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October 24-26, 2023

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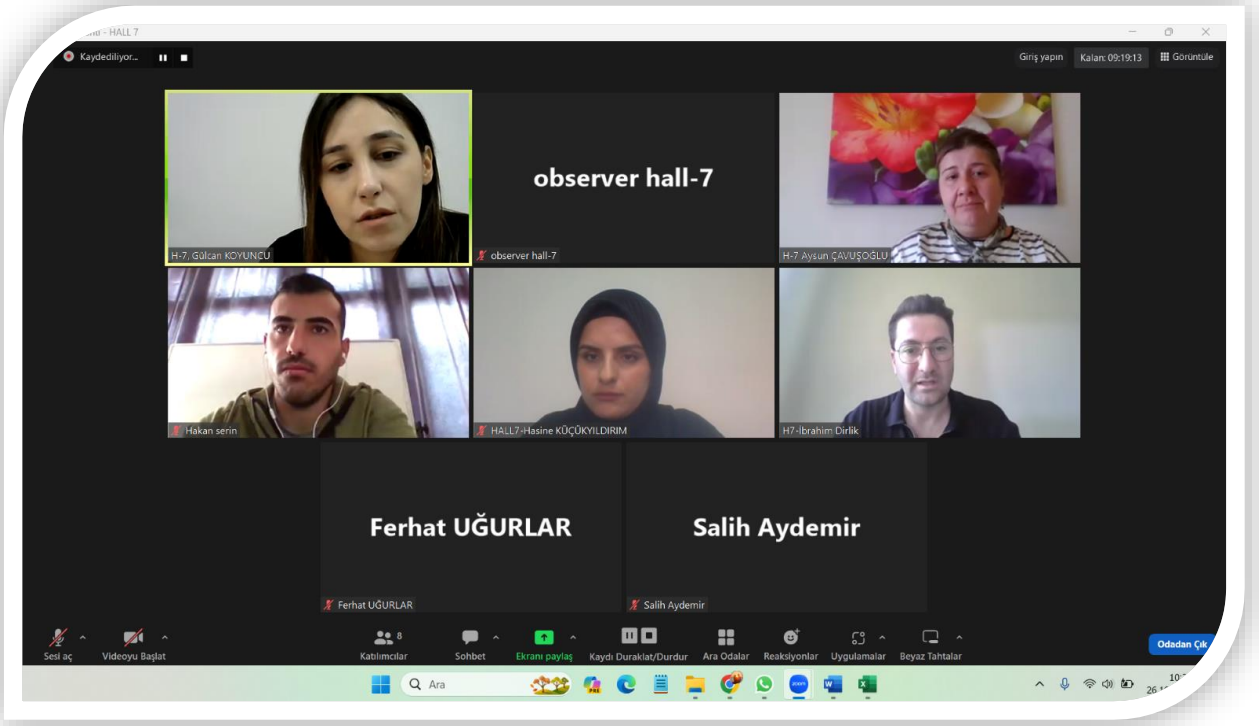

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25.10.2023 / HALL-1 / SESSION-1

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09 00 : 11 00	10 00 : 12 00

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PARIS LOCAL TIME	ANKARA LOCAL TIME
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HEAD OF SESSION: Prof. Dr. Ayse Gul INCE

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Assoc. Prof. Dr. Pınar KOÇ	Amasya University TÜRKİYE	ANALYSIS OF COINTEGRATION RELATIONSHIP BETWEEN AGRICULTURAL INCOME AND EMPLOYMENT VIA THE FOURIER FUNCTION
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Prof. Dr. Mehmet KARACA **Prof. Dr. Ayse Gul INCE**	Akdeniz University TÜRKİYE	CELLULOSE SYNTHASES SPECIFIC MICROSATELLITE PRIMERS IN GOSSYPIUM HIRSUTUM L.
Prof. Dr. Mehmet KARACA **Prof. Dr. Ayse Gul INCE**	Akdeniz University TÜRKİYE	GRAFTING INDUCED DIFFERENTLY METHYLATED CYTOSINES IN LONG NON-CODING RNAS OF COTTON

ONLINE PRESENTATIONS

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PARIS LOCAL TIME	ANKARA LOCAL TIME
09 ^{00} : 11 ^{00}	10 ^{00} : 12 ^{00}

HEAD OF SESSION: Assist. Prof. Dr. Gülcan KOYUNCU

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Agr. Eng. İbrahim DİRLİK **Prof. Dr. Cengiz KAYA** **Res. Assist. Ferhat UĞURLAR**	Harran University TÜRKİYE	GREENHOUSE ENVIRONMENT MONITORING AND SMART IRRAGATION SYSTEM FOR MORE EFFICIENT PRODUCTION
Hakan SERİN **Assist. Prof. Muslu Kazım KÖREZ**	Selçuk University TÜRKİYE	BIBLIOMETRIC ANALYSIS OF STUDIES ON BABESIOSIS DISEASE IN VETERINARY MEDICINE
Hasine KÜÇÜKYILDIRIM **Prof. Dr. Salih AYDEMİR**	Harran University TÜRKİYE	SLOW RELEASE MECHANISM OF COATED FERTILIZERS AND AFFECTING FACTORS
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ONLINE PRESENTATIONS

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Dr. Bogdan-Catalin SERBAN Dr. Octavian BUIU Dr. Marius BUMBAC Dr. Cristina Mihaela NİCOLESCU	National Institute for Research and Development in Microtechnologies–IMT Bucharest ROMANIA Valahia University of Targoviste ROMANIA	NOVEL GRAVIMETRIC ETHANOL SENSOR
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ONLINE PRESENTATIONS

26.10.2023 / HALL-6 / SESSION-2

PARIS LOCAL TIME	ANKARA LOCAL TIME
11 30 : 13 30	12 30 : 14 30

HEAD OF SESSION: Dr. Malihe JAHANI

Authors	Affiliation	Presentation title
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Andrey Popatanasov	Bulgarian Academy of Sciences BULGARIA	EFFECTS OF HORMOPRIMING WITH CYTOKININS ON THE GERMINATION OF CAPSICUM ANNUUM CV. KURTOVSKA KAPIJA
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Dr. EL AMMARI Mohamed **Prof. Brhadda Najiba** **Dr. EL BAHJA Fatima** **Dr. ELWAHAB Fathalah** **Dr. BOUKITA Hassan** **Dr. FAHAD Kaoutar** **Prof. BOUZAKRAOUI SAID** **Prof. ZIRI Rabea**	Ibn Tofail University MOROCCO Regional Center of Agricultural Research of Kenitra MOROCCO Ibn Tofail University MOROCCO	USE OF PLANT ESSENTIAL OILS AS BIOINSECTICIDES IN AGRICULTURE IN NORTH AFRICA ADVANCES AND PERSPECTIVES
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Delbrin Ahmed	University of Duhok IRAQ	THE NUMBER OF SUBUNIVERSES, CONGRUENCES, WEAK CONGRUENCES OF SEMILATTICES DEFINED BY TREES
Toudamrini Hanane **Algouti Abdellah** **Algouti Ahmed** **Benkaroum Hajar** **Agli Saloua** **Aboulfaraj Abdelfattah** **Nassiri Oumayma**	University of Cadi Ayyad MOROCCO	IMPACT STUDY OF LOCALIZED IRRIGATION ON SOIL SALINIZATION IN THE REGIONS OF AL HAOUZ AND KELAA DES SRAGHNA
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EFFECTS OF HORMOPRIMING WITH CYTOKININS ON THE GERMINATION OF CAPSICUM ANNUUM CV. KURTOVSKA KAPIJA

Andrey Popatanasov

Bulgarian Academy of Sciences, Sofia, Bulgaria

ABSTRACT

According to some authors Bulgaria is considered as one of the secondary centers of origin for the important crop species Capsicum annuum L. due to the favorable climate, widespread acceptance and centuries of cultivation and breeding efforts. One of the results of these efforts is the cv. Kurtovska kapija – one of the most widespread varieties in cultivation in the region. Its remarkable balance of high yield while maintaining and improving the nutritive values and deliciousness of the fruits earned the praise and affection of the highly demanding local consumers and growers of this crop. As a result locally it is grown under variety of environmental conditions and scenarios, sometimes not very favorable for the plant. In other crops it is known that pre-sowing treatments with some plant growth regulators can have beneficiary effects on the plant development under normal and stressful conditions. Therefore in this study was placed as aim to explore the effects of some plant growth regulators with cytokinin action, on the early stages of the ontogenesis of some important for the growers and farmers parameters, since the early stages of the plant development are one of most crucial ones for the long term survival, growth and yield for the crop.

The results revealed that there is significant improvement of the germination start compared with the non-treated controls with all tested plant growth regulators. However, the results from the other parameters may have different trends depending on the application scenario of the used plant growth regulators.

Key words: Capsicum annuum, cv. Kurtovska kapija, cytokinin, hormopriming, hormone

INTRODUCTION

According to some authors Bulgaria is considered along with Guatemala as one of the secondary centers of origin for the important crop species Capsicum annuum L. which originated from Mexico, Central America (Bosland 1996; Malik et al. 2011). Partly this is due

to the favorable climate, widespread acceptance as crop and incorporation in the local cuisine by the Bulgarian consumers and farmers and centuries of breeding efforts and development of astonishing cultivation technology, which brought fame and respect to the Bulgarian gardeners and researchers throughout Europe (Tütünkov-Hrisztov, 2019). Nowadays the pepper is the second most grown and consumed vegetable in Bulgaria (Angelova, et al., 2016). Among of the results of these breeding efforts is the cv. Kurtovska kapija – one of the most widespread varieties in cultivation in Bulgaria and the neighbor regions (Bogevska, et al., 2017; Георгиева, 2013). Its remarkable balance of high yield while maintaining and improving the nutritive values and deliciousness of the fruits earned the praise and affection of the highly demanding local consumers and growers of this crop (Георгиева, 2013; Todorova, & Pevicharova, 2021). In fact the cv. Kurtovska kapija is so delicious that it was officially recorded in the "Treasury of Tastes" of the renown international organization for authentic foods "Slow Food" and it has prominent place in the Bulgarian annual Pepper and Tomato Festival where every visitor can get nearly ecstatic experiences with the publicly made pepper and tomato culinary masterpieces (Hristova, 2022; Peneva, & Kazakova-Mateva, 2015). As result of such appreciation locally it is grown under variety of environmental conditions and scenarios, sometimes not very favorable for the plant.

In other crops as wheat, lettuce, etc. it is known that pre-sowing treatments with some plant growth regulators can have beneficiary effects on the plant development under normal and stressful conditions (Iqbal, et al., 2006; Hudecek et al., 2023).

Cytokinins are class of plant hormones which are involved in diverse processes related to the growth and development of plants such as root formation, cell division, chloroplast development, apical dominance, seed development, leaf senescence, stomatal behavior, antioxidant system etc. (Iqbal, et al., 2006; Hudecek et al., 2023). The various cytokinins from other side can differ by the strength of their action or even trigger different effects depending on the organism, stage of ontogenesis, physiological state etc. (Iqbal, and Ashraf, 2005; Hudecek et al., 2023). For example benzylaminopurine (BAP) is more active than kinetin and other cytokinins during germination, and also in breaking the dormancy of celery and lettuce seeds (Iqbal, and Ashraf, 2005).

Therefore in this study was placed as aim to explore the effects of some plant growth regulators with cytokinin action, on the early stages of the ontogenesis of some important for the growers and farmers parameters, since the early stages of the plant development are one of most crucial ones for the long term survival, growth and yield for the crop.

MATERIALS AND METHODS

For the present study were used seeds of the sweet pepper cv. Kurtovska kapija (Genchev ET) and for the pre-sowing treatment (hormopriming) were used one of the following cytokinins: the naturally occurring kinetin, benzylaminopurine and the synthetic thiadiazuron at concentrations 1mg/L. For each group were prepared 50 seeds with 3 replicates placed in between two layers of filter paper and moistened with water in plastic containers and the seeds were incubated at room temperature. Germination and development were observed on daily basis until the end of the trial. The germination parameters were calculated as relative to the controls which served as baseline.

RESULTS AND DISCUSSION

The results revealed that there is significant improvement of the germination start compared with the non-treated controls with all tested plant growth regulators. Hydropriming and kinetin treatment are comparable starting earlier than the controls (fig. 1), even earlier to them were the groups with the other two cytokinins – BAP and thiadiazuron.

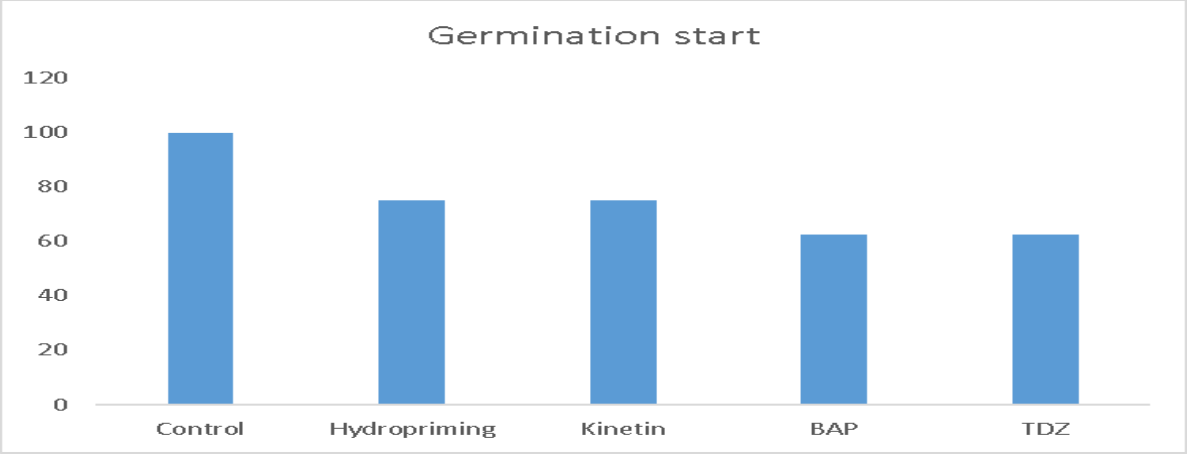

Figure 1. Germination start in relative values taking the control as baseline.

As for the germination percentage all primed groups showed improvements compared to the controls. However the cytokinin treated groups had lower values of the germination percentage than the hydroprimed seeds. With kinetin being best, followed by BAP and thiadiazuron.

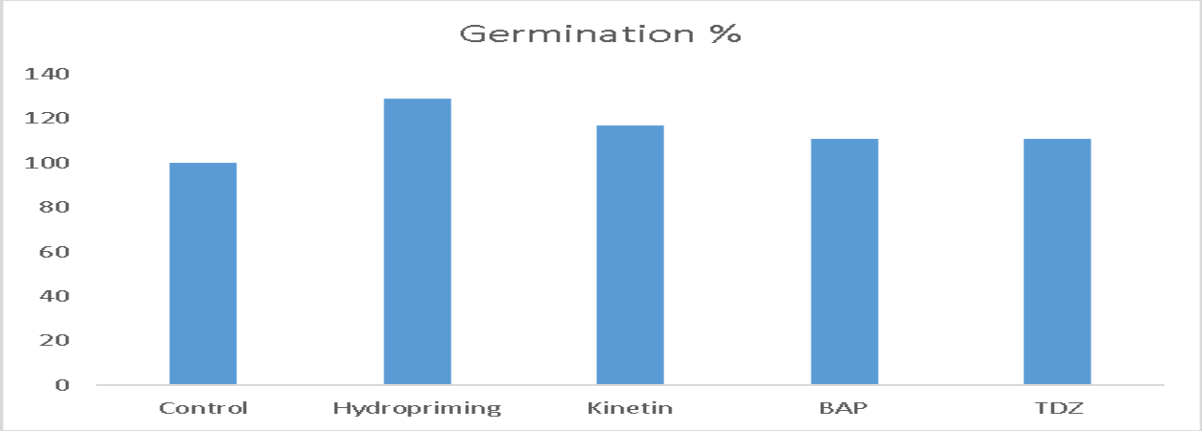

Figure 2. Germination percentahe in relative values taking the control as baseline.

The parameter seedling size had less stellar results. While in all primed groups the seedling size was increased, for the hormoprimed groups the values decreased, with BAP and thiadiazuron scoring lowest and rather close to the controls.

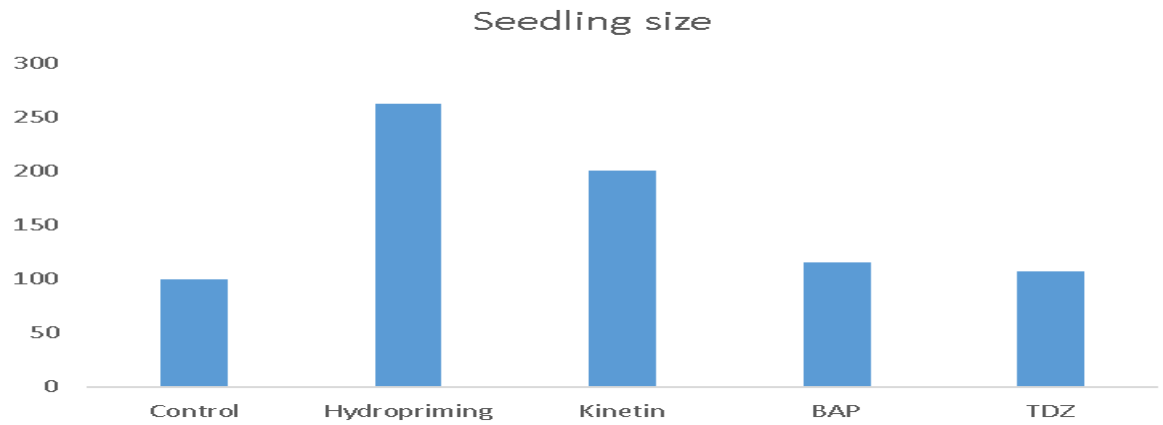

Figure 3. Seedling size in relative values taking the control as baseline.

However, the results from the other parameters may have different trends depending on the application scenario of the used plant growth regulators.

At the used dose in general the applied cytokinins had various degree of inhibitory effect on the seedling growth and development. Such findings are with partial concordance with the study of Barbosa, er al. comparing from various priming techniques where excessive dose of 0.2% of kinetin was used (which is several times higher than the dose used in the present study). In that study the applied kinetin dose greatly inhibited all germination parameters and produced predominant percentage of abnormal seedlings (Barbosa, er al., 2016). In the current study

although it was utilized much lower dose cytokinins, it seems that it is still in the inhibitory zone of action, although with less pronounced effects. Probably another contributing factors for such results are the thickness and the properties of the tissues and mater surrounding the pepper embryo.

CONCLUSIONS

With the used dose of cytokinins the hormopriming had partly stimulatory effect and partly inhibitory effect according to various parameters and descriptors of the germination and early growth stages. The results also varied for the different agents with cytokinin action which probably is related to the different binding affinity to the cytokinin receptors. Further research is needed to determine optimal scenario of hormopriming with cytokinins of this remarkable and important for the Bulgarians pepper cultivar.

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GREENHOUSE ENVIRONMENT MONITORING AND SMART IRRAGATION SYSTEM FOR MORE EFFICIENT PRODUCTION

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ABSTRACT

Technologies that increase productivity, profitability and quality in agriculture are becoming increasingly widespread, making the work of producers easier. Automation systems in agriculture entail the execution of production processes without human effort. The primary objective of this study is to elucidate how a producer can automate greenhouse management and plant irrigation by employing certain electronic components in their facilities. This system, in addition to saving time for producers, represents a crucial design for the efficient utilization of water resources and its transfer to future generations. The system utilizes sensor technology, comprised of a microcontroller, relay, DC motor, essential sensors, and a battery. This system includes four adapted sensors: soil moisture, humidity, temperature and light sensors, each of which measures environmental changes within the greenhouse and intervenes independently. Data obtained from soil moisture sensors capable of real-time measurement are processed by the microcontroller and irrigation is started when there is insufficient water in the soil and stopped when it reaches the optimum level. These critical levels were determined through calibration of the soil moisture sensor according to the soil conditions utilized in the design. This design facilitates the remote monitoring and control of data through a developed mobile application. It seems promising in terms of reducing yield losses that may occur due to insufficient or excessive irrigation, saving time and energy, and using limited water resources effectively.

Keywords: Smart Irrigation, Sensor-based Systems, Agriculture, Arduino, Soil Moisture sensor

A REVIEW OF THE ROLE OF ZINC IN PLANTS

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ABSTRACT

Zinc (Zn) is an important micronutrient for plants. This element plays an essential role in many enzyme reactions, metabolic processes and oxidation-reduction reactions, for this reason it is considered as one of the important and necessary elements in the process of growth and development in plants. In addition, zinc plays an essential role in the structure of many enzymes involved in the processes of nitrogen metabolism, energy transfer and protein synthesis. Zinc deficiency in plants affects and delays the growth and development processes and causes a sharp decrease in yield. Zinc plays a very important role in plant metabolism by affecting the activity of hydrogenase and carbonic anhydrase enzymes, stabilization of ribosomal structure and cytochrome synthesis. Plant enzymes that are activated by zinc are mainly involved in the metabolism of sugars, maintaining the integrity of cell membrane structure, protein synthesis, regulation of auxin hormone synthesis, and pollen formation. In plants, the regulation of the expression of genes that play an important role in bearing environmental stress depends on the presence of this element. The absence or deficiency of zinc in plants leads to the occurrence of abnormalities in plants, that external symptoms can be seen in the form of symptoms such as severe reduction in plant growth, leaf chlorosis and shrinking of leaves, as well as plant sterility. The deficiency of zinc can also affect the quality of the products collected from the farm and garden, as the plant becomes weak and simply by exposure to intense light or increase of the temperature will be damaged. Some researches show that this element affects the ability of plants to absorb and transport water and also partially reduces the harmful effects of short-term salinity and heat stress. Zinc is a very key factor in the synthesis of the amino acid tryptophan, which is one of the precursors of indole acetic acid (IAA). Moreover, this element helps to maintain the structural position of macromolecules inside the membrane as well as ion transport systems. The interaction of this element with phospholipids and sulfhydryl groups of membrane proteins helps to maintain the integrity of the membrane. Zinc plays a vital role in the development and functioning of flowering organs such as anthers, pollen sacs, pollen grains and pistils.

Keywords: Zinc, Micronutrient, Plant Growth, Cell Membrane Integrity, Flowering Organs Development, Auxin Synthesis

BIOLOGICAL METHODS FOR POST-HARVEST CONTROL OF R. STOLONIFER ROT IN PEACHES AND NECTARINES

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Abstract

"Combatting stolon rot (R. stolonifer) in peaches and nectarines after harvest is crucial for preserving fruit quality. This study examines various biological methods aimed at minimizing post-harvest losses. We explore the use of biopesticides based on antagonistic microorganisms, such as Trichoderma spp. and Bacillus spp., which have demonstrated their effectiveness in reducing the growth of R. stolonifer on stored fruits. Additionally, enhancing storage microbiology by introducing beneficial microorganisms has been studied to enhance the resistance of peaches and nectarines to stolon rot. Furthermore, approaches involving natural predators to control disease vectors after harvest have been examined. Lastly, sustainable agronomic practices, such as crop rotation and integrated pest management in warehouses, have been evaluated to reduce disease pressure. This research highlights the increasing importance of biological methods in preserving the quality of peaches and nectarines after harvest, providing environmentally friendly solutions for the fruit preservation industry."

Keywords: R. Stolonifer, Peaches, Nectarines, Biological Control, Post-Harvest

FERTILITY, HATCHABILITY, MORTALITY AND GROWTH PERFORMANCE OF INDIGENOUS, SASSO AND THEIR F1 CROSS CHICKEN GENOTYPES IN ETHIOPIA

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ABSTRACT

Three chicken genotypes were involved in the study with the objectives of evaluating fertility, hatchability, and growth performance of three chicken genotypes. For the experiment, 1550 (600 of indigenous, 450 of Sasso, 500 of crossed) eggs were labeled and incubated. The data were analyzed using SAS. Relatively higher proportion of fertility was observed for the eggs collected from Sasso (89.6%) followed by crossed eggs (72.8%). Correspondingly, hatchability was higher for Sasso. Body weight was increased from 27.9 to 321.7g for indigenous, 36.8 to 431.2g for Sasso, and 32.4 to 353.4g for crossbred from week0 to week7. Agroecology, genotypes, and sex had significant effect ($p<0.05$) on growth performance of the chickens for almost all ages of their experiment period across different agro-ecologies. Agroecology by genotype had a significant ($p<0.05$) influence on the growth performance of the chickens during week11 and week15. The interaction between agroecology and sex was significantly influenced growth rate of the chickens in all weeks of their age, except the chickens at their 11^{th} weeks of age. Genotype by sex interaction had highly significant effect in the growth performance of the chickens at their 11^{th}, 15^{th} and 20^{th} weeks' age. The chickens' growth has

been influenced by the interaction among agroecology, genotype, and sex. Higher proportion of indigenous (22%) and Sasso (24%) birds were died in highland in between W7-13, however higher proportion of crossbred birds were lost in lowland for same week interval. Considering the most parameters of chickens, midland agroecology is more promising for their production. This is because, better feed resources, climatic condition, and awareness of farmers how to manage their birds.

Key words: Agroecology, Fertility, Hatchability, Growth performance, Mortality

SYNTHESIS OF TURMERIC EXTRACT INCORPORATED GELATIN BASED PACKAGING FILM WITH SPECIAL REFERENCE TO ITS ANTIOXIDANT POTENTIAL

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Abstract

Packaging plays a pivotal role in order to extend the shelf life of food commodities. The aim of current research was to synthesize the gelatin based packaging film with the incorporation of turmeric extract. Ultrasonic assisted extraction of turmeric was carried out by using ethanol as a solvent and obtained extract was subjected TPC, DPPH, FRAP and $ABTS^{+}$ determination. For the purpose, the gelatin based film were produced by casting technique, and characterized through the application of FTIR, XRD and SEM for their structural elucidation. Moreover, the physical parameters including film solubility, tensile strength, thickness, elongation at break and water permeability were performed. The results showed that turmeric extract contain the total phenolic content 2.77±0.01 GAE mg/g, and their activity showed that DPPH 32.44±0.2, FRAP 42.96±0.05, $ABTS^{+}$ 714.48±0.27 GAE mg/g. Furthermore, FTIR spectra of films

showed the stretchings of various peaks which showed the presence of different functional groups including amide I peak of control film, which was shifted in film containing 1% and 2% extract respectively. XRD showed that characteristic peak of triple helical structure of gelatin shifted from $2\theta \approx 10°$ to $2\theta \approx 13°$ in film T_2 and T_3. SEM micrographs showed that increased turmeric extract concentration led to homogeneous films. The physical tests of the film showed that film solubility, tensile strength, elongation at break, and water permeability decreased with increasing concentration of turmeric, while the thickness of the film increased with increasing turmeric concentration. In conclusion, it was assessed that turmeric extract incorporated in gelatin-based biofilm significantly enhanced its structural as well as physical properties, which could be suitable for the fabrication of biodegradable biofilm for the sustainable packaging.

Keywords: Food packaging, Gelatin film, Turmeric extract, antioxidant activity,

THE NUMBER OF SUBUNIVERSES, CONGRUENCES, WEAK CONGRUENCES OF SEMILATTICES DEFINED BY TREES

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Abstract

We determine the number of subuniverses of semilattices defined by arbitrary and special kinds of trees via combinatorial considerations. Using a result of Freese and Nation, we give a formula for the number of congruences of semilattices defined by arbitrary and special kinds of trees. Using both results, we prove a formula for the number of weak congruences of semilattices defined by a binary tree; we discuss some special cases. We solve two apparently nontrivial recurrences applying the method of Aho and Sloane.

HOLEY CARBON NANOHORNS – BASED MATRIX NANOCOMPOSITE FOR RELATIVE HUMIDITY RESISTIVE SENSOR

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ABSTRACT

Humidity is one of the most frequently monitored physical parameters and is of a significant importance in multiple areas of domestic and industrial activities: indoor air quality control, pharmaceutical industry, textile and paper industry, electronics, the automotive industry, meteorology, chemical engineering, etc. Thus, manufacturing of high-performance humidity sensors has become prioritary in the last decades. Measuring and controlling humidity and temperature are critical aspects of crops management. Along with semiconductor metal oxides (SnO_2, ZnO, etc.), ceramic materials (Al_2O_3), polymers, (poly (3,4-ethylene dioxythiophene), poly (3,4-ethylene dioxythiophene – polystyrene sulfonate)), perovskites ($BaTiO_3$), electrolytes (LiCl), nanocarbon materials are intensively used as sensing elements in the design of humidity sensors.

In this study, a resistive humidity sensor for moisture detection at room temperature is presented. The thin film proposed as a critical sensing element is a binary nanocomposite based on oxidated carbon nanohorns (CNHox) – agarose at the w/w ratio of 9/1. The synthesis of oxidated carbon nanohorns is carried out by two different methods, using the treatment in water plasma, respectively the treatment in oxygen plasma. Both of these plasma-treatments ensure the hydrophilization of carbon nanohorns by grafting carboxyl, carbonyl, hydroxyl, and epoxy groups. In addition, the optimal degree of hydrophilization of the carbon nanohorns, to minimize the hysteresis and achieve an appropriate sensitivity, can be controlled by changing the plasma power as well as the exposure time.

The RH sensor includes a Lexan substrate, interdigitated electrodes, and a sensing layer obtained via drop-casting procedure. The electrodes were connected by successive deposition of Cr (10 nm) and Au (100 nm). The width of the electrodes is about 200 microns, with a separation of 6 mm between them. They can be linear or have an interdigitated configuration. The morphology and the composition of the sensing layers were investigated through scanning electron microscopy (SEM), X-ray diffraction (XRD), and Raman spectroscopy. The RH monitoring capability of the sensing layers was investigated by applying a current between the two electrodes, and measuring the resulted voltage while exposing the assemby at different RH levels. Resistance of the thin film increased when the sensors were exposed to atmosphere with the relative humidity in the range of 0 to 100%.

The use of oxidized carbon nanohorns / agarose nanohybrid, deposited as a sensitive layer by the drop-casting method on a dielectric substrate, has significant advantages, such as:

- improving the mechanical properties and processability of the sensitive layer;
- the presence of oxidized carbon nanohorns confers a high specific surface/volume ratio as well as a notable affinity for water molecules;
- agarose is a hydrophilic polymer and improves the dispersion of oxidized carbon nanohorns through hydrogen bonding;
- the manufactured devices show a room temperature response comparable to that of a commercial capacitive humidity sensor; also it is characterized by an excellent linearity, rapid response and recovery times, as well as a good sensitivity.

Keywords: holey carbon nanohorns, resistive sensors, relative humidity, agarose, nanocomposite

NOVEL NANOHYBRID AS SENSING LAYER FOR RESISTIVE RELATIVE HUMIDITY MONITORING

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ABSTRACT

Relative humidity sensors have received increasing attention in the last years due to their importance in a large variety of residential, industrial, and commercial applications such as building heating, air conditioning and ventilating (HVAC systems), handheld devices, medical field (medical air line, incubators, sterilizers), food/beverage processing, chemical industry (dehumidifiers, smelting furnaces, dryers), pharmaceutical processing, electronics (semiconductor fabrication plants, clean room controls) agriculture (drip irrigation), weather station and so forth.

In this study, a resistive humidity sensor for moisture detection at room temperature is presented. The thin film proposed as a critical sensing element is based on binary nanohybrid based on oxidated carbon nanohorns (CNHox) – indium oxide (In_2O_3) at the w/w ratios of 1/1.

The RH sensor includes a silicon (470 microns) substrate coated with SiO_2 (1 micron), interdigitated electrodes, and a sensing layer obtained via drop casting. The electrodes were connected by the successive deposition of Cr (10 nm) and Au (100 nm). The width of the electrodes is about 200 microns, separated by a 6 mm gap, and they can be linear or have an interdigitated configuration. The morphology and the composition of the sensing layers were investigated through Scanning Electron Microscopy (SEM), X-ray diffraction (XRD), and RAMAN spectroscopy. The RH monitoring capability of the sensing layers was investigated by applying a current between the two electrodes and measuring the voltage, while exposing the device at different values of relative humidity. The nanohybrid-based thin film's resistance increased when the sensors were exposed to relative humidity ranging from 0 to 100 %.

The use of oxidized carbon nanohorns / In_2O_3 nanohybrid, deposited as a sensitive layer by the sol-gel method on a dielectric substrate, has significant advantages:

- improves the mechanical properties and processability of the sensitive layer;
- the presence of oxidized carbon nanohorns gives a high specific surface/volume ratio;
- the presence of In^{3+} ions confers the sensor's increased sensitivity; according to the HSAB (Hard Soft, Acids and Bases) theory, water is classified as a hard base, while In^{3+} cations are hard acids, so a "hard acid - hard base" interaction between water molecules and the sensitive layer is very likely to act in obtaining the superior sensing properties;
- detection over a wide temperature range;
- the hydrophilic character of oxidized carbon nanotubes (and therefore the affinity for water molecules) can be modulated by changing some parameters such as plasma power, exposure time, nitric acid solution concentration, reflux duration , etc.).
- the quick response of the sensor to variations in the relative humidity value.

Keywords: HSAB theory, resistive sensors, relative humidity, oxidized carbon nanohorns, indium oxide

NOVEL GRAVIMETRIC ETHANOL SENSOR

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ABSTRACT

The monitoring of ethanol concentration is an important process in various fields of industrial activity such as: the wine industry (for example, monitoring fermentation processes), the biofuel industry, the management and safety of car traffic (sensors for measuring alcohol, portable or even included in the dashboard of cars), the pulp industry, the medical field (for example, breathing monitoring).

Last but not least, thanks to the antifungal and antimicrobial properties, ethanol is used in the food packaging. Moreover, ethanol, along with carbon dioxide, is the main spoilage metabolite of freshly cut fruit.

In this study, a room temperature surface acoustic wave (SAW) ethanol sensor is presented. The device includes a piezoelectric substrate, a pair of interdigital transducers, as well as a sensing layer for ethanol gas detection. The electrical signal, applied to one of the transducers, generates a surface acoustic wave that propagates to the other transducer, the mechanical wave being converted into an electrical signal.

The manufactured sensor uses as sensing layer a matrix nanocomposite based on oxidated carbon nano-onions (CNOox) -graphene oxide (GO).

The sensor used is of the "delay line" type, dual, made on a quartz piezoelectric substrate. The sensor features a dual delay line to compensate the thermal drift. Thus, one delay line is covered with the binary nanocomposite matrix sensitive to the variation of ethanol concentration, the second delay line being the piezoelectric substrate without sensitive layer. To obtain a signal due exclusively to the chemical interaction of ethanol molecules with the binary nanocomposite matrix, the signal associated with the delay line without the sensitive layer can be subtracted from the signal of the delay line covered with the sensitive layer. The sensing layers are deposited on a piezoelectric quartz substrate by the "drop casting" or spin coating method.

The use of binary matrix nanocomposite of the CNOox - GO type confers several notable advantages:

• the presence of CNOox confers a high specific surface / volume ratio, affinity for ethanol molecules ("mass loading"), as well as a variation of the resistance of the sensitive layer upon contact with them ("electric loading");

• the presence of GO confers a high specific surface / volume ratio, affinity for ethanol molecules ("mass loading"), being a dispersing medium for oxidized onion-type nanocarbon materials.

• the fast response of the sensor to variations in the ethanol concentration value;

• reversibility;

•detection at room temperature;

• superior mechanical properties.

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Keywords: oxidated carbon nano- onions, graphene oxide, surface acoustic wave (SAW) sensor, ethanol

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OXIDATED CARBON NANO- ONIONS BASED TERNARY NANOHYBRID AS SENSING ELEMENT FOR RESISTIVE HUMIDITY SENSOR

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ABSTRACT

Relative humidity monitoring is an essential process in various areas of domestic and industrial activities such as indoor air quality control, pharmaceutical industry, textile and paper industry, electronics, the automotive industry, meteorology, the pharmaceutical industry (storage, synthesis and quality control of medicinal products), agriculture (moisture measurement technique in agricultural silos, soil moisture control) and so forth. Along with polymers (polyvinylpirrolidone), semiconductor metal oxides (TiO_2, CuO, etc.), ceramic materials ($MgAl_2O_4$) perovskites ($BaHfO_3$), polyelectrolytes (quaternary ammonium salts, sulfonate salts, and phosphonium salts), nanocarbonic materials are intensively used as key sensing elements in the design of humidity sensors.

In this study, a resistive humidity sensor for moisture detection at room temperature is presented. The thin film proposed as a critical sensing element is a ternary nanohybrid based on oxidated carbon nano-onions (ox-CNOs)/NaCl/polyvinyl alcohol (PVA).

The RH sensor includes a Kapton substrate, interdigitated electrodes, and a sensing layer obtained via drop casting method. The electrodes were connected by successive deposition of Cr (10 nm) and Au (100 nm). The width of the electrodes is about 200 microns, with a separation of 6 mm between them. They can be linear or have an interdigitated configuration. The morphology and composition of the sensing layers- based ternary nanohybrid were investigated through scanning electron microscopy (SEM), atomic force microscopy and Raman spectroscopy. The RH monitoring capability of the sensing layers was investigated by applying a current between the two electrodes, and measuring the resulted voltage while exposing the assemby at different RH levels. Resistance of the thin film increased when the sensors were exposed to atmosphere with the relative humidity in the range of 0 to 100%.From the point of view of the detection principle, the resistance of the conductive layer varies with the level of relative humidity.

The use of ox-CNOs/NaCl/PVA ternary nanohybrid deposited as a sensitive layer by the drop-casting method on a dielectric substrate, has significant advantages, such as:

• Ox-CNOs confer a high specific surface / volume ratio, affinity for water molecules, as well as a variation in the resistance of the sensitive layer upon contact with them throughout the relative humidity (RH) range;

• detection at room temperature;

•polyvinyl alcohol is a hydrophilic polymer that exhibits low hysteresis.

•the presence of Na+ cations confer the ternary nanohybrid an increased sensitivity, by increasing the number of active sites available for an interaction with water molecules. According to the HSAB (Hard Soft, Acids and Bases) theory, Na^+ cations are hard acids, while water is classified as a hard base, so a hard acid-hard base interaction is to be expected between water molecules and the moisture-sensitive layer.

IMT authors would like to acknowledge the financial support provided by the Romanian Ministry of Education and Research via the “MICRO-NANO-SIS PLUS” Nucleu program, grant number PN 19 16, and the UEFISCDI contract PED no. 673/2022.

Keywords: oxidated carbon nano- onions, resistive sensors, relative humidity, polyvinyl alcohol

OXIDATED CARBON NANO- ONIONS BASED MATRIX NANOCOMPOSITE FOR NOVEL RESISTIVE HUMIDITY SENSOR

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ABSTRACT

Moisture monitoring is an essential process in different areas such as agriculture and forestry, hydrology, and civil engineering. Soil moisture measurement is a key tool for activities in agriculture. The moisture content of grains has a huge impact on the market value of the crops. Soil moisture detection has been used for monitoring and evaluating construction sites, mining operations, forest areas, landscape sites, etc.

In this study, a resistive humidity sensor for moisture detection at room temperature is presented. The thin film proposed as a critical sensing element is a matrix nanocomposite based on oxidated carbon nano-onions (ox-CNOs)/tannic acid.

The sensor substrate is made of silicon (470 microns) coated with SiO_2 (1 micron). The electrodes were connected by successive deposition of Cr (10 nm) and Au (100 nm). The width of the electrodes is about 200 microns, with a separation of 6 mm between them. They can be linear or have an interdigitated configuration. The morphology and composition of the sensing layers- based ternary nanohybrid were investigated through scanning electron microscopy (SEM), atomic force microscopy and Raman spectroscopy The relative humidity sensing capability is investigated by applying a constant current between the two electrodes and measuring the voltage at different values of the relative humidity level to which the sensitive layer was exposed. %.. From the point of view of the detection principle, the resistance of the conductive layer varies with the level of relative humidity. Resistance of the thin film increased when the sensors were exposed to atmosphere with the relative humidity in the range of 0 to 100.

The use of ox-CNOs/tannic acid matrix nanocomposite deposited as a sensitive layer by the drop-casting method on a dielectric substrate, has significant advantages, such as:

• the rapid change in the resistance of the sensitive layer to variations in the relative humidity value;

• improving the mechanical properties and processability of the sensitive layer;

• oxidated carbon nano-onions confer a high specific surface / volume ratio;

• detection over a wide temperature range;

• the hydrophilic character of tannic acid and oxidated carbon nano-onions;

• tannic acid can form hydrogen bonds both with the hydrophilized substrate (Si/SiO_2) and with the oxidized carbon nanohorns.

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Keywords: oxidated carbon nano- onions, resistive sensors, relative humidity, tannic acid

MATRIX NANOCOMPOSITE FOR NOVEL RESISTIVE HUMIDITY SENSOR

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ABSTRACT

RH sensors have received increasing attention in the last years due to their importance in agriculture. For instance, soil moisture is vital in monitoring farming activities, managing water supply, etc.

In this study, at room temperature relative humidity resistive sensor is presented. The thin film proposed as a critical sensing element is a ternary matrix nanocomposite based on oxidated carbon nano-onions (ox-CNOs)/oxidated carbon nanohorns (CNHox)/ sodium lignosulfonate.

The dielectric substrate is made of Kapton and can have a thickness between 50 microns and 5 millimeters. Electrodes can be deposited on the surface of the dielectric substrate by direct

printing, sputtering or evaporation. The electrodes can be made of the same material (chrome, gold) or of different materials. They can be linear or have an interdigitated configuration. The relative humidity sensing capability is investigated by applying a constant current between the two electrodes and measuring the voltage at different values of the relative humidity level to which the sensitive layer was exposed. The morphology and composition of the sensing layers-based ternary nanohybrid were investigated through scanning electron microscopy (SEM), atomic force microscopy and FTIR spectroscopy. The RH monitoring capability of the sensing layers was investigated by applying a current between the two electrodes, and measuring the resulted voltage while exposing the sensor at different RH levels. Resistance of the thin film increased when the sensors were exposed to atmosphere with the relative humidity in the range of 0 to 100%. From the point of view of the detection principle, the resistance of the conductive layer varies with the level of relative humidity.

The use of the ternary nanocomposites described above, deposited as sensitive layers by the "drop casting" method on a Kapton substrate, presents several significant advantages:

• the rapid change in the resistance of the sensitive layer to variations in the relative humidity value;

• improving the mechanical properties and processability of the sensitive layer;

• the presence of nanocarbon materials gives a high specific surface / volume ratio;

• detection over a wide temperature range;

• the hydrophilic nature of oxidized carbon nanohorns, as well as of onion-type oxidized nanocarbon materials;

• the dispersing character of sodium lignosulfonate that facilitates obtaining a sensitive layer with a uniform distribution of the nanocarbon material;

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Keywords: oxidated carbon nano- onions, oxidated carbon nanohorns resistive sensors, relative humidity, sodium lignosulfonate

NOVEL RESISTIVE ETHANOL SENSOR

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ABSTRACT

Moisture monitoring is an essential process in different areas such as agriculture and forestry, hydrology, and civil engineeringIn the last years, humidity sensors have been played a pivotal role for controlling the food degradability

The sensitive layers described in this invention, which can be used to obtain resistive relative humidity sensors, are oxifluorinated carbon nanohorns (generically labeled ox-CNHs-F), oxifluorinated carbon nano-onions (generically labeled ox-CNOs -F), as well as binary nanocomposite based on ox-CNHs-F/ox-CNOs-F type at 1;1 w/w ratio.

The synthesis of ox-CNHs-F and ox-CNOs-F is achieved by the treatment of single carbon nanotubes as well as onion-type carbon materials in F2-N2 and Ar-O2 plasma.

The functionalization of nanocarbon materials in F2-N2/ and Ar-O2 plasma has the advantage (by varying the type of plasma, the exposure time, as well as its power) that it can ensure an optimal C:F:O atomic ratio, synchronously conferring a appropriate sensitivity as well as a reduction in hysteresis.

The sensor substrate is made of silicon (470 microns) coated with SiO_2 (1 micron). The electrodes were connected by successive deposition of Cr (10 nm) and Au (100 nm). The width of the electrodes is about 200 microns, with a separation of 6 mm between them. They can be linear or have an interdigitated configuration. The morphology and composition of the sensing layers- based ternary nanohybrid were investigated through scanning electron microscopy (SEM), atomic force microscopy and Raman spectroscopy The relative humidity sensing capability is investigated by applying a constant current between the two electrodes and measuring the voltage at different values of the relative humidity level to which the sensitive layer was exposed. %.. From the point of view of the detection principle, the resistance of the conductive layer varies with the level of relative humidity. Resistance of the thin film increased when the sensors were exposed to atmosphere with the relative humidity in the range of 0 to 100.

The use as sensitive layers of ox-CNHs-F, ox-CNOs-F, as well as binary nanocomposites of the type ox-CNHs-F/ ox-CNOs-F several significant advantages:

- the presence of oxygenated functions, generated by the treatment of simple nanocarbonic materials in Ar-O2 plasma, ensures the degree of hydrophilicity necessary for the interaction with water;

- fluorine atoms, through the electron-attracting effect, increase the number of carriers both in carbon nanohorns and in onion-type nanocarbon materials. As in both nanocarbonic structures conduction is achieved through gaps (p-type carriers), the material's sensitivity to water molecules increases;

- the presence of fluorine atoms reduces the hysteresis through their hydrophobic effect;

- due to the increased electronegativity, the fluorine atoms increase the polarity of the surface of the nanocarbon material, creating temporary dipoles that facilitate the interaction with water molecules.

- chemical and thermal stability;

- superior mechanical properties;

- detection at room temperature;

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Keywords: oxifluorinated carbon nanohorns, oxifluorinated carbon nano-onions, resistive sensor, relative humidity

ANALYSIS OF COINTEGRATION RELATIONSHIP BETWEEN AGRICULTURAL INCOME AND EMPLOYMENT VIA THE FOURIER FUNCTION

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ABSTRACT

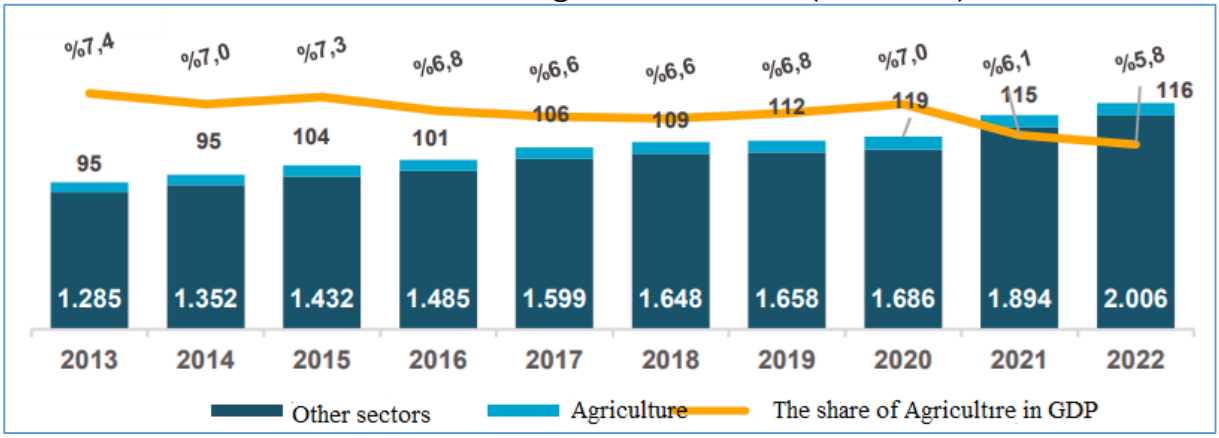
The aim of this study is to investigate the cointegration relationship between agricultural income and agricultural employment in Turkey for the period of 2005Q1-2023Q2. Agricultural income and agricultural employment are variables used in the model. In the study, firstly, the stationary degrees of the variables were determined and it was concluded that the Fractional Fourier ADL test is suitable to examine the cointegration relationship between the variables. According to the results of the study, there is no statistically significant relationship between agricultural income and agricultural employment in the long term in Turkey.

Keywords: Agricultural Income, Agricultural Employment, Fractional fourier ADL

1.INTRODUCTION

Türkiye is one of the important countries due to its biological diversity, rich climate, geographical conditions, and the existence of an agriculture-based industry. Türkiye is among the top ten countries in the production of 55 agricultural products (TBB, 2023). However, the share of agriculture in GDP has decreased for the years. Table 1 illustrates the change in the share of agriculture in GDP in Turkey for the period of 2013-2022. The share of agriculture in GDP in Turkey was 7.4, but, it decreased to 5.8 in 2022.

Table 1: The share of agriculture in GDP (2013-2022)



Source: TBB, 2023:12

Decreasing the share of agriculture in GDP led to a reduction in agricultural employment. Table 2 shows employment by economic activity. Agricultural employment decreased to 15.8 in 2022 while it was 25.5 in 2005.

Table 2: Employment by Economic Activity

Period	Agriculture	Industry	Construction	Services
2005	25.5	21.4	5.7	47.4
2006	23.4	21.8	6.0	48.8
2007	22.0	21.9	6.1	49.9
2008	21.8	22.2	6.1	50.0
2009	23.3	20.2	6.3	50.2
2010	23.3	21.2	6.5	49.0
2011	22.8	21.0	7.2	49.0
2012	21.7	20.6	7.2	50.5
2013	20.6	21.0	7.3	51.2
2014	20.3	20.7	7.4	51.6
2015	20.2	20.2	7.2	52.4
2016	19.5	19.5	7.3	53.6
2017	19.2	19.2	7.5	54.0
2018	18.4	19.8	7.0	54.8
2019	18.2	19.9	5.6	56.4
2020	17.7	20.5	5.8	55.9
2021	17.2	21.3	6.2	55.3
2022	15.8	21.7	6.0	56.5

Source: TURKSTAT

Table 3 shows agricultural employment by gender. When agricultural employment by gender, it is seen that female's share in agricultural employment is higher than males. Although it varies from year to year, both female's and male's share in agricultural employment reduced during the period of 2005-2023.

Table 3: Agricultural Employment by Gender

Period	Male				Female			
	Agriculture	Industry	Construction	Services	Agriculture	Industry	Construction	Services
2005	18.6	23.0	7.3	51.0	46.7	16.5	0.5	36.3
2006	16.9	23.6	7.8	51.8	43.1	16.5	0.7	39.7
2007	15.8	23.7	7.9	52.6	41.1	16.6	0.7	41.6
2008	15.8	24.2	7.9	52.2	39.6	16.3	0.8	43.3
2009	17.3	21.8	8.4	52.6	40.0	15.9	0.7	43.5
2010	16.9	23.0	8.6	51.5	40.2	16.4	0.9	42.5
2011	16.7	22.9	9.7	50.8	39.0	15.9	0.8	44.3
2012	16.2	22.6	9.7	51.5	35.8	15.6	0.8	47.7
2013	15.4	22.9	9.9	51.8	33.4	16.1	0.9	49.6
2014	15.5	22.5	10.1	51.8	31.5	16.4	1.1	51.1
2015	15.7	22.2	10.0	52.1	30.6	15.5	0.9	53.0
2016	15.5	21.6	10.1	52.8	28.5	14.9	1.0	55.5
2017	15.3	21.2	10.5	53.0	28.0	14.8	1.0	56.3
2018	14.9	21.9	9.8	53.3	26.0	15.2	0.9	57.9
2019	14.9	22.1	7.8	55.2	25.2	15.2	0.8	58.9
2020	15.3	22.6	8.0	54.0	23.1	15.9	0.8	60.2
2021	14.7	23.5	8.6	53.3	22.7	16.6	0.9	59.7
2022	13.6	23.9	8.4	54.1	20.6	17.1	0.9	61.5

Source: TURKSTAT

2.DATA SET AND METHODOLOGY

The aim of this study is to investigate whether there is a cointegration relationship between agricultural income and agricultural employment. Agricultural GDP and agricultural employment statistics were compiled from TURKSTAT. Table 4 shows the variables used in the model.

Table 4: Data Set

Statistics	Notation	Database
Agricultural GDP	lnincome	TURKSTAT
Agricultural employment	lnemployment	TURKSTAT

All variables including the model must be first-degree stationary to analyze the cointegration relationship between variables. In this study, the Fractional Fourier Unit Root Test developed by Omay (2015) was applied to determine the degree of the stationary of the variables. The Fourier ADF Unit Root Test was developed by Enders & Lee (2012). Table 4 illustrates the results of the Fractional Fourier ADF Unit Root Test.

Table 5: The results of Fractional Fourier ADF

	FFADF				ADF			
					Düzey		Fark	
Değişken	**Frekans**	**F Kisit**	**k**	**FFADF**	**τ**	**p**	**τ**	**p**
lnincome	0.80	4.546	1.00	-3.904	-2.437	0.1351	-3.049	0.0360**
lnemployment	1.10	5.937	11.00	-2.578	-1.743	0.4050	-3.697	0.0064*

Critical values for F statistic are 8.78, 10.28 and 13.48 for 10 %, 5 %, and 1 % significance levels, respectively. The critical values are obtained from Omay (2015). Critical values for individual statistics are compiled by Bozoklu et al. (2020).

2.1. Fourier Fractional ADL Cointegration Test

Fourier cointegration tests are tests considering smooth structural breaks. Banerjee et al. (2017) developed the Fourier ADL cointegration test by including trigonometric functions in the ADL cointegration test. The Fourier ADL cointegration test is formulated as follows;

$$\Delta y_{1t} = \beta_0 + \phi_1 \sin\left(\frac{2\pi kt}{T}\right) + \phi_1 \cos\left(\frac{2\pi kt}{T}\right) + \delta_1 y_{1,t-1} + \delta' y_{2,t-1} + a\Delta y_{2t} + e_t \qquad (1)$$

Where, t, T and π represent trend term, sample size, and pi constant. k is the number of optimal frequencies representing smooth structural breaks. Ilkay et al. (2021) revised the Fourier ADL testi by using fractional frequency. The null hypothesis expresses there is no cointegration between variables. If the calculated test statistic is higher than the critical value as absolute value, the null hypothesis is rejected. Rejecting the null hypothesis means there is cointegration relationship between variables.

2.2.Econometric Estimation

Table 6 illustrates the results of the Fractional Fourier ADL cointegration test. According to Table 6, there is no cointegration relationship between agricultural GDP and agricultural employment

Table 6: The Results of the Fractional Fourier ADL Cointegration Test

H_0	Test Stat	f	Min AIC	Conclusion
There is no cointegration between agricultural income and agricultural employment	-3.754	0.10	-3.501	No cointegration

Critical values for the Fractional Fourier ADL cointegration test are -4.742, -4.134 and -3.821 for 1 %, 5 % and % 10 significance level, respectively.

CONCLUSION

Climate changes, wars and pandemics caused by environmental degradation negatively affect agricultural production both locally and globally. Although agricultural GDP varies over the years, the share of the agricultural sector in GDP has decreased uninterruptedly. As of 2022, the share of the agricultural sector in GDP in Turkey is 5.8%. Although it fluctuates over the years, it can be said that agricultural employment has generally decreased. Although the share of women in agricultural employment is higher than that of men, the decrease in the share of women in agricultural employment is greater than that of men. The increase in women's education level and increasing incentives for women's employment accelerated the shift of women from the agricultural sector to the service sector. The results of the study show that there is no statistically significant relationship between agricultural GDP and agricultural employment. The increase in agricultural input costs, decreases in productivity due to drought, use of smart agricultural techniques and mechanization, increases in demand for higher education, and migration negatively affect agricultural employment and these factors prevent the positive impact of the increase in agricultural GDP on agricultural GDP. It is necessary to support rural development and strengthen the agricultural sector in order to overcome the problems caused by intense urbanization and increasing environmental problems and to reduce food security concerns, which have especially increased recently.

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FEED INTAKE, DIGESTIBILITY AND WEIGHT GAIN OF RED SOKOTO GOAT FED FUNGUS TREATED Parkia biglobosa FLOWER MEAL

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Abstract

This experiment was carried out to evaluate the effect of fungus-treated Parkia biglobosa flower meal on the feed intake, digestibility and weight gain of Red Sokoto goats. Twelve (12) experimental goats with an average weight of 14kg were randomly allocated into four (4) treatments with three replicates per treatment in a completely randomized design. The diets formulated had four (4) inclusion levels of Aspergillus niger treated Parkia biglobosa flower meal at 0%, 5%, 7.5% 10% as T1, T2, T3 and T4 respectively. Feed and water were provided ad-libitum while standard management practices were followed. The experiment lasted for 8 weeks and Data collected at the end of the experiment showed significant difference in feed intake ($P<0.05$), with T4 having the highest value, while final body weight, weight gain and feed conversion ratio did not record significant difference at ($P>0.05$). The digestibility coefficients of dry matter, crude protein, crude fibre and ether extract were also significantly different among the treatments ($P<0.05$), with T1 having the highest values for all parameters

except crude protein, which was highest in T4. The study concluded that fungus treated Parkia biglobosa flower meal improved feed intake which resulted in improved body weight gain with the highest weight gain and Protein digestibility. Therefore, Aspergillus niger-treated Parkia biglobosa flower meal has the potential to enhance growth performance, feed conversion ratio, and nutrient digestibility. In conclusion farmers should consider incorporating fungus-treated Parkia biglobosa flower meal into the diet of goats as a potential alternative protein source. This study recommended the inclusion of fungus-treated Parkia biglobosa flower meal at 10% inclusion as a valuable resource in goat nutrition.

Keywords: Parkia bilobosa flower meal, Aspergillus niger, feed intake, digestibility, weight gain.

INTRODUCTION

The world's demand for animal protein is growing continuously due to the increasing human population and improved standard of living necessitating increasing animal production. In developing countries like Nigeria, the main reason for the present low consumption of animal protein is the low livestock productivity rather than low livestock numbers.(NRC, 2007). Conventional protein ingredients like the GNC is very expensive and in high demand by monogastric animals.

Parkia biglobosa flower commonly known as Bututun Dorowa (Hausa language), is a distinctively large red globe capitulum that composes of up to 2500 individual flowers arranged around a spherical bud. The capitulum measures 45-70mm long, 35-60mm in diameter and is divided into two parts: apical ball and basal portion (Hopskins, 1983).

P. biglobosa is a perennial tree legume which belongs to the sub-family Mimosidae and the family Leguminosae. It grows in the savanna region of west Africa up to the southern edge of the sahel zone 130N (Campell-Platt 1980). the trees are not normally cultivated but ares seen in population of two or more in the savanna region of Nigeria. (Hopkins, 1983). The flowers are used as food in the Northern- Western Nigeria when mixed with groundnut cake and other ingredients. The flower is eaten as it is by children (Jaiyi, et al 2009).

The protein requirements of goats in Nigeria are not met due to the high cost of conventional protein feedstuffs. There is high competition for conventional protein feedstuffs (ie. GNC) between man and monogastric animals leading to scarcity and unavailability.There is need to source for cheaper and readily available alternative feed ingredients that are not in high demand by man or monogastric animals. This research was directed towards the utilization of fungus treated parkia biglobosa flower meal by goats.

Experimantal Site

The study was conducted at the Department of Animal Science, of the University of Abuja Main Abuja.

Collection and processing of Parkia biglobosa

Mature Parkia biglobosa flower was collected from Parkia trees found around the University of Abuja, Main Campus and British villages around Gwagwalada region. The capitulum inflorescence was removed from the main bud of the whole flower, after which it was sundried. The flower was futher milled and autoioclaved after which it was ready to be innoculated with the aspergillus niger.

Autoclaving of Parkia biglobosa Flower

Sack was used in collecting Mature parkia biglobosa flower from Parkia trees around the University of Abuja, Main Campus and British villages around Gwagwaladsa region. The capitulum inflorescence was was removed from the main bud of the whole flower, after which it was sundried. The flower was futher packed into a sack and transported for milling and autoclaved after which it was ready under 30 minutes to kill toxic microorganisms in the Parkia biglobosa. After it was autoclaved, the Parkia bioglobosa flower was placed in a bowl and was futher innoculated with the Aspergillus niger leaving it for two weeks. When the Aspergillus stated growing on the Parkia biglobosa flower, a spoon was used to turn it over.

Fungus Used

Fungus (Aspergillus niger) was obtained from the Department of Microbiology, University of Ilorin, it was sub-cultured in the Department of Microbiology, University of Abuja ob PDA

under proper supervision, After which the fungus was used to inoculate the already autoclaved Parkia biglobosa flower meal.

Animal management

A total of twelve weaned goats were used for the experiment. The goats were treated against ecto and endo parasites using ivomec. The animals were replicated three times with one animal per replicate.

Parameters Evaluated

Parameters evaluated were as follows:

(!) Feed intake

(2) Weight gain

(3) Digestibility of the animal

Treatment Table

The below represent the various treatment that were used for the experiment and the composition of the complete diet that were formulated alongside the already processed Aspergillus niger treated Parkia biglobosa flower fed to the goats.

Table 1: Composition of the experimental diets

Ingredients (%)	**T1**	**T2**	**T3**	**T4**
Cassava peels/waste	54.00	54.00	54.00	54.00
Rice husk	35.00	35.00	35.00	30.00
Groundnut Cake	**10.00**	**5.00**	**2.50**	**---**
Aspergillus treated Parkia biglobosa flower	**-----**	**5.00**	**7.50**	**10.00**
Salt	0.50	0.50	0.50	0.50
Vitamin premix	0.50	0.50	0.50	0.50
total	100.00	100.00	100.00	100.00

Statistical analysis

Data collected were subjected to analysis of variance (ANOVA) using Completely Randomized Design Model (CRD). treatment means were separated using Duncan (1955) Multiple Range Test (DMRT).

Table 2: Proximate composition (%) of the Experimental Diet

Parameters (%)	T1 (0%)	T2 (50%)	T3 (75%)	T4(100%)
Dry matter	81.62	79.12	78.49	81.55
Crude protein	14.87	13.99	14.93	15.17
Ether extract	5.28	5.75	6.08	6.09
Ash	8.04	8.21	8.82	8.89
Crude fibre	11.42	11.01	10.42	10.70
Gross energy(kcal/kg)	2409.50	2446.40	2420.00	2543.85

Table 3. Performance Characteristics of Red Sokoto Goat Fed Fungus Treated Parkia biglobosa Flower.

PARAMETERS	T1	T2	T3	T4	±SEM
Initial body weight (kg)	10.00	10.32	10.00	10.16	0.22
Final body weight (kg)	12.18	11.46	11.17	12.00	0.16
total weight gain (g/buck)	2180.00	1140.00	1170.00	2160.00	15.00
Total weight gain g/buck/day	38.93	20.36	20.89	38.57	1.96
Feed conversion ratio (g)	1.77	4.10	2.85	2.00	0.52

Table 4:Feed Intake of Red Sokoto Goat Fed Fungus Treated Parkia biglobosa

PARAMETERS	T1 (0%)	T2 (50%)	T3 (75%)	T4 (100%)	±SEM
Total feed intake	2670.00a	2300.00d	2410.00c	2610.00b	0.15
Daily feed intake (g/buck/day)	47.68a	41.07d	43.04c	46.61b	0.86

Table 5:**Digestibility Coefficient of Red Sokoto Goat fed Aspergillus Treated Parkia biglobosa Flower Meal.**

PARAMETERS(g/dm)	T1	T2	T3	T4	±SEM
Dry matter	69.70a	65.00c	60.09d	66.26b	3.82
Crude protein	86.66a	75.00c	65.00d	85.50b	9.78
Crude fibre	80.00a	66.66c	50.00d	74.28b	10.71
Ether extract	85.00a	60.00c	55.00d	77.50b	4.19

Result and Discussion

The feed intake was significantly different ($p< 0.05$) across the treatments. The highest feed intake value of 2670.00g and 2610.00g was recorded in treatments 1 and 4 respectively.The highest total weight gain of 2180.00 was recorded in treatment 1 which did not differ significantly ($P>0.05$) with 2160 recorded in treatment 4, however this was significantly different ($P<0.05$) from 1140.00 and 1170.00 recorded in treatments 2 and 3 respectively.Similarly, the highest final body weight value of 12.18 was recorded in treatment 1 which did not differ significantly ($P>0.05$) with 12.00 recorded in treatment 4, however this was significantly different ($P<0.05$) from 11.46 and 11.17 recorded in treatments 2 and 3 respectively. Dry matter, crude protein, crude fibre and ether extract digestibility were significantly affected ($P<0.05$) by the treatments, highest value of dry matter, crude protein, crude fibre and ether extract were recorded in treatment 1. Treatment 4 had significantly higher value for dry matter, crude protein, crude fibre and ether extract ($p <0.05$) than treatment 2 and the least values for these parameters were recorded in treatment 3.

The chemical composition of the experimental diet showed that the diet contains adequate dry matter and nutrient requirements to support normal rumen function.(NRC 2007).Crude Fiber decreased as the inclusion level of treated P. biglobosa flower meal increased, indicating degradation by the fungus thereby impacting digestibility. This corresponds with Ikhimioya et al, (2019) who recorded decreased fibre values with the inclusion of biological treated Parkia biglobosa pod. The over all result showed that fungus-treated Parkia biglobosa flower meal

inclusion in the diet improved performance in terms of final weight gain and total weight gain this may be as a result of higher feed intake and digestibility showing acceptability of the diet.

Conclusion and Recommendation

It can be concluded that dietary inclusion of Fungus-treated Parkia biglobosa flower meal has the potential benefits of improving growth performance, feed efficiency and nutrient digestibility in goats. Farmers and producers should consider incorporating Aspergillus -treated Parkia biglobosa flower meal in goat diets as a potential alternative protein source.

Future research could include, evaluating the effects of dietary inclusion Parkia biglobosa flower meal on meat quality parameters, assessing the potential for toxicity at higher inclusion levels and comparing the cost-effectiveness of alternative protein sources for goat diets.

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USE OF PLANT ESSENTIAL OILS AS BIOINSECTICIDES IN AGRICULTURE IN NORTH AFRICA ADVANCES AND PERSPECTIVES

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Abstract

Chemical pesticides are more prevalent worldwide than organic alternatives, causing harm to humans and the environment. This study evaluates biological pest control strategies, focusing on essential oils from aromatic plants as bioinsecticides, which have insecticidal properties.This review aims to provide a comprehensive overview of the use of essential oils as bioinsecticides in North Africa. It will examine the efficacy of these oils against a variety of insect pests, explore the underlying mechanisms of action, discuss environmental and economic considerations, and highlight future prospects for this promising approach. By

combining traditional knowledge with scientific advances, this study aims to contribute to more sustainable and resilient agriculture in the North African region

To get an idea of research activity in this field in all North African countries, we analyzed a sample of over 54 articles published over 5 years by researchers in North African countries, between 2010 and 2015, The largest number of publications on botanical insecticides among North African countries comes from Egypt, followed by Tunisia, Algeria, Morocco and Libya, with little difference between the last three.

Nearly half of the research we looked at used Coleoptera insect species, while Lepidoptera and Diptera were used less frequently, various types of botanical preparations (extracts, essential oils and powders) were evaluated in studies carried out in North Africa. More than half (48%) of the studies were conducted on essential oils, and almost as many (42%) on plant extracts. On the other hand, only 2% of studies used plant powders in their biological tests. The remaining 8% of studies used a combination of these forms.

Keywords: Plant Essential Oils, Bioinsecticides, Agriculture, North Africa

FRANCE'S COMPETITIVENESS AND LEVEL OF SPECIALIZATION IN AGRICULTURAL AND LIVESTOCK PRODUCTS

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ABSTRACT

This study analyzed France's competitiveness and level of specialization in agricultural and livestock products. The product groups subject to the analysis consist of 3-digit products in the Standard International Trade Classification (SITC) Revision 3 category (SITC 0, SITC 1, and SITC 4). In the study where 44 product groups were analyzed, Revealed Comparative Advantages (RCA) was used to determine competitiveness, and the Michaely index (MI) was used to determine the level of specialization. According to the results of the RCA analysis, France has competitiveness in 23 of 44 product groups. There is a strong competitive advantage in 2 product groups, medium in 7 and weak in 14. According to the results of the MI analysis, France specialized in 18 of the 44 product groups and could not specialize in 26 product groups.

Keywords: Export Competitiveness, RCA Index, Specialization, Michaely Index

INTRODUCTION

France is one of the leading countries in the European Union (EU) regarding agriculture and animal husbandry. 29.024 thousand hectares of the country's surface area is agricultural land, and 53.4% of the surface area is considered agricultural land, while 31.4% is covered by forested land. The main agricultural products are cereals, sugar beets, wine, fruits and vegetables, dairy products, and animal products. The main agricultural products produced in France are grain, sugar beet, wine, fruit and vegetables, dairy products, and animal products

(Karlı et al. 2018: 321-322). In this context, it can be said that the agriculture and livestock sectors are crucial to the French economy.

The Northern part of France is known for its large wheat farms (Stum and Camaret, 1990: 1298). The production of dairy products, pork, poultry, and apples is mainly located in the West of the country (Bickley, 1969: 1). Beef production is mainly located in central France, while wine, vegetable, and fruit production has spread from the central regions of the country to Southern France (David et al. 2010). The Uruguay Round Talks of the Common Agricultural Policy (CAP) and the General Agreement on Tariffs and Trade (GATT) envisaged several reforms in the agricultural sector of the French economy. France's competitive advantage in the agricultural and livestock sector is often directly related to the high quality of its products, such as cheese and wine, and their world renown. France has the highest number of cattle among the European Union countries (Saygın and Demirbaş, 2017: 74-75). In addition to the superiority of the number of cattle, France is also rich in animal diversity (Ergün and Bayram, 2021: 160). It is also the only country with herds of cows and calves on a large scale. Production in French industry mainly includes grazing and livestock for export. These productions take place in France in different geographical and climatic zones. There are 19 million cattle in France, thus leaving behind Germany and Spain. France exports about 1.2 million grazing and livestock, and 90% of the animals are livestock. The Italian market is behind France's 85% and the Spanish's 11%. Every year, France's livestock exports (fattening, pasture, and slaughter) contribute approximately 1.2 billion Euros to the country's economy (FranceAgriMer, 2023).

Therefore, the study analyzed the specialization and competitiveness of France in the agricultural and livestock sectors. The study covers the years 2000-2022. Standard International Trade Classification (SITC) Revision 3, 3-digit agricultural and livestock products were discussed in the study. In the study where 44 product groups were analyzed, the results will be discussed in other sections.

METHODOLOGY AND EMPIRICAL ANALYSIS

The most commonly used method to determine countries' competitive advantage is Balassa's RCA index. The RCA index compares the export performance of countries in that sector with the world's performance and measures the competitiveness of that product or sector in this way.

The RCA Index is formulated as (Balassa, 1965):

$$RCA_{jkt} = \frac{X^{j}_{kt} \,/\, X^{j}_{t}}{X^{w}_{kt} \,/\, X^{w}_{t}}$$

Suppose RCA > 1, the country in question specializes in the export of that product and has competitiveness. If RCA< 1, the country in question could not specialize in exporting that product and has a competitive disadvantage. If 1< RCA< 2, there is weak competitiveness, 2 < RCA< 4, medium competitiveness, and above 4 and 4 strong competitiveness (Çeştepe, 2012).

The Michaely index is an index created by Michael Michaely in 1962. It has been put forward as an alternative to other specialization indices. The Michaely index is formulated as follows (Michaely, 1962):

$$MI^{j}_{k} = \frac{X^{j}_{k}}{\sum X^{j}_{k}} - \frac{M^{j}_{k}}{\sum M^{j}_{k}}$$

The expression seen as Xij in the formula; country j represents exports in sector i, and Mij represents the country j's imports in sector i. ∑ Xij shows the country's total exports, ∑ Mij shows the country's total imports. The first part of the formula (before the minus sign) shows the percentage share of a particular sector in national exports, and the second part shows the percentage share of a particular sector in national imports (Laursen, 2015). The index value is between -1 and +1. If the value of the index is positive (0 < MI < 1), the country specializes in that sector, while a negative value is not.

Table 1: SITC Rev. 3 Agricultural and Livestock Products

Product Code	Product Name	Product Code	Product Name
001	Live animals	056	Vegetables, preserved
011	Meat of bovine animals	057	Fruit and nuts, fresh or dried
012	Other meat and meat offal	058	Fruit, prepared or preserved
016	Meat, salted, dried or smoked	059	Fruit and vegetable juices
017	Meat, prepared or preserved	061	Sugars, molasses, and honey
022	Milk, cream, and milk products	062	Sugar confectionary
023	Butter	071	Coffee and coffee substitutes
024	Cheese and curd	072	Cocoa
025	Eggs	073	Chocolate and cocoa preparations
034	Fish, fresh, chilled, or frozen	074	Tea
035	Fish, dried, salted or smoked	075	Spices
036	Crustaceans and molluscs	081	Animal feeds, excl. unmilled cereals
037	Marine prod., prep. or preserved	091	Margarine and shortening
041	Wheat, unmilled	098	Edible products and prep. n.e.s.
042	Rice	111	Non-alcoholic beverages n.e.s.
043	Barley, unmilled	112	Alcoholic beverages
044	Maize, unmilled	121	Tobacco, unmanuf.; refuse
045	Other cereals, unmilled	122	Tobacco, manufactured
046	Meal and flour of wheat	411	Animal oils and fats
047	Other cereal meals and flour	421	Fixed soft vegetable fats/oils
048	Cereal, flour, and starch preparation	422	Other fixed vegetable fats/oils
054	Vegetables, fresh, chilled or frozen	431	Animal/vegetable fats/oils, processed

Note: This classification is from the World Integrated Trade Solution (WITS) database.

The study used SITC Rev. 3, 3-digit classification of agricultural and livestock products (SITC 0, SITC 1, and SITC 4). In this classification, which covers 44 product groups, the code and names of the product groups are shown in Table 1. Balassa's RCA index and Michaely index were used to analyze product groups. Index scores are shown in Table 2 and Table 3.

Table 2: Results of RCA Index

Product Code	Product Name	RCA Values	Competitiveness Degree
001	Live animals	3,480	Medium
012	Other meat and meat offal	1,268	Weak
017	Meat, prepared or preserved	1,266	Weak
022	Milk, cream, and milk products	2,589	Medium
023	Butter	1,641	Weak
024	Cheese and curd	3,635	Medium
025	Eggs	1,866	Weak
041	Wheat, unmilled	3,173	Medium
043	Barley, unmilled	5,319	Strong
044	Maize, unmilled	2,069	Medium
046	Meal and flour of wheat	1,645	Weak
047	Other cereal meals and flour	1,856	Weak
048	Cereal, flour, and starch preparation	2,153	Medium
054	Vegetables, fresh, chilled or frozen	1,182	Weak
056	Vegetables, preserved	1,217	Weak
061	Sugars, molasses and honey	1,622	Weak
072	Cocoa	1,294	Weak
073	Chocolate and cocoa preparations	1,738	Weak
081	Animal feeds, excl. unmilled cereals	1,333	Weak
098	Edible products and prep. n.e.s.	1,457	Weak
111	Non-alcoholic beverages n.e.s.	2,613	Medium
112	Alcoholic beverages	5,693	Strong
411	Animal oils and fats	1,816	Weak

Source: It was calculated by the authors using data from the COMTRADE database.

According to the analysis of the RCA index (Table 2), 23 of France's 44 product groups have a competitive advantage, and 21 have a competitive disadvantage. Of the competitive product groups, it has a strong advantage in 2, medium in 7, and weak in 14.

The product groups with substantial advantages are;

- barley, unmilled and
- alcoholic beverages.

The product groups in which medium advantage are;

- live animals
- milk, cream, and milk products
- cheese and curd
- wheat, unmilled
- maize, unmilled
- cereal, flour, and starch preparation
- non-alcoholic beverages n.e.s.

The product groups with weak advantages are;

- other meat and meat offal
- meat, prepared or preserved
- butter
- eggs
- meal and flour of wheat
- other cereal meals and flour
- vegetables, fresh, chilled, or frozen
- vegetables, preserved
- sugars, molasses, and honey
- cocoa
- chocolate and cocoa preparations
- animal feeds, excl. unmilled cereals
- edible products and prep. n.e.s.
- Animal oils and fats.

Table 3: Results of Michaely Index

Product Code	Product Name	MI Values
001	Live animals	0,0030
012	Meat of bovine animals	0,0002
017	Meat, prepared or preserved	0,0001
022	Milk, cream, and milk products	0,0030
024	Cheese and curd	0,0031
025	Eggs	0,0002
041	Wheat, unmilled	0,0059
043	Barley, unmilled	0,0017
044	Maize, unmilled	0,0024
045	Other cereals, unmilled	0,0001
046	Meal and flour of wheat	0,0002
047	Other cereal meals and flour	0,0001
048	Cereal, flour, and starch preparation	0,0011
081	Animal feeds, excl. unmilled cereals	0,0005
098	Edible products and prep. n.e.s.	0,0015
111	Non-alcoholic beverages n.e.s.	0,0014
112	Alcoholic beverages	0,0173
411	Animal oils and fats	0,0003

Source: It was calculated by the authors using data from the COMTRADE database.

According to the results of the Michaely Index (Table 3), it is seen that France specializes in 18 out of 44 product groups, while it does not specialize in 26 product groups. Unlike the RCA index, the Michaely Index uses not only export data but also import data. According to the results of the Michaely Index, France imports more than it exports in most product groups (26 product groups with a low level of specialization), which is not enough to explain the existence of competitiveness by looking at export data alone.

CONCLUSION

It provides information on analyzing the foreign trade competitiveness of countries, determining their foreign trade partners and products subject to trade, and increasing their production. In particular, determining the competitiveness of countries with a significant foreign trade volume in the agriculture and livestock sector, such as France, is essential in terms of the contribution of the studies to the literature.

The study calculated France's competitiveness and specialization level in the agricultural and livestock sector. In the study where 44 product groups were analyzed, France has a competitive advantage in 23 product groups according to the RCA index and 19 product groups according to the Michaely index.

According to the RCA index, the results show that France has a strong advantage in classifying unmilled barley and alcoholic beverages. As stated in the methodology, RCA analysis compares the export performance of the countries in that sector with the export performance of the world and analyzes accordingly. Although the analysis based on the countries' exports shows the countries' export competitiveness in that sector, it does not show whether they are sufficiently specialized. Therefore, the Michaely index was used to find the level of specialization. Since this index also includes import data for that sector, it gives more accurate results than the RCA index. Finally, although there are slight differences, the results of both analyses confirm that France specializes in similar product lines.

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STUDIES ON POWDERY MILDEW CAUSED BY *PODOSPHAERA PANNOSA* IN *ROSA* SPP.

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ABSTRACT

Powdery mildew is a broad-spectrum plant disease that can be systematically encountered in distance or close plant species and infects many agricultural or naturally growing plants. One of the most affected taxonomic groups is *Rosa* genus that has important plant species in ornamental and in horticultural production and utilization as well as in natural habitat and ecosystem. It is known that most of the *Rosa* spp. are sensitive to one of the powdery mildew pathogens *Podosphaera pannosa* disease and thus there are product losses. Although ornamental, garden, or medicinal roses are most understood when rosa is mentioned, the other members of Rosa genus used for medicinal, direct consumption, ornamental, and aromatic purposes also suffer from the disease. The disease symptoms, detection and protection methods may vary from plant to plant and from study to study. In this review article important points in previous studies on powdery mildew in *Rosa* spp. will be presented, and perspectives of the detection, characterization, signs and symptoms, protection and control methods will be discussed.

Keywords: Plant Protection, *Podosphaera pannosa*, Powdery Mildew, *Rosa* spp., Roses

INTRODUCTION

Rosa spp. powdery mildew caused by *Podosphaera pannosa* (Wallr.) de Bary (Homotypic Syn. *Sphaerotheca pannosa* (Wallr.) Lev. (NCBI, 2023) is a pathogen that has been named many times in its scientific journey. According to Mycobank Database *Erysiphe pannosa*, *Sphaerotheca pannosa* var. *pannosa*, *Erysiphe pannosa*, *Albigo pannosa*, and *Leucothallia pannosa* are its obligate synonyms (MYCOBANK, 2023). The pathogen belongs to *Podosphaera* genus in Erysiphaceae family in Erysiphales order in Leotiomycetes class in Pezizomycotina subphylum in Ascomycota phylum in Fungi kingdom (EPPO, 2023; NCBI, 2023). The *Podosphaera* genus has dozens of species that cause diseases in plants that consisted agronomic crops or weeds e.g., strawberry, cucurbit, bean, eucalypt, cherry, quince, hop, apple, *Euphorbia* spp., *Vaccinium* spp., *Spiraea* spp., and *Ribes* spp. besides *Rosa* spp. (Agrios, 2005; EPPO, 2023).

Figure 1. *Podosphaera pannosa* on a rose at early stage in a greenhouse cultivation

Rosa spp. have major economically important plants these are growth and utilized for cut-flower, landscape ornamental, perfume oil, medicinal, culinary usage aims (Hummer and Janick, 2009). *Podosphaera pannosa* (Syn. *Sphaerotheca pannosa*) is the most screening and occurring pathogen in open air garden roses for multi purposes and in greenhouse roses that aimed cut or pot flower. The disease emerges from year-to-year, causes flower reducing by attacking buds, young leaves, and growing tips. The fungus produces white mycelium that grows on the surface of the rose plant tissues (Figure 1) and then sending globose haustoria into the epidermal cells. On roses under the open field condition, fungus overwinters mostly as mycelium in the buds. On roses under greenhouse, the fungus survives as mycelium and conidia, greenhouse roses are susceptible throughout the year, although it varies depending on the regions. The control of rose powdery mildew is achieved by applying of sulphur or other systemic and contact fungicides. New methods such as spraying of defence activating compounds, of sodium bicarbonate solution and of ultrafine oils have also started to be applied (Agrios, 2005).

In the review article it is aimed to evaluate the studies that have achieved successfully on detection, isolation, genetics, hosts, symptoms, and controlling of the rose powdery mildew.

Hosts and Symptoms of *Podosphaera pannosa*

Rosa spp. are the main hosts of the *Podosphaera pannosa* and the well-known symptoms on the roses are blister-like areas on young leaves that become covered with a grayish-white, powdery looking fungus. When the leaves began to extend, leaf curling, white patches, distortion, and necrotic tissues can be seen. The symptoms are also seen on young green shoots, and buds before opening. The buds may can fail to open or can be caused improperly opening. Flowers also can be symptomatic with discoloration, dwarfed looking and eventually die (Agrios, 2005).

According to one of the first reports and the genetic studies on *Podosphaera pannosa*, the species has some hosts besides *Rosa* spp.. In one of the study, scientists obtained one sample from residential garden at Mililani city in Hawaii in 2013 on *Catharanthus roseus* (L.) G. Don. and they emphasized that the report was the first of *P. pannosa* in Apocynaceae genera and was the second *Podosphaera* genus in the family (Romberg et al.,2014).

Vajna and Rozsnyay (2006) firstly observed the *P. pannosa* on *Prunus cerasus* in a 5-year-old orchard in 2002 with white epiphytic mycelia, and conidia on leaves, thin irregular colonies on either side of leaves in July and curling and blistering leaves in later times. This was the first report to their knowledge in sour cherry in Hungary and elsewhere.

In *Rosa cymosa* which is an ornamental and traditional medicine plant, powdery mildew was determined in 2022 that cause colonizing both of leaf sides, rolling up the leaves along the main veins. At the same time mature leaves and main stems had covered with pathogen. The results of the detailed studies showed that the powdery mildew was *P. pannosa* and this was the first in the plant species in Guizhou province in China (Tan et al., 2023).

Although *Podosphera pannosa* is mostly known as powdery mildew of *Rosa* spp. and some *Prunus* spp., in France the pathogen was the first described in *Prunus cerasus* in 2011. The pathogen caused typical powdery mildew symptoms as covered by pathogen on the lower surfaces of leaves with white and dense mycelium besides discoloration on the upper side of leaves, necrotic patches, and blisters (Hubert et al., 2012).

Powdery mildew is an important problem in greenhouses and hedges of *Eucalyptus* spp. in Brazil. The sympoms of the pathogen on the eucalypt plants are leaf and shoot distortion, shoot discoloration, growth reduction and production losses. The cross-inoculation study which was held from a single clade containing *P. pannosa* showed that the species can infect both rose and eucalypt (Fonseca et al., 2017).

Cornejo et al. (2019) had been observed signs and symptoms of powdery mildew in a mandarin cultivar in an orchard. The symptoms were dusty colonies on the upper surface of young leaves and young stems, leaf chlorosis, deformation, stunting and fruit russeting. The morphological and molecular studies with the fungus showed that the pathogen was *P. pannosa*. To their knowledge this is the first detection of *P. pannosa*, attacking W. Murcott mandarins in Chile and the world.

Detection, Isolation and Assessment of *Podosphaera pannosa* in *Rosa* spp.

Scientists have to observe, detect and assess the symptoms and signs of *Podosphaera pannosa* because of proving the pathogen. In the other side there can be methodology differences in experiment to experiment.

In a study monoconidial isolates of the pathogen *Podosphaera pannosa* were taken naturally infected *Rosa* spp. plants and than the single conidia transferred to *in vitro* grown susceptible genotypes. Re-growth single conida or conidiophores were transferred again and the step was repeated 5 times to be sure for reach genetically uniform pathogen. For testing of resistance of

plants, roses that were grown in climate chamber and greenhouse. The leaflets on water-agar in *Petri* also were used for visual analysis of the pathogen. Disease index was calculated as percentages between 0-100% from the leaf areas covared with conidiophores, and resistance evaluations showed as 10% or more covarage is susceptible (Linde and Debener, 2003).

In another study, monospore isolations of the pathogen were maintained *in vitro* grown plants as before mentioned study and then artificial inoculations were realized in greenhouse grown plants by spore suspension of conidia in tap water via immediately spraying method. In the study 0-6 disease score table as percentage of leaf covered mycelium was used to evaluate the symptom development on the tetraploid roses population (Yan et al., 2006).

A study has been worked in a greenhouse to assess supplementary LED light on the growth parameters and *P. pannosa* development on miniature *Rosa* x *hybrida*. For this aim spore distrubution fans were used for naturally inoculation and disease evaluation with 0-5 score with mycelium, and conidia covarage area percentage on both shoot and leaf have been used (Matysiak, 2021).

Genetics of *Podosphaera pannosa*

One of the genetic studies of *Podosphaera pannosa* (Wallr.:Fr) de Bary was discussed by Leus et al. (2006). In the study 26 monoconodial isolates of the pathogen *Podosphaera* had been collected from roses and *Prunus* spp. from 6 countries. The 24 of these were determined as *Podosphaera pannosa.* In addition, 18 of these were found as highly virulent on roses and avirulent or weakly on *Prunus avium*. After the first group, the second group showed highly virulent on both roses and *P. avium*. The study has emphasized that different strains of the pathogen *P. pannosa* can exist with varying host specificity.

Another study about races of the pathogen has been worked using single conidial isolates from ten rose genotypes. All eight isolates of the *P. pannosa* from ten rose genotypes were ascribe to different races. In addition, five races isolated from one location had been exhibited a high racial diversity. At the same time the study showed that, Rpp1 is the first resistance gene against rose powdery mildew (Linde and Debener, 2003).

Control and Management of *Podosphaera pannosa* in *Rosa* spp.

In a study, silicon application to roots was carried out to overcome the powdery mildew, caused by *Podosphaera pannosa*, in greenhouse potted roses with the aim of finding alternative way to chemical control. K_2SiO_3 material was used at a rate of 3.6 mM (100 ppm) via watering before inoculation with *P. pannosa*. Two of the four genotypes of roses were moderately resistant, and the other two were highly susceptible. Disease severity was determined visually using a magnifying glass at certain days after inoculation in some interval, and finally using a stereo microscope at 9th day after inoculation on detached leaves. The conclusions of the scientists were that; i) Root application of Si resulted insignificant reductions in powdery mildew infection and growth, and did not prevent the disease completely, ii) Si is relatively easy to apply in greenhouse systems and caused the reduction in disease severity up to 48.9% and delay in onset of symptom expression, iii) Si can be a supplement especially in resistant genotypes in integrated disease management (Shetty et al., 2012).

In another study, engineered nanomaterials (ENMs) to control and protection of *Podosphaera pannosa* on the rose (*Rosa hybrida* 'Samantha') was realized. For this aim multi-wall carbon nanotubes (MWCNTs), reduced graphene oxide (rGO), copper oxide (CuO) nanoparticles, and titanium dioxide (TiO_2) nanoparticles were used, and they were prepared as 50 or 200 mg/L suspensions in deionized water. The treatments on leaves at water-agar Petri were applied with the suspensions, and the pathogen conidia mixtures separately. After a 19-day standard infection test, the growth of the pathogen on rose leaves was evaluated, and the obtained results of the study that; i) The four engineered nanomaterials inhibited infection of the powdery mildew at the concentration 200 mg/L, whereas only CuO nanoparticles decreased fungal growth at 50 mg/L, ii) The used engineered nanomaterials increased plant resistance to infection by altering endogenous phytohormones especially zeatin riboside, iii) Espacially CuO nanomaterials in both of two used doses showed the highest effectiveness at the fungal infection (Hao et al., 2019).

Yan et al. (2006) described partial resistance to *P. pannosa* in their study that aimed creation of new cultivars which have resistance to the pathogen. For this aim tetraploid rose population obtained by crossing two tetraploid genotypes and its parents were tested via two monospore isolates. The results showed that both isolates exhibited a wide and significant variations among genotypes for resistance and the result was continuous. The study is important for controlling the disease via genetic selection and breeding. Similarly, Bao et al. (2022) observed differences in powdery mildew resistance among 3 *Rosa multiflora* genotypes in their study. They emphasized that secondary metabolites, cytologic differences as epidermis, chitinase, and salicylic acid pathway are key factors in *Rosa multiflora* defense against the pathogen infection.

Qiu et al. (2015) investigated gene transformation to enhance resistance to *Podosphaera pannosa* in *R. multiflora*. For this purpose *Mlo* gene, that is well-known as broad-spectrum resistance gene against plant diseases pathogen found in cereal, was used. The results showed that the plants to which gene were transferred are resistant to the diseases and for ornamental plants it can be an environmentally sustainable solution.

Matysiak (2021) investigated the effects of LED-light spectra on plant growth, photosynthetic performance, and powdery mildew development in rosa. The study have been conducted in a greenhouse with a miniature rose cultivar. The LED light treatments were red, blue, white, and their mixture with far-red in high and low degrees. There were statistically differences in plant growth and disease development. The study showed that red LED is more successful than other light treatments on *P. pannosa*. Light spectra modification can be useful and can be alternative to chemical usage.

For develop an alternative a new method, a phylloplane microflora diversity of rose and their parasitic effect on *P. pannosa* of the plant have been studied by Kumar and Chandel, (2018a). In the study 8 fungal and 2 bacterial isolates were isolated from the phylloplane of rosa leaves. The results indicated that all the isolates effected on the pathogen in *in vitro*. Especially *Trichoderma* sp. was found the best in conidial germination inhibition.

Marzani et al. (2021) used 13 plant extracts from different plant organs of 13 different plants to test the effects on powdery mildew in rose under greenhouse environment. Garlic extract from bulb, ginger extract from tuber, and rosemary extract from leaf were found out the most

efficient on powdery mildew of rose and miniature rose. They emphasized that the plant extract can be used as biofungicides in ecofriendly manner.

In a detailed study (Kumar and Chandel, 2018b) eight fungicides, seven biocontrol agents, nine bioproducts and eight botanicals were used for obtaining anti-sporulant activity of *P. pannosa* on rose. Maximum reduction in conidia production was recorded in difenoconazole, hexaconazole, tebuconazole and trifloxystrobin+tebuconazole. Among the other used agent there were successful products. The study indicate that there were chemical products that suppress the disease and biocontrol agents, bioproducts and botanicals can be used as alternative way to chemical fungicides.

A study (Wanasiri et al., 2020) that consisted of five anti-fungal agent including *Bacillus subtilis*, *Ampelomyces* sp., salicylic acid, fresh cow's milk and carbendazim indicated that all of them effective on spore germination inhibition and disease severity efficiency of *P. pannosa* on rose over control plots under greenhouse. The study emphasized that salicylic acid followed by *Bacillus subtilis* and Carbendazim that shared same statistical group, were the more effective for conidia inhibition than others at spray treatment. The first two have indicated that their usage can be alternative to chemical fungicides.

CONCLUSION

Fungal decay in growing area and nature of *Podosphaera pannosa* is responsible very high levels of economic losses in *Rosa* spp. in addition to risk of transmission to another economic plant species as *Prunus* spp. It should also be kept in mind that powdery mildew diseases can easily reach near and far distances. To ensure global economic, and environmental sustainability, it is necessary to be aware of this disease and control and combat it with right methods at the right time. Cultivation of high-resistant roses obtained as a result of breeding studies, use of new generation eco-friendly pesticides, use of bio-control and bio-product may be a few options. Before all of this, identifying the disease correctly is the first step. According to the review article, although the plant disease *Podosphaera pannosa* is well-known, as many studies as hoped could not be reached. In this manner further studies need to be realized for reach the more detailed knowledges.

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SAEMAUL UNDONG (YENİ KÖY HAREKETİ) KIRSAL KALKINMA MODELİ'NİN ŞANLIURFA KIRSALINDA TARIMSAL ÖRGÜTLENMENİN SAĞLANMASINDA UYGULANABİLİRLİĞİ ÜZERİNE BİR TARTIŞMA

A DISCUSSION ON THE APPLICABILITY OF SAEMAUL UNDONG (NEW VILLAGE MOVEMENT) RURAL DEVELOPMENT MODEL IN ENSURING AGRICULTURAL ORGANIZATION IN ŞANLIURFA RURAL AREA

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ÖZET

Saemaul Undong ya da Yeni Köy hareketi, Park Chang Hee iktidarı tarafından 1970 yılında, Güney Kore'nin kırsalının sosyo-ekonomik koşullarının iyileştirilerek, yoğun sanayileşme politikaları sonucunda kentsel alanda ortaya çıkan büyüme ve refah artışının kırsal kesimde de sağlanması için uygulanan kırsal kalkınma projesidir. Saemaul Undong'un amacı kırsal kesimin geçmişten süregelen yoksulluk, savaş sonrasında artan temel gıda ürünleri üretim eksikliği, altyapısızlık gibi sorunları çözmek ve kent ile kır arasındaki gelir dengesizliğini azaltmaktır. Saemaul Kırsal Kalkınma Projesi, devletin kalkınma girişimlerinin yanında köylünün de kendi köylerini dönüştürmede başrol alacakları, devlet görevlileri ve yerel yöneticilerin gözetiminde gerçekleştirilecek faaliyetler bütününden oluşmaktadır. Saemaul Undong hareketi, kalkınma girişiminin başlangıçta devletin mali destek, danışmanlık ve gözetmenlik hizmeti ile başlayacağı ve bir süre sonra köylülerin kendilerinin sahiplenerek kırsalı dönüştüreceği inancıyla başlatılan, devletin resmi kırsal kalkınma projesi özelliği taşımaktadır. Diğer taraftan proje, politika ve uygulanma aşamasında tavandan tabana bir yönetim ve organizasyon özelliği taşımakla birlikte, proje paydaşlarına duyurulması anından itibaren yerelde köylünün katılımının olacağı ve olması gerekliliği vurgulanmıştır. Bu çalışmada öncelikli olarak Saemaul Undong (Yeni Köy Hareketi) Kırsal Kalkınma Modeli'nin Şanlıurfa ili kırsalının yapısal dinamikleri dikkate alınarak uygulanabilirliği araştırılacak ve tartışılacaktır. Şanlıurfa ili Türkiye'nin toplam tarım alanının %12,6'sını oluşturan GAP Bölgesinde yer almaktadır. Şanlıurfa GAP Bölgesi içinde tarım alanları büyüklüğü bakımından %40'lık pay ile birinci sıradadır. Türkiye pamuk ve antep fıstığı üretiminin yaklaşık %45'i Şanlıurfa'da üretilmektedir. Şanlıurfa pamuk ve mercimek üretiminde birinci sırada, mısır üretiminde ikinci sırada, yağlı tohum ve tahıl üretiminde de ilk sıralarda yer almaktadır. Aynı zamanda GAP bölgesi içerisinde hayvansal üretimde de ilk sıradadır. Şanlıurfa ili tarım ve hayvancılıkta sahip olduğu potansiyel ve üretim miktarlarına karşın, TÜİK 2022 yıllık ortalama eşdeğer hanehalkı kullanılabilir fert geliri en düşük olan bölgeler (toplam 26 bölge) içerisinde bulunmaktadır. Bölgeler arasında karşılaştırma yapıldığında Şanlıurfa ilinin bulunduğu Güneydoğu Anadolu Bölgesi tarımsal örgütlenmenin en az olduğu bölgedir. Diğer taraftan Şanlıurfa ili için yapılan araştırmalarda kooperatif tipi örgütlenme modelinin benimsenmesinde, kendi kendine yardım düşüncesine bağlı olarak tabandan oluşması gereken hareketin oluşmadığı ve mevcut kooperatiflerde evrensel kooperatifçilik ilkelerinin geçerli olmadığı görülmüştür. Dolayısıyla temel ilkelere sahip kooperatif tipi örgütlenme modellerinin

başarılı olamayacağı, Şanlıurfa ili kırsalının yapısal dinamiklerine uygun bir örgütlenme modelinin geliştirilmesi kaçınılmazdır.

Keywords: Kırsal kalkınma, kırsalda örgütlenme, Saemaul Undong, Şanlıurfa-Turkiye.

ABSTRACT

Saemaul Undong or New Village movement is a rural development project implemented in South Korea rural area in 1970 by Park Chang Hee government in order to ensure the growth and welfare increase also in rural area like urban area by improving socio-economic conditions. The aim of Saemaul Undong is to solve the problems of rural areas such as poverty, the lack of production of basic food products that increased after the war, lack of infrastructure, and to reduce the income imbalance between the city and the countryside. Saemaul Rural Development Project consists of a set of activities to be carried out under the supervision of state officials and local administrators, in which the villagers will take a leading role in transforming their own villages, in addition to the development initiatives of the state. The Saemaul Undong movement has the characteristics of the official rural development project of the state, which was initiated with the belief that the development initiative would initially begin with financial support, consultancy and supervision services of the state, and after a while the villagers would adopt and transform the rural. On the other hand, although the project has a top-down management and organization feature in the policy and implementation phase, it has been emphasized that there will be and should be the participation of local villagers from the moment it is announced to the project stakeholders. In this study, first of all, the applicability of the Saemaul Undong (New Village Movement) Rural Development Model in Şanlıurfa will be researched and discussed, taking into account the structural dynamics of the rural areas of Şanlıurfa province. Şanlıurfa province is located in the GAP Region, which constitutes 12.6% of Turkey's total agricultural area. Şanlıurfa ranks first in the GAP Region in terms of agricultural area size with a share of 40%. Approximately 45% of Türkiye's cotton and peanut production is produced in Şanlıurfa. Şanlıurfa ranks first in cotton and lentil production, second in corn production, and first in oilseed and grain production. It also ranks first in animal production in the GAP region. Despite the potential and production amounts that Şanlıurfa province has in agriculture and animal husbandry, it is among the regions (26 regions in total) with the lowest annual average equivalent household disposable income according to TÜİK 2022. When comparing between regions, the Southeastern Anatolia Region, where Şanlıurfa province is located, is the region with the least agricultural organization. On the other hand, in the research conducted for the province of Şanlıurfa, it was seen that in the adoption of the cooperative type organization model, the movement that should be formed from the bottom based on the idea of self-help was not formed and the principles of universal cooperatives were not valid in the existing cooperatives. Therefore, it is inevitable that cooperative type organizational models with basic principles will not be successful, and that an organizational model suitable for the structural dynamics of the rural area of Şanlıurfa province should be developed.

Key words: Rural development, rural organization, Saemaul Undong, Şanlıurfa-Turkey.

GİRİŞ

Kırsal yaşam alanları bir ülkenin sınırları içerisinde bulunan köy yerleşkelerinin tamamıdır (Deavers, 1992; Soysal, 1998). Kırsal alanların ekonomik etkinlikleri doğal kaynakların kullanımına bağlı olarak tarımsal faaliyetlere dayanmaktadır. Bu alanlarda toplumsal ilişki düzeyini birincil ilişkiler belirler. Kırsal yaşam alanlarında toplumsal yaşam üzerinde geleneklerin, örf ve adetlerin baskın olarak biçimlendirme etkisinin olduğu görülmektedir. Bununla birlikte kırsal yaşam alanlarında ekonomik, sosyal, kültürel, toplumsal gelişmeler ve değişimler oldukça yavaş gerçekleşir (Deavers, 1992; DPT, 1994; Pamuk, 2015; G. Sevinç, Davran ve Sevinç, 2018; Wiggins ve Proctor, 2001). Kırsal alanda değişimlerin ve gelişmelerin yavaş olarak gerçekleşmesi bu alanlarda mutlak ve göreli yoksulluğun yaşanmasını kaçınılmaz kılmaktadır (Ateş, 2017; De Janvry, Sadoulet ve Murgai, 2002; Weber, Jensen, Miller, Mosley ve Fisher, 2005). Dünya yoksul nüfusunun yaklaşık %70'inin kırsal yaşam alanlarında bulunması bunu ispatlamaktadır (World Bank, 2016). Dolayısıyla ülkelerin kalkınmasında öncelikli olarak kırsal yaşam alanlarında kalkınmanın sağlanması, ekonomik ve politik hedeflerin başında gelmektedir.

Kırsal kalkınmada ana hedef kırsalda yaşayan toplulukların ekonomik, toplumsal ve kültürel niteliklerinde olumlu yönde değişimin sağlanmasıdır (De Janvry ve diğerleri, 2002; Moseley, 2003). Kırsal alanlarda yaşanan bu değişim gelir ve refah seviyesini iyileştirecek, kırsal alanlar ile kentsel alanlar arasındaki fiziksel ve alt yapı eşitsizliklerini giderebilecektir (Collin, 2004; De Janvry ve diğerleri, 2002; Eraktan ve Yıldırak, 1989; Kuter ve Ünal, 2013). Kırsal kalkınmaya yönelik çabaların devletin bu konudaki çabalarıyla birleştirilmesi, kırsalda yaşayan toplulukların ulusun tümüyle entegrasyonunun sağlanması, kırsal kalkınmaya yönelik politikaların ve uygulamaların başarısını arttıracaktır (Gledhill, 1995; Kalkınma Bakanlığı, 2018; Thurlow, Dorosh ve Davis, 2019).

Ülkeler uygulayacağı kırsal kalkınma politikalarını seçerken nitel ve nicel birçok değişkene ve birikime bağlı kalarak karar almak durumundadırlar. Örneğin o ülkenin kırsal toplumunun sosyo-kültürel yapısı, kırsal alanların fiziksel altyapısı, sahip olunan doğal kaynakların miktarı ve niteliği gibi birçok değişken kırsal kalkınma politika tercihini ve başarısını doğrudan etkilemektedir.

Kırsal kalkınma hususunda başarılı olan ülkelere bakıldığında, başarı hikâyesinin ilk basamağının tarımsal faaliyetlere verilen önem ve bu faaliyetlerin örgütlü bir biçimde yapılmasının sağlanması olduğu görülmektedir (Banaszak, 2008; Çıkın, 2016; Helmberger, 1966; Ribašauskienė ve diğerleri, 2019; M. R. Sevinç, 2021). Daha önce bahsedildiği üzere kırsal alanların ekonomik etkinliğini tarımsal faaliyetler oluşturmaktadır. Tarımsal faaliyetler temel olarak doğal kaynakların kullanımı ile bitkisel ve hayvansal üretim yapmaktır. Ancak günümüzde tarımsal faaliyetler üretim kararı alma aşamasından, nihai hayvansal ve bitkisel ürünlerin pazara ya da tüketiciye sunulmasına kadar geçen bir sürece karşılık gelmektedir (M. R. Sevinç, 2021; Yavuz ve Çağlayan, 2005). Tarım sektörü yapısal olarak birçok risk ile karşı karşıyadır. Bu risklerin bir kısmı kontrol edilebilir olsa da bir kısmı etkisi azaltılabilir ancak kontrol edilemez niteliktedir (Boehlje ve Trede, 1977; Duong, Brewer, Luck ve Zander, 2019; Jankelova, Masar ve Moricova, 2017; M. R. Sevinç, 2021). Tarım sektöründe bu risklerin kontrol edilebilmesi ya da olumsuz etkilerinin asgari düzeye indirilebilmesi ise tarımsal

örgütlenme ile mümkün olmaktadır (Banaszak, 2008; Boehlje ve Trede, 1977; Helmberger, 1966; M. R. Sevinç, 2021).

Şanlıurfa ili insanoğlunun ilk olarak yerleşik hayata geçtiği, tohumu kullanarak ilk defa bitkisel üretim yaptığı, Dicle ve Fırat havzalarının oluşturduğu "Bereketli Hilal" coğrafi alanı içerisinde yer almaktadır (Cançelik, 2021; Çıvgın, 2016; Ötümlü, 2006; Shiferaw ve diğerleri, 2013). Şanlıurfa ili gerek hayvansal gerekse bitkisel üretim potansiyeli yüksek, beşeri sermaye bakımından genç nüfusu fazla, Türkiye'nin en büyük dünyanın ise sayılı entegre projeleri arasında yer alan GAP sınırları içerisinde yer alan bir ildir. Şanlıurfa ilinde kırsal kalkınmanın en önemli aktörlerinden olan tarıma dayalı örgüt ya da birlik yapılanmalarında niceliksel olarak sorun bulunmamaktadır. Şanlıurfa İl Tarım ve Orman Müdürlüğü verilerine göre Şanlıurfa ilinde 2023 yılı Ekim ayı itibariyle 13 adet üretici birliği, 4 adet yetiştirici birliği ve 89 adet tarımsal kalkınma kooperatifi bulunmaktadır. Bu örgütsel yapılar içerisinde tarımsal kalkınma kooperatiflerinin tamamı (89 adet) ise fiili olarak aktif değil pasif durumdadır. Ortaya çıkan bu tablo Şanlıurfa ili kırsalında tarıma dayalı örgütlenmede sorunların olduğu ve bu nedenle tarımsal potansiyelin yeterince kullanılmadığını göstermektedir.

Bu çalışmada Saemaul Undong (Yeni Köy Hareketi) Kırsal Kalkınma Modeli'nin, Şanlıurfa ili kırsalında tarıma dayalı örgütlenmede uygulanabilirliği tartışılacaktır. Saemaul Undong Modeli'nin nitelikleri dikkate alınarak Şanlıurfa ilinde uygulanabilir ve başarılı olabilir tarıma dayalı örgütlenme modeli önerisi sunulması çalışmanın ana amacıdır. Çalışmada öncelikli olarak Şanlıurfa ilinin tarımsal ve kırsaldaki toplumsal yapısına ilişkin bilgilere değinilecektir. Sonrasında Saemaul Undong (Yeni Köy Hareketi) Kırsal Kalkınma Modeli'nin genel niteliklerinden bahsedilecektir. Son olarak Şanlıurfa ilinde uygulanabilir ve başarılı olabilir tarıma dayalı örgütlenme modeli önerisi, Saemaul Undong Modeli baz alınarak tartışılacaktır.

ŞANLIURFA İLİNİN TARIMSAL POTANSİYELİ VE TARIMA DAYALI ÖRGÜTLENME YAPISI

Şanlıurfa ili, 19242 km^2 yüzölçümü, ikisi merkez olmak üzere toplam on üç ilçesi ile Türkiye'nin Güneydoğu Anadolu Bölgesi'nde yer almaktadır. Toplam nüfusu 2,1 milyon kişi olup, nüfusun %66'sı 30 yaşın altında genç nüfustan oluşmaktadır. Türkiye'nin üçüncü büyük tarım arazisine sahip, 24,9 milyar TL yıllık tarımsal geliri ve 112 ülkeye yapılan ihracatla 208,6 milyon dolar ihracat geliri elde eden önemli bir tarım şehridir (Karacadağ Kalkınma Ajansı, 2023a; Şanlıurfa Valiliği, 2023). Şanlıurfa ili aynı zamanda 1989 yılında hazırlanan Master Plan ile tarım, sanayi, ulaştırma, eğitim, sağlık, kırsal ve kentsel altyapı yatırımlarını da içine alan, Türkiye Cumhuriyeti tarihinin en kapsamlı ve maliyetli bölgesel kalkınma projesi olan "Güneydoğu Anadolu Projesi (GAP)" illerinden bir tanesidir (GAP, 2023).

GAP Bölgesi yüzölçümü bakımından 76014 km^2 alanıyla Türkiye'nin %9,7'sini oluşturmaktadır. Türkiye'de ekonomik olarak sulanabilir alanların %20'si GAP Bölgesi'nde yer almaktadır. Aynı zamanda Fırat-Dicle su havzalarını içinde barındıran bölge Türkiye su potansiyelinin %28'ine sahiptir. Bölge sahip olduğu su ve toprak potansiyeli nedeniyle "Bereketli Hilal" olarak adlandırılmaktadır. Ülkedeki toplam tarım alanının %12,6'sı GAP Bölgesi'ndedir. GAP Bölgesi'nde işlenen tarım alanı ve uzun ömürlü bitkilerin alanı toplamda 2,9 milyon hektardır. Bu alanın %79'u işlenen tarım alanıdır. GAP Bölgesi'nde işlenen tarım alanının ülke geneline oranı %11,8 iken uzun ömürlü bitkilerin alanının ülke geneline oranı ise

%17'dir. Ülkedeki toplam tarım alanının %12,6'sı GAP Bölgesi'ndedir (GAP, 2023; TÜİK, 2022a). GAP Bölgesi Türkiye geneline göre 1016 m^3/yıl ile 2,8 kat daha fazla kullanılabilir su potansiyeline sahiptir. Türkiye'deki ekonomik olarak sulanabilir arazilerin %11'ine sahip olan Şanlıurfa, GAP'ın sulama projelerinden en fazla pay alan ildir (GAP, 2023). Şanlıurfa, Türkiye'deki tarım alanlarının yaklaşık %5'ini oluşturmakta ve bu konumu ile Konya ve Ankara'dan sonra arazi dağılımı bakımından üçüncü sıraya yerleşmektedir. Bu büyük potansiyelinden dolayı GAP içerisinde "tarım ve tarıma dayalı ihracat üssü" olarak değerlendirilmektedir (Karacadağ Kalkınma Ajansı, 2023a; TÜİK, 2022a).

Şanlıurfa pamuk, antep fıstığı ve mercimek üretiminde Türkiye'de birinci sırada, mısır üretiminde ikinci sırada, yağlı tohum ve tahıl üretiminde de yine ilk sıralarda yer almaktadır. Ürün desenini incelediğimizde yetiştirilen ürünler üretim miktarları bakımından sırasıyla kırmızı mercimek, pamuk, antep fıstığı, mısır (dane), arpa, buğday, biber, patlıcan ve aspirden oluşmaktadır (Karacadağ Kalkınma Ajansı, 2023b; TÜİK, 2022a). TÜİK'in 2022 yılı verilerine göre Türkiye'nin büyükbaş hayvan varlığının %1,89'u küçükbaş hayvan varlığının ise %4,13'ü Şanlıurfa ilinde bulunmaktadır (TÜİK, 2022a).

TÜİK'in il bazında gayri safi yurtiçi hâsıla iktisadi faaliyet kollarına göre 2020 yılı GSYH sektörel dağılımında tarım, ormancılık ve balıkçılık sektörünün Şanlıurfa ili toplam GSYH içindeki payı %22,4'tür. Türkiye ekonomisine göre Şanlıurfa'nın tarımsal üretim ile yaratılan değerin, toplam üretim içindeki payı oldukça yüksektir. Tarımsal üretim değeri olarak Şanlıurfa 81 il içinde altıncı sırada yer almaktadır (Karacadağ Kalkınma Ajansı, 2023a).

Şanlıurfa ilinin tarım ve hayvancılıkta sahip olduğu potansiyel ve üretim miktarlarına karşın, TÜİK 2022 yıllık ortalama eşdeğer hanehalkı kullanılabilir fert geliri en düşük olan bölgeler (toplam 26 bölge) içerisinde bulunmaktadır (TÜİK, 2022b). Tarım sektöründe üreticilerin gelirlerinin iyileştirilmesi ve ekonomik olarak faaliyetlerinin devamlılığı, üretilen ürünleri değerinde ve uygun bir pazarlama ağı içerisinde pazarlayabilmelerine bağlıdır. Üreticiler için en uygun ve güçlü bir pazarlama yapısının oluşması ise ancak örgütlenme ile mümkündür. Gelişmiş ülkelerde tarım sektöründe tarımsal örgütlenme başarılı bir şekilde uygulanmakta ve tarım ürünleri bu örgütler aracılığı ile pazarlanmaktadır.

Tarımsal örgütler içerisinde kooperatifler birçok ülkede kırsal ve ulusal ekonominin kalkınmasında büyük rol oynamaktadır (Banaszak, 2008; Çıkın, 2016; Helmberger, 1966; Ribašauskienė ve diğerleri, 2019; M. R. Sevinç, 2021). Türkiye'de ise tarımsal kooperatiflerin sayısı fazla olmakla birlikte birçoğu fonksiyonel olarak faaliyet göstermemektedir (Çıkın, 2016; G. Sevinç, 2018; M. R. Sevinç, 2021).

Tarım ve Orman Bakanlığı verilerine göre Türkiye'de 2022 yılı itibari ile 1163 sayılı kanun kapsamında 10561 tane tarıma dayalı kooperatif bulunmaktadır (Tarım ve Orman Bakanlığı, 2022). Şanlıurfa İl Tarım ve Orman Müdürlüğü verilerine göre Şanlıurfa ilinde 2023 yılında 89 adet kooperatif bulunmaktır. Ancak Şanlıurfa ilindeki kooperatifler fiili olarak aktif olmayıp pasif durumdadırlar. Bölgeler arasında karşılaştırma yapıldığında Şanlıurfa ilinin bulunduğu Güneydoğu Anadolu Bölgesi tarımsal örgütlenmenin en az olduğu bölgedir. Diğer taraftan Şanlıurfa ili için yapılan araştırmalarda kooperatif tipi örgütlenme modelinin benimsenmesinde, kendi kendine yardım düşüncesine bağlı olarak tabandan oluşması gereken hareketin oluşmadığı ve mevcut kooperatiflerde evrensel kooperatifçilik ilkelerinin geçerli olmadığı görülmüştür (Ayalp, 2020; Efe, 2022; Rastgeldi, 2021).

SAEMAUL UNDONG (YENİ KÖY HAREKETİ) KIRSAL KALKINMA MODELİ

Kore, Güney Kore ve Kırsal Kalkınma Yaklaşımlarının Temeli

20. yüzyılın ortalarında yaşanan (1939-1945) ve günümüzde ülkelerin siyasi ve politik yapısı üzerinde oldukça etkili olan II. Dünya Savaşı sonrasında, dünya ülkeleri kendilerini komünist ve kapitalist olmak üzere iki kutuplu bir soğuk savaşın içerisinde buldu (Cuming, 2010; Jervis, 1980; Sandler, 1999). Savaş döneminde ABD ve Rusya (Sovyet) aralarında yaptığı anlaşma ile Kore'nin kendileri ile beraber İngiltere ve Çin'in de dâhil olduğu dört ülkenin vesayeti altında bir statüye sahip olmasına karar verdiler. Sovyet Rusya'nın 1945 yılında Uzak Doğu Savaşı'na katılması kararı ile beraber Kore 38. Enlem çizgisinden ikiye ayrılarak iki farklı statüye ve yönetim biçimine sahip oldu. Güney Kore'de Mayıs 1948'de ABD gözetiminde yapılan seçim ile "Güney Kore Cumhuriyeti", Eylül 1948'de Kuzey Kore'de Sovyet Rusya gözetiminde yapılan seçim ile de "Kuzey Kore Halk Cumhuriyeti" kurulmuştur (Armaoğlu, 2018; Bulut, 2018; Murat, 2021).

Kore oldukça dağlık bir coğrafyaya sahip, topraklarının yalnızca %22'si ekilebilir durumda olan bir ülkedir. Hava koşullarına bağlı olarak sadece yaz aylarında tarım yapılabilmekte ve mevsimsel işsizliğe ve tarımsal kaynakların yetersiz kullanımına yol açan oldukça soğuk ve uzun süreli kış mevsimlerinde neredeyse hiçbir tarımsal üretim yapılamamaktadır. Dolayısıyla, kalkınma sürecinde, Kore'de refah seviyesinin arttırılması oldukça zor bir mücadele gibi görünmekteydi (Abafita, Mitiku ve Ryang, 2013; Jun, 2019; J.-H. Park, Duan, Kim, Mitchell ve Shibata, 2010).

Güney Kore, Japon kolonisi olduğu dönemde (1910-1945) ve Kore Savaşı (1950) döneminde aşırı derecede gıda kıtlığı sıkıntısı yaşamıştır. 1950-1970 yılları arasında tarımsal politikalar, pirinç üretiminde kendi kendine yeterli olmayı sağlamakla birlikte, öncelikli olarak ülke gıda ambarını oluşturacak olan tahıl üretiminde verimliliği arttırmaya yönelik olmuştur (Jung, 2016). Savaş sonrasında (1950-1953) hükümet kırsal toplum kalkınma programları yürütmeye başlamıştır. Güney Kore Hükümeti 1950'lilerin ilk yarısında, Kore'nin Birleşmesi ve Rehabilitasyonu için Birleşmiş Milletler Komisyonu'nun önerisiyle, savaş sonrası rehabilitasyon programlarının bir parçası olarak, bir kırsal kalkınma hamlesi planlamıştır. 1958'de 2137 köyde modern tarımsal teknoloji, sosyal refah kuruluşları, toplum sağlığı ve hijyenini kapsayan kırsal kalkınma programını uygulamıştır (Asian Development Bank, 2012). Güney Kore Japonya'dan bağımsızlığını 1948 yılında ilan ettiği zaman dünyanın en yoksul ülkelerindendir. Ekonomisinin tarıma dayalı olduğu söylenebilir.

Güney Kore'nin bugünkü başarısının altında Konfüçyüs öğretisini temel alan Park Chung Hee yönetiminin çabalarının oldukça önemli bir yeri vardır. Park Chung Hee yönetimi 1961 yılında askeri bir darbe ile yönetimi ele almıştır. Park Chung Hee yönetimi 1961'den itibaren gıda üretimi ve tarımın modernleşmesine ciddi anlamda öncelik vermiştir (Erkök, 2019; Jung, 2016). Park Chung Hee yönetimi 1962 yılında teknokratlar tarafından görevlendirilmesi yapılan "Ekonomik Planlama Kurulunu" oluşturmuştur. Yine aynı yıl beş yıllık kalkınma planı hazırlanarak öncelikli olarak ekonomik büyümenin sağlanması hedeflenmiştir (Erkök, 2019). İlk hazırlanan kalkınma planının tam uygulanması Kırsal Kalkınma Ajansı'nın kurulduğu 1965'te gerçekleşmiş ve tüm kırsal kalkınma programları Altı Yıllık Kırsal Kalkınma Planı

(1966-1971) altında birleştirilmiştir. Bu plan üç ana amacı içermektedir (Asian Development Bank, 2012):

i. Ulusal kırsal topluluklarda demokratik liderliğin inşa edilmesi,
ii. Tarımsal üretimin modernizasyonu ve işgücü dâhil kırsal kaynakların seferberliği ile aile gelirinin arttırılması,
iii. Köylülerin kendine yardım çabalarının teşvik edilmesi.

Amaçların tek taraflı ve aynı anda 33100 köyde uygulanılmasından dolayı, planın uygulanılmasında çok istekli olunmasına rağmen tüm amaçlar yerine getirilememiştir (Asian Development Bank, 2012).

Kore Hükümeti 1967'den itibaren ikincil sanayiler ve ihracata yönelik endüstrileşmeye odaklanmıştır. Bu strateji kırsal alanda tarımsal geliri arttırmaya, tarım ve sanayinin eş anlı gelişimine ve tarım sektöründe üretimi arttırarak kendi kendine yeterliliği sağlamaya önem veren bir stratejidir (Jung, 2016). Hükümetin sanayileşmeye yönelik 1. Beş Yıllık Kalkınma Planı (1962-1966) kentsel gelirlerde ciddi anlamda artışı sağlarken, sonrasında kırdan kente hızlı göç ile beraber kırsal ve kentsel gelirler arasında büyük dengesizliğe yol açmıştır (Asian Development Bank, 2012). Sonuç olarak Kore hükümeti bu dönemde tarımsal gelir artışıyla birlikte endüstrinin gelişimini de sağlamıştır.

Kore hükümeti tarafından 1960'larda başlatılan ihracata yönelik sanayileşme politikası sonucu, tarım sektörü ortalama yıllık büyüme oranı %3,5 iken sanayi sektörü büyüme oranı %9,6 olmuştur. Kırsal alanların sosyal ve ekonomik durumları oldukça kötüye gitmiştir. Devletin finansal kaynaklarını kısıtlaması ve kent-kır arasındaki bu büyük açığı gidermek için büyük miktarda gerekli olan sermaye ihtiyacını karşılayamaması, sürdürülebilir ekonomik kalkınmayı tehdit eden ve sosyal çatışmayı arttıran iç pazarda tüketici piyasalarında düşüşe ve gıda ithalatının artmasına yol açmıştır (Zhang ve Li, 2019). Kırsal ve kentsel alanlarda gelir artış oranları arasındaki dengesizlik, Park Chung Hee yönetiminin birinci ve ikinci beş yıllık kalkınma planlarında, kentsel sanayileşmenin yanında aynı anda kırsal kalkınmanın da sağlanması anlayışına yöneltmiştir (Asian Development Bank, 2012).

Saemaul Undong (Yeni Köy Hareketi)

1960'larda Güney Kore nüfusunun büyük çoğunluğunu kırsal nüfus oluşturmaktadır. 1970 yılında kırsal nüfus oranı ise %59,3'tür. Güney Kore kırsal nüfusunun büyük çoğunluğu son derece yoksul bir hayat sürmektedir. Kırsal hane halkının %27,9'u mutlak yoksulluk içerisinde yaşamaktadır (Han ve Claassen, 2017).

Bu dönemde Güney Kore kırsalında köylülerin çoğu elektriği olmayan, çatısı kamıştan yapılmış evlerde yaşayan, düşük gelirli küçük çaplı çiftçi ailesiydi. Kırsal nüfus sağlık hizmetleri dâhil birçok kamu hizmetinin olmadığı, düşük verimlilikte üretim koşullarında, kaynak erişimini sınırlı olduğu, altyapının neredeyse bulunmadığı köylerde yaşamaktaydı. Halk arasında alkolizm, kumar, sinizm, umutsuzluk yaygındı. Kırsaldaki tüm bu olumsuzlukları giderebilmek ve kırsalda kalkınmayı sağlayabilmek amacıyla Saemaul Undong (Yeni Köy Hareketi) başlatıldı (Abafita ve diğerleri, 2013; Asian Development Bank, 2012; Han ve Claassen, 2017).

Saemaul Undong 1970'lerde Güney Kore'de ulusal kırsal kalkınma programı olarak oluşturulmuştur. Temmuz 1969'da Güney Kore'de, bazı köyleri enkaz haline getiren şiddetli

sel felaketi sonucu tetiklenmiştir. Sonrasında, Cumhurbaşkanı Park Chung Hee, ülke genelinde, Gyeongsang ilinin kuzeyinde bulunan Chung-do köyünü de kapsayan ve ağır derecede hasar gören yerleri ziyaret etmiştir. Bu sırada Chungdo köylülerinin ortaklaşa olarak, selden hasar gören bağlantı yollarını onardıklarını gözlemlemiştir. Bu gözlem, cumhurbaşkanı Park için, kendine yardım düşüncesini ülke genelinde yaygınlaştırmak için ilham kaynağı olmuş ve 1970 yılında Saemaul Undong'u başlatma amacı ortaya çıkmıştır (Jwa, 2018; S. J. Lee ve Kim, 2017; Zhang ve Li, 2019).

Hükümetin sel felaketi sonucu ortaya çıkan kıtlığın olumsuz etkilerini önleyebilmek amacıyla 22 Nisan 1970'de yerel yönetim tarafından bir toplantı düzenlemiştir. Toplantıda Cumhurbaşkanı Park, çocukluğuna ait köy hikâyesini anlattıktan sonra sel felaketinde şahit olduğu kendine yardım, dayanışma ve işbirliği erdemlerinden bahsetmiştir. Cumhurbaşkanı, çiftçileri teşvik edici sözcüklerle çağrıda bulunmuştur (Jwa, 2018; C.-N. Kim, 2011; S. J. Lee ve Kim, 2017). Cumhurbaşkanı Park'ın toplantıda; "Yoksulluktan kaçınmak için kendi kendinize yardım ediniz. Ne sorumluluğu başkalarının üzerine atarak, devleti yeterince yardım etmemekle suçlayarak ne de yoksulluğun kaderiniz olduğuna inanarak yoksulluktan kurtulamazsınız. Biz devlet olarak kendine yardım etmek istemeyene yardım edemeyiz. Herkes, çiftçiler, yerel yönetimler, tarım işçileri bir araya gelerek Yeni Bir Köy (Saemaul Undong) inşaa etmelidirler" sözleri ile hareketin başlangıcına dair ilk adımı atmıştır (C.-N. Kim, 2011).

Saemaul Undong'un özü, kırsalda yoksulluğun ortadan kaldırılması ve refah seviyesinin arttırılmasında çiftçilere yardım ederek, aynı zamanda köylülük ruhunu yücelterek, yeniden yapılanma ve yaratıcılık ruhunu oluşturarak yeni bir kırsal alan inşa etmek ve geliştirmektir. Sürdürülebilir kırsal kalkınma ile kırsal ve kentsel alanların koordineli olarak kalkınması sağlanması da hedefler arasındadır (Reed, 2010; Zhang ve Li, 2019).

Saemaul Undong'un ilk hedefi, kırsal kesimdeki insanları çalışkanlığın, kendi kendine yardımın ve işbirliğinin faydaları konusunda ikna ederek zihniyetlerini değiştirmek olarak belirlemişti. Sonrasında ise kırsal köylüler arasında katılımcı bir yaklaşıma ve toplum temelli liderliğin teşvik edilmesine yönelik topluluk örgütlenmesinde değişiklikler yapmaktı. Saemaul Undong'un üçüncü hedefi ise kırsal altyapıyı iyileştirmek ve çiftçilerin ekonomik getirisini artırmaktı. Kısacası hareket, kırsal toplulukların geçim koşullarını iyileştirmeye yönelik entegre bir programdı (Jwa, 2018; Reed, 2010; UNDP, 2015). Saemaul Undong'un hedeflerinin nasıl tanımlanacağı konusunda farklı yorumlar olsa da çoğu kişi amacın ekonomik, sosyal ve davranışsal iyileştirmeler yaratmak olduğu konusunda hemfikirdi. En geniş kabul gören hedefler şunlardır (S. Park, 2009):

i. Gelir yaratma,
ii. Yaşam ortamı ve temel kırsal altyapının iyileştirilmesi,
iii. Kapasite geliştirme ve tutum değişikliğidir.

Saemaul Undong kırsal kalkınmaya yönelik farklı bir model geliştirmiştir. Modelde çok katmanlı bir yapının oluşturulması, yukarıdan başlayarak aşağıya doğru uzanan komuta ve kontrol birimlerinin bulunduğu, bununla birlikte kırsaldaki doğal liderlerinde sürece entegrasyonunun sağlandığı bir örgüt yapısı üzerinde durulmuştur. Bu örgüt yapısı özetle devlet ile kırsal toplumun uyumlu çalışmasının ya da entegrasyonunun temsili olacaktır. Örgütsel yapının arkasındaki fikir hareketi salt devlet eliyle yapılan bir uygulamadan ziyade,

kırsal toplum ile devlet kurumlarının eş güdümlü çalışmasına teşvik edilmesidir (Abafita ve diğerleri, 2013; Jwa, 2018; S. Y. Lee, 2019). Bu amaçla Park Chung Hee Hükümeti öncelikli olarak İçişleri Bakanlığı'na bağlı "Saemaul Undong Bürosu" kurulması talimatını vermiştir. Bu büro Saemaul Undong'un bütün hedef ve politikalarının ortaya çıkarılmasından, sahada uygulanıp kontrol edilmesine kadar hemen hemen her süreçten sorumludur (S. Y. Lee, 2019).

Saemaul Undong Bürosu aracılığıyla, Saemaul Undong merkezi hükümetin bakanlıklarının yanı sıra tüm merkez ve taşra teşkilatının dâhil olduğu, hükümet yönetiminin tüm düzeylerini içeren bir yapı haline bürünmüştür. Bu yapı idari piramit aracılığıyla hiyerarşik bir şekilde yönetilmiştir. Bu hiyerarşik idari yapıya uygun olarak hükümet, köylüleri ve işçileri hükümet yönetiminin her düzeyinde harekete geçirmek için hükümet-sivil komiteler kumuştur (Asian Development Bank, 2012; S. Park, 2009; Reed, 2010).

Saemaul Undong'un en alt seviyesinde köy idaresi olan ri/dong kalkınma komitesi (köy komitesi), Saemaul Undong projelerini, hem devlet tarafından hem de köylüler tarafından seçilen Saemaul Liderlerinin birlikte atadığı köy şeflerinin liderliğinde uygulamıştır. Up/myon uygulama komitesi (kasaba komitesi) Saemaul liderleri ve yerel yönetim ofislerinin danışmanlığındaki topluluk üyeleri tarafından belirtilen Saemaul Undong proje uygulamalarında ortaya çıkan sorunlara çözüm üretmeye çalışmışlardır. İlçe komitesi, belediye başkanı ve yerel idari yetkililerin rehberliğinde bölgesel topluluk düzeyinde Saemaul Undong'a rehberlik etmiş ve koordinasyon sağlamıştır. İl komitesi, vali, il idaresi ve vali yardımcısı, üniversite profesörleri, tarım ve balıkçılık kooperatifleri il yöneticileri, yerel yayın kuruluşları yöneticileri ve müfettişlerin de dâhil olduğu eğitim liderlerinin rehberliğinde ilgili ildeki Saemaul Undong için kapsamlı plan oluşturmuştur (Asian Development Bank, 2012; Jwa, 2018; K.-D. Kim ve Kim, 1977). Kırsal topluluklardaki Saemaul Undong projelerinin finansmanı hükümet kontrolündeki Ulusal Tarım Kooperatifi Federasyonu ve Ulusal Balıkçılık Kooperatifi Federasyonu'nun yanı sıra kamu mali kurumları tarafından sağlanmıştır (Asian Development Bank, 2012).

Saemaul Undong'un (Yeni Köy Hareketi) Etkileri

Saemaul Undong temel olarak köy halkını çalışkanlık, kendi kendine yardım etme ve işbirliği ruhunu geliştirmek için cesaretlendirmiştir. Bunun sonucunda Saemaul Undong, Güney Kore halkının düşünce yapısını kronik yenilgi duygusundan yeni umuda, daha iyi bir vizyona ve yüksek coşkuya çeviren yapabilirim ruhunu besleyerek ulusal sosyal sermaye inşa etmiştir (Fitria, Hwang ve Shin, 2021).

Saemaul Undong, 1970'li yıllarda endüstriyel gelişmeyle biriken kaynakları kullanarak, kırsal ile kentsel alan arasındaki gelişmişlik farkının azaltılması amacıyla ortaya çıkmıştır. 1970 yılında hükümet çimentonun aşırı üretimine ilişkin bir rapor almış ve üretim fazlasının kırsal kesimdeki halka dağıtılması için hızlı bir plan hazırlamıştır. Hükümet ilk olarak 34655 tarım ve balıkçılıkla uğraşan köylerin her birine 355 paket çimentoyu toplum refahının arttırılması amacıyla kullanılması koşuluyla ücretsiz olarak dağıtmıştır. Çimentoyla birlikte köylere ulaşım yolları, küçük köprüler, çatılar, kuyular, hamamlar ve yıkama alanları ile dere bentlerinin inşası da dâhil olmak üzere köylerin üstlenebileceği yaklaşık 20 proje fikri sunulmuştur. Plan kamuoyunda olumlu tepki almış ve Hükümetin öngörüsünün ötesinde önemli sonuçlar elde edilmiştir (C.-N. Kim, 2011; K.-D. Kim ve Kim, 1977; S. Y. Lee, 2019; Moore, 1985; S. Park, 2009).

Newsweek, 17 Kasım 1975'te Saemaul Undong'un bazı etkileyici sonuçlarını (s. 19-20) şöyle bildirmiştir (Jwa, 2018): "Başkan ve Saemaul liderlerinin açıkladığı gibi, programın amacı Güney Kore ruhunu yeniden canlandırmak, Güney Kore'yi teşvik etmektir. Ulusal birlik ve kalkınma için kendi kendine yardım ahlakını aşılamaktır. İstatistiksel olarak sonuçlar etkileyicidir. Hareket, yaklaşık 16000 köyün su tedarik sistemlerini iyileştirdiğini, binlerce köy toplantı salonu inşa ettiğini ve bazen köylülerin istekleri dışında bir milyondan fazla sazdan çiftlik evinin çatısını modern kiremitle değiştirdiğini iddia etmektedir. Saemaul kırsaldaki tarıma dayalı küçük ev işletmelerinde, hane başına düşen kırsal gelirin 1970'te 747 ABD dolardan 1974 yılında 1760 ABD dolara yükselmesine yardımcı olmuştur."

Saemaul Undong aracılığı ile kırsal alanlarda fiziki altyapıların yenilenmesi, üretimde yeni teknolojilerin kullanılması, pazara olan ulaşım kanallarının iyileştirilmesi sağlanmıştır. Böylelikle kırsalda refah ve gelir seviyesinde olumlu değişimlerin yaşanması sağlanmıştır. Kırsal alandaki mutlak yoksulluk oranında 1970'den 1978 e gelince azalma yaşanmıştır. Kırsaldaki hane geliri 1970'den 1978'e gelinceye kadar yaklaşık altı kat artış göstermiştir. Diğer taraftan kırsal kesimde yaşayanların gelir kaynakları da çeşitlenmiş ve tarım dışı gelirin payı da artış göstermiştir (S. Y. Lee, 2019; Moore, 1985; S. Park, 2009). Güney Kore İçişleri Bakanlığı'nın (1980) raporuna göre 1977 yılına gelindiğinde köylerin %98'i "kendi kendine yetebilir" hale gelmiş, kentsel ve kırsal alanlar arasındaki gelir farkı daralmış, böylece kırsal alanlarda hane başına düşen gelir 1974'ten itibaren kentsel alanları geride bırakacak şekilde artmıştır (Jwa, 2018).

Saemaul Undong eğitimlerine 1972'den 1979'a kadar 500 bin kişiden fazla 1981'e gelindiğinde 800 bin kişiden fazla katılım olmuştur. Saemaul Undong liderlerine göre bu eğitimler köylüler arasında işbirliği ruhunu geliştirmiş, üretimde yeni teknolojilerin öğrenilmesini sağlamış, üretimde verimlilik ve kaliteyi arttırmış, köylülerin öz güvenini arttırarak geleceğe dair daha umutlu olmalarını sağlamıştır (Asian Development Bank, 2012; K.-D. Kim ve Kim, 1977; S. Park, 2009; UNDP, 2015).

SONUÇ VE ÖNERİLER

Kırsal alanlarda nicelik ve nitelik bakımından olumlu yönde değişimlerin yaşanması bir ülkenin genelini etkileyebilecek bir sürecin başlaması demektir. Güney Kore'de 1970'lerde başlayan Saemaul Undong günümüz dünyasında güçlü bir ekonomiye sahip Güney Kore'nin inşasının ilk adımı olarak gösterilebilir. Kırsal alanda uygulanacak toplum temelli kırsal kalkınma yaklaşımlarının ne kadar başarılı olabileceğinin de ispati niteliğindedir. Saemaul Undong bugün gelişmekte olan birçok Asya, Afrika ve Latin Amerika ülkesinde başarı hikâyesi olarak anılan, kendi ülkelerinin ekonomik ve sosyal yapısına uygun olarak revize edilip uygulanmaya çalışılan ve Güney Kore'nin kırsal kalkınmada ulusal markası haline gelen bir projedir.

Saemaul Undong'un Şanlıurfa ili kırsalında kalkınmanın sağlanabilmesine ilişkin model olarak uygunluğunun tartışılması bu çalışmanın ana amacıdır. Şanlıurfa ili kırsalı gerek bitkisel gerekse hayvansal üretimde ciddi bir potansiyele sahiptir. Bu potansiyele rağmen Türkiye'nin yoksulluk sıralamasında üst sıralarda yer almaktadır. Bu tablonun ortaya çıkmasında Şanlıurfa kırsalının toplumsal yapı dinamiklerinin etkisinin olduğu birçok akademik çalışmada belirtilmiştir. Yapılan akademik çalışmalarda ortaya konulan en önemli bulgular; toplumun

eğitim seviyesinin düşüklüğü, sorgusuz biat ile güçlenen aşiret yapısı, değişimlere ve yeniliklere kapalı sosyo-kültürel birikimdir. Bu nedenlerle kırsal alanda kalkınmanın en önemli ayaklarından olan örgütlenmeye ilişkin çabalar ve uygulamalar, Şanlıurfa kırsalında genellikle başarısızlıkla sonuçlanmıştır. Diğer taraftan bu durum değişime zaten kapalı olan toplumda umutsuzluk duygusunun çok daha baskın bir şekilde yaşanmasını ortaya çıkarmıştır. Dolayısıyla kırsal toplumun yoksulluk kıskacından kurtulma çabalarının birçoğu kısır bir döngü içerisinde kaybolup gitmiştir.

Saemaul Undong'u başarılı kılan ilk husus Güney Kore kırsalında toplumun birlikte hareket edebilme davranışını başlatabilmesidir. Şanlıurfa kırsalı açısından bakıldığında yüzyıllardır varlığını koruyan aşiret kültürü, toplumda bireylerin birlikte hareket edebilme kabiliyetini özünde barındırmaktadır. Önemli olan bu birlikte hareket edebilme kabiliyetinin yönlendirilebilmesidir. Saemaul Undong bunu Güney Kore kırsalında yukarıdan başlayarak aşağıya doğru uzanan, güçlü bir hiyerarşik yapı ile başarmıştır. Hiyerarşik yapı içerisinde kırsaldaki bireylere de görev ve sorumluluklar verilmiş ve Saemaul Undong'un bir parçası olmaları sağlanmıştır. Bu hiyerarşik yapı kırsaldaki her bireye verilen eğitimler sayesinde kırsal toplum tarafından benimsenmiş ve sahiplenmiştir. Ayrıca kırsala yapılan yatırımlarda bu sahiplenmeyi pekiştirerek, kırsal toplum ile devlet arasında çok güçlü bir bağın ortaya çıkmasına vesile olmuştur.

Şanlıurfa kırsalında Güney Kore kırsalından farklı olarak devlet otoritesi dışında aşiret otoritesi de hüküm sürmektedir. Dolayısıyla kırsalda olumlu yönde değişimlerin sağlanmasına yönelik atılacak adımların önündeki ilk engel, aşiret otoritesini kaybetmek istemeyen aşiret liderleri ya da bu sistemden fayda sağlayan bireyler tarafından konacaktır. Bu noktada devlet, öncelikli olarak kırsalda otoritesinin varlığını hissettirmelidir. Kırsalda istenilen ya da öncelikli olarak hedeflenen düzeyde gelişim sağlanıncaya kadar, ihtiyaç duyulduğunda aşiret otoritesini kullanabilme yetkisine sahip, toplumsal kalkınmanın öneminin farkında olan kişiler ile uyum içerisinde çalışılmalıdır. Kırsalda yaşayan bireyleri aşiret baskısına maruz bırakan yine bu bireylerin içinden çıkamadıkları yoksulluk kıskacı ve düşük eğitim düzeyidir. Kırsalda toplumsal refah sağlandığında ve eğitim düzeyi arttığında aşiret baskısının da zamanla etkisinin azaldığı görülebilecektir. Ancak bu refah artışı ve yüksek eğitim düzeyi kırsal toplumunun geneline yayılmadıkça, başarılı olma olasılığı düşük olacaktır. Bu amaçla hedefe yönelik başarı olasılığının en yüksek olduğu tarımsal örgütlenme biçimi kooperatifçiliktir. Her ne kadar Şanlıurfa kırsalında kurulan kooperatiflerin tamamı bugün pasif olsa da bu başarısızlığın altına yine Şanlıurfa kırsalının toplumsal dinamiklerinin ve aşiret sistemi varlığının etkisinin olduğu unutulmamalıdır. Dolayısıyla kooperatifçilik çabalarının bu hususların göz önünde bulundurularak ortaya konulması gerekmektedir.

Şanlıurfa kırsalında tarımsal faaliyetler içerisinde bulunan üretici ya da yetiştiriciler, birlikler ve ziraat odaları ile hibe ve destekler dolayısıyla sürekli irtibat halindedirler. Birlikler ve ziraat odaları yarı özerk idari yapıları ile başarı odaklı faaliyetler gerçekleştirme amacında olan bölgedeki aşiret yapısını ve niteliklerini bilen yönetim ve personeli ile aslında üretici ve yetiştiricilerin çok yakından tanıdığı ve güvendiği birimlerdir. Bölgede yapılan akademik çalışmalarda bu görüşü destekler niteliktedir. Dolayısıyla Güney Kore kırsalında başarılı kalkınmanın sağlanmasında önemli bir görev üstlenen "Saemaul Undong Bürosu" tarzında bir yapılanma, birlikler ve ziraat odaları içerisinde kurularak aktif hale getirilebilir. Birlikler ve ziraat odalarında aktif olacak bürolarda devlet tarafından kalifiye personel ataması yapılarak,

bu personele kooperatiflerin kurulmasına ilişkin yetkiler verilebilir. Bu personel üretici ya da yetiştiricilerin kooperatif kurmaları, bu kooperatifi ayakta tutarak ürünlere katma değer yaratacak yatırımların yapılması ve ürün piyasasında rekabet edebilme kabiliyetinin kazandırılması hususunda karar alma ve uygulama mercii olarak görevlendirilmelidir. Bu süreçte kooperatif faaliyetlerine ilişkin yönetim, denetim ve kayıt altına alma işlemleri konusunda üst yetki devlet tarafından atanan bu personelde olmakla beraber kooperatif ortaklarının kendi aralarında seçecekleri az sayıdaki üretici ya da yetiştirici de bahsi geçen işlemlerde gözlemci olarak görev almalıdır. Kooperatiflerin faaliyetlerine başlayıp ekonomik ve sosyal olarak riskli dönem atlatılıncaya kadar bu işlemler devlet tarafından atanan personel tarafından yürütülmelidir. Riskli dönem atlatıldıktan, kooperatifçilik hareketinin ve ilkelerinin üretici ve yetiştiricilerden oluşan kooperatif ortaklarınca benimsendikten sonra evrensel kooperatif yönetim sistemi devreye girmeli ve kooperatifin ortaklara devri gerçekleştirilmelidir.

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BIBLIOMETRIC ANALYSIS OF STUDIES ON BABESIOSIS DISEASE IN VETERINARY MEDICINE

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ABSTRACT

Babesiosis is typically characterised by fever and intravascular haemolysis leading to progressive anaemia, haemoglobinuria and, jaundice. Babesia species can vary according to climatic conditions. Babesiosis is transmitted to humans through the bite of an infected tick, but can also be transmitted through blood transfusion and transplacental transmission from mothers. In this study, we aim to reveal the intellectual, social and, conceptual structure of the field by performing a bibliometric analysis of studies on Babesiosis. For this purpose, the term "Babesiosis" is searched in the Web of Science database and articles in the field of veterinary sciences in English are included in the study. In the 43 years from 1980 to 2023, a total of 1000 articles are written on the subject. The number of authors is 3489 and the number of single author studies is 55. The number of citations per article is 20.11 and the total number of references is 17303. When the leading journals in the field are evaluated in terms of the h-g-m index, the two journals with the highest h and g index are Veterinary Parasitology and Journal of Medical Entomology. The two journals with the highest m-index are Veterinary Parasitology and Journal of Veterinary Internal Medicine. When the authors are ranked according to the h-g-m index, the three authors with the highest h-index are Remo G. Lobetti, Linda S. Jacobson and, Vladimir Mrljak. The three authors scoring the highest according to the m-index are Vladimir Mrljak, Renata Barić Rafaj and, Amelia Goddard. The three authors with the highest g-index are Vladimir Mrljak, Ikuo Igarashi and, Remo G. Lobetti. When the universities with the highest number of publications in this field are examined, University of Pretoria, Obihiro University of Agriculture and Veterinary Medicine and, University of Zagreb are in the top 3. The countries with the highest number of studies on Babesiosis are USA, South Africa and, Japan. Countries with a multiple country publication (MCP) rate of 50% and above are those with a high level of international collaboration on babesiosis research. The United Kingdom is identified as the country that has exceeded this threshold. When analysing the most frequently used keywords, Babesiosis with 208 repetitions, Babesia and dog with 90 repetitions, Babesia Canis with 85 repetitions and, cattle with 76 repetitions took the top 5 positions. When the results are evaluated, since Babesiosis is affected by seasonal conditions, South Africa came to the forefront in this field. When the studies in this area are evaluated by species, it is found that there are more studies on dogs and cattle than on other species.

Keywords: Babesiosis, Babesia, Babesia Canis, Dog, Cattle

NUTRITIONAL ANALYSIS OF FRESH BANANA FRUITS (MUSA SPP.) GROWN IN SOUTH TUNISIA

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Abstract

Partial nutritional analysis including total polyphenols, vitamin C, total soluble solids (°Brix), soluble sugars and mineral constituents carried out for the banana fruits derived from six triploid Musa accessions grown in coastal oasis of south of Tunisia. Results showed that pH values ranged from 5.44 to 6.01. The °Brix values varied between 4.00 g/100 g (Fresh weight) FW in 'Arbi IRA', and 1.33 g/100 g FW in 'Lobnani'. Carbohydrates were quantified in all tested samples of the six accessions of banana fruits whereas sucrose was detected only in four accessions. The highest values of glucose, fructose and sucrose were 2.7, 3.37and 1.8 g/100 g FW, respectively. Total polyphenols content ranged from 46.0 to 55.08 mg GAE /100g FW. Vitamin C was detected in smaller quantity. Regarding the mineral composition K, Mg and P were found in relatively large quantities in banana fruits whereas the levels of Na and Ca were medium. Significant disparities were detected in mineral contents of banana samples. The micro-elements composition such as zinc, copper, iron and magnesium varied according to the tested accessions. The analysis showed a high Fe content of up to 1945 mg/100g dried matter. Therefore, banana fruits exhibited to provide recommended daily supplies of Fe, K and other mineral elements.

Key words: Musa, Banana, South Tunisia, Chemical content, Minerals.

PLANT EPIGENETIC RESEARCH: CONTRASTING WGBS WITH BISEQ

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ABSTRACT

The genome employs both epigenetic and genetic pathways to generate responses to various internal and external stimuli. Epigenesis refers to the process by which chemical modifications occur in the genome, as well as changes in chromatin structure, that are independent of alterations in the DNA sequence. DNA cytosine methylation is a crucial epigenetic mechanism that regulates all genetic processes, including gene transcription and transposition, DNA replication and repair, cell differentiation, gene silencing, and imprinting. It also influences vernalization, heterosis, drought and salt tolerance, biodefense, transgenic expression, and the expression of foreign DNA in cells. Cytosine methylation is a prevalent occurrence in plants, typically shown in three distinct sequences. These sequences are CG, CHG, and CHH (where H represents A, C, or T). Two approaches are often used to study DNA cytosine methylation. WGBS is a second next-generation sequencing technique, and BiSeq was initiated using the Sanger sequencing. We employed BiSeq in a number of plant species, including cotton, and we are preparing to apply the WGBS approach to study plant epigenetics. In this work, we compared benefits and drawbacks of the WGBS and BiSeq approaches. In summary, both of the methods start with the use of sodium bisulfite treatment of genomic DNA, the number of targets greatly differ, BiSeq usually involves in cloning and Sanger sequencing. The process of WGBS begins with the random fragmentation of DNA into tiny pieces in the presence of a spike, to which adapters are ligated. NGS technologies are used to sequence size-selected library fragments. Despite having significant differences, these two sequencing methods might be applied to the same study. With the aid of tables and figures, we address a few technical features of these bisulfite sequencing techniques in the current work.

Keywords: BiSeq, 5-methylcytosine, methylation, NGS, PCR, sequencing

INTRODUCTION

Today, technological advancements have presented unparalleled prospects for the surveillance of chromatin changes, gene expression, and genomic structure. The initial documentation of various conventional epigenetic phenomena, like as transposable element inactivation, imprinting, paramutation, transgene silencing, and co-suppression, primarily originated from studies conducted on plants. The integration of classical genetic investigations with recently developed sequencing technology has enabled the examination of several epigenetic phenomena with an unprecedented level of precision, a capability that was previously inconceivable until recent years. The current period presents a stimulating opportunity to engage in the research of plant epigenetics (Olkhov-Mitsel & Bapat, 2012; Hernandez et al., 2013; Kurdyukov & Bullock, 2016; Beck et al., 2021; Ince & Karaca, 2021).

The term 'epigenetic' pertains to heritable patterns of gene expression that are determined by the gene's DNA sequence. The investigation of plants has yielded a multitude of significant contributions to the discipline of epigenetics. The prevalence of epigenetic regulation in plants can be attributed to their specific patterns of development, lifestyle characteristics, and evolutionary trajectory. Plants rely significantly on alterations in gene expression to effectively react to environmental stimuli, and it is highly probable that the regulation of gene expression by chromatin changes plays a pivotal role in these responses. Furthermore, it has been shown that plants have a decreased level of chromatin "resetting" during the process of sexual reproduction in comparison to animals. This particular trait has the potential to facilitate the transfer of epimutations that are acquired over the lifespan of plants. Moreover, a significant proportion of plant species has the capacity for asexual reproduction, leading to the generation of vegetative clones. The mechanism presents promising pathways for the propagation of epigenetic states via mitotic inheritance, finally culminating in the emergence of notable characteristics. The investigation of epigenetics in plants holds significant scholarly significance (Kurdyukov & Bullock, 2016; Ince & Karaca, 2021; Karaca & Ince 2023; Van Antro et al., 2023).

The genome employs both epigenetic and genetic pathways to generate responses to various internal and external stimuli. Epigenesis refers to the process by which chemical modifications occur in the genome, as well as changes in chromatin structure, that are independent of alterations in the DNA sequence. These modifications and structural changes are a consequence of cells or tissues detecting and responding to signals generated by environmental factors or internal signals. The resulting information is then encoded in the epigenome. The primary hypothesis posited in the project proposal asserts that the genome effect plays a crucial role in influencing the epigenome. Furthermore, it is postulated that the manipulation of the epigenome is feasible, and that valuable insights into the fundamental principles of epigenome engineering can be accumulated. The ramifications of epigenesis provide challenges of an intricate kind due to its deviation from the criteria outlined in the modified central dogma of molecular biology (Ince & Karaca, 2021; Sun et al., 2022; Agius et al., 2023; Karaca & Ince 2023; Van Antro et al., 2023).

The responsibilities of a genome encompass generating a comprehensive reaction to various internal and external stimuli, overseeing the functioning of the host cell through this response, and, when required, safeguarding and transmitting genetic material to ensure the

perpetuation of future generations. The functions carried out by the genome are accomplished through the utilization of both epigenetic and genetic mechanisms (Ahn et al., 2017; Crespo-Salvador et al., 2018). The process of epigenesis is believed to encompass a sequence of cellular processes that can give rise to a novel phenotype. This occurs through chemical modifications that occur independently of alterations in the DNA sequence, as well as changes in the structure of chromatin. These modifications are triggered by signals originating from either the environment or internal factors, which are detected by the cell or tissue and subsequently elicit a response (Gapper et al., 2014).

The epigenetic result is determined by the presence of epialleles. An epiallele refers to a heritable variation in chromatin structure that results in a persistent allelic difference. According to Eichten et al. (2014), classification of epialleles can be categorized into three distinct states: pure, selective (facilitate), and obligate (obligate) epialleles. The pure epiallelic state is characterized as an epiallelic condition that is wholly autonomous from genetic information, whereas the obligatory epiallelic state is contingent upon genetic variation. The condition of facultative epiallele status refers to the situation in which genetic variation has a role in determining the alternative chromatin state. The term "chromatin state" encompasses various components such as histone variations, histone modifications (such as methylation and acetylation), DNA methylation, and impacts and modifications of small RNA molecules (Eichten et al., 2014).

DNA methylation is a prominent method of epigenetic diversity in eukaryotic genomes. It involves the enzymatic alteration of DNA and chromatin. Special methyltransferases could methylate nuclear DNA (nDNA). The predominant form of DNA methylation involves the addition of a methyl group (-CH3) to the C5 site of cytosine. Cytosine methylation is a prevalent occurrence in plants, typically shown in three distinct sequences. These sequences are CG, CHG, and CHH (where H represents A, C, or T). The process of DNA hypermethylation, mediated by methylase enzymes, has been found to be associated with the suppression of gene expression in promoter regions, but it is associated with gene activation in coding sequences (Ince & Karaca, 2021; Karaca & Ince, 2023).

DNA cytosine methylation has a role in the activation of transcription and the regulation of gene expression after transcription. The condition of methylation is characterized by its dynamic nature, as the actions of methyltransferases can be counteracted by demethylases, hence allowing for reversibility. In addition to protein enzymes, short RNAs have a role in the process of DNA methylation through the mechanism known as RNA-guided DNA methylation (RdDM) (Yaari et al., 2019).

This article provides a concise introduction to DNA methylation determination methods and compares the merits and drawbacks of bisulfite sequencing with whole genome sequencing techniques.

METHODS FOR DNA METHYLATION ANALYSIS

Currently, a range of techniques are employed to address global and gene-specific cytosine methylation (Figure 1). Methods for analysing DNA methylation in research typically involve the use of restriction enzyme-based, bisulfite-based, affinity-based, or a combination of these methodologies. The determination of methylation can be categorized into three main methodologies, which include the following methods: (i) Bisulfite-based: Whole genome bisulfite sequencing, Reduced representation bisulfite sequencing, Massively Clonal sequencing platforms, Denaturing HPLC, Bisulfite methylation profiling, Bisulfite sequencing, Bisulfite padlock probes (BSPP), Pyrosequencing, Methylation-specific PCR (MSP), Methylation sensitive melting curve analysis (MS-MCA), Methylation sensitive high resolution melting (MS-HRM), Sensitive melting analysis after real-time (SMART)-MSP, Methylation-specific fluorescent amplicon generation (MS-FLAG), Methylation sensitive single nucleotide primer extension (MS-SNuPE), (ii) Affinity-based: Methylated DNA immunoprecipitation (MeDIP), Methylated CpG island recovery assay (MIRA), Methyl binding domain proteins MBD column chromatography, MeDIP-PCR, (iii) Restriction enzymes-based: Restriction landmark genome scanning (RLGS), HpaII tiny fragment Enrichment by Ligation-mediated PCR (HELP), Luminometric methylation assay, Methyl-Seq, Methylation sensitive cut counting (MSCC), Methylated CpG island amplification (MCA), Methylation amplification DNA chip (MAD) and promoter-associated MAD (PMAD), Comprehensive high-throughput arrays for relative methylation (CHARM), Microarray-based methylation assessment of single samples (MMASS), Methylscope, Methylation hybridization (DMH), Methylation SNP (MSNP), Methylation sensitive arbitrary-primed PCR (MS-AP-PCR), Amplification of intermethylated sites (AIMS), TD-MS-RAPD-PCR. Some of these are shown in Figure 1 and Figure 2 according to their usage strategies. Typing and profiling of DNA methylation with these technologies are suitable for high-throughput applications that encompass established and new methods used for (A) identifying DNA methylation and (B) confirming DNA methylation-based biomarkers, while outlining their primary benefits and constraints (Laird, 2010; Olkhov-Mitsel & Bapat, 2012; Karaca et al., 2019; Agius et al., 2023).

The primary consideration is that the selected methodology must provide an objective response to the biological inquiry posed by the researcher. Nevertheless, it is imperative to consider various additional crucial factors in the selection of a DNA methylation analysis method. These factors encompass the objectives of the study, such as the identification of newly occurring epigenetic alterations or the examination of established methylation sites in particular genes of interest. Additionally, the quantity and quality of the DNA sample(s), the desired level of sensitivity and specificity, the reliability and ease of use of the method, the accessibility of bioinformatics software for data analysis and interpretation, the availability of specialized equipment and reagents, as well as the associated costs, all play a significant role in the decision-making process. The researcher can select from different ways based on whether they are studying a gene that is already known or one that is unknown. According to Kurdyukov & Bullock (2016), these methods can be organized and presented in Figure 2.

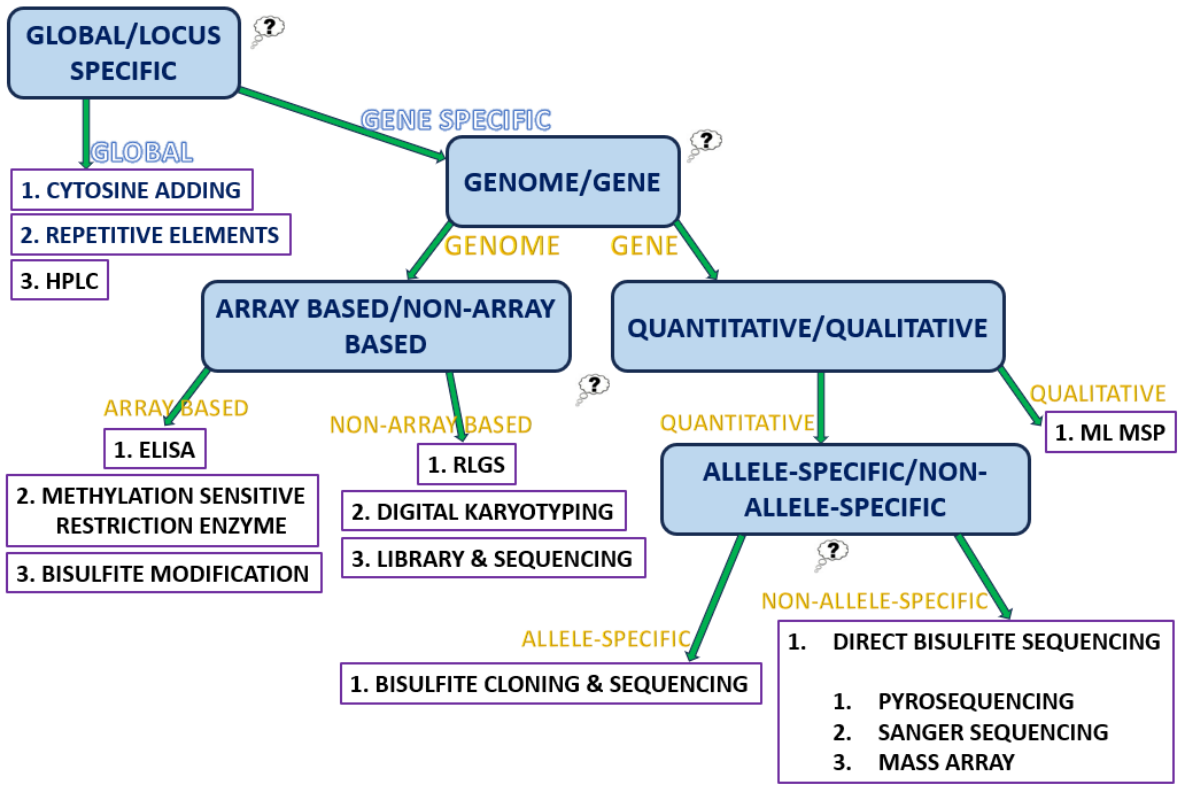

Figure 1. Some methods for DNA methylation analysis.

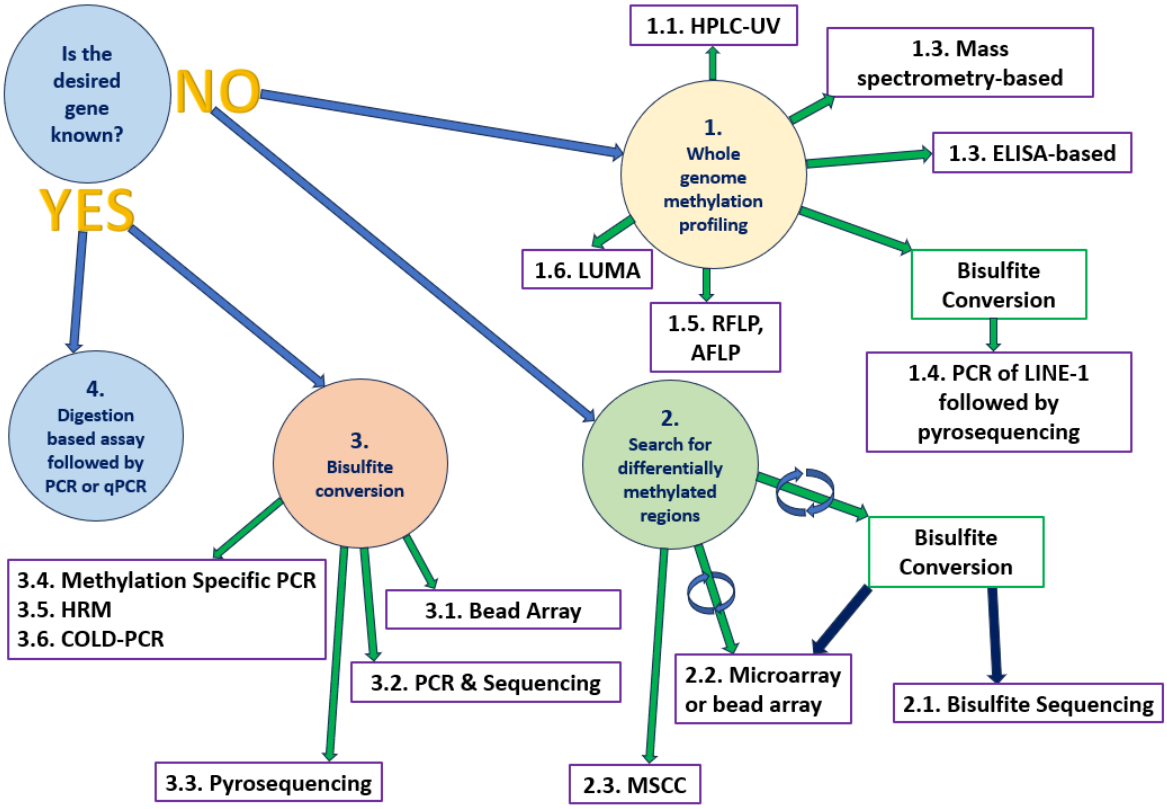

Figure 2. Algorithm for selecting an appropriate approach for analysing DNA methylation adapted from Kurdyukov & Bullock (2016).

Determination of Differentially Methylated Regions and Differentially Methylated Cytosine

The techniques outlined in this article can be employed to ascertain the global alterations in the DNA methylation state of the sample(s) under investigation. Nevertheless, "what is the process of identifying and evaluating particular genes/regulatory areas of interest that exhibit differential methylation?" is an important question. Bisulfite sequencing and whole genome bisulfite sequencing are crucial techniques used to identify Differentially Methylated Regions or Differentially Methylated Cytosine (Karaca & Ince, 2023).

Bisulfite Sequencing (BiSeq)

Existing DNA sequencing technologies lack the capability to differentiate between methyl cytosine and cytosine. The bisulfite-assisted deamination method is widely recognized as the gold standard technique for detecting DNA cytosine methylation (Baumann and Doerge, 2011). This method allows for the determination of the methylation status of individual cytosine nucleotides over the entire genome, making it particularly well-suited for large-scale DNA sequencing approaches. Following the sulfonation events carried out by methyl particles, cytosine sulfonate is formed through bisulfite interaction at the carbon of the cytosine base. Subsequently, the emergence of ammonium takes place, accompanied by deamination breaks. The formation of uracil sulphonate occurs as a consequence of this reaction. During the final process, desulfination reactions occur, resulting in the formation of uracil through the removal of bisulfite (HSO_3) from uracil sulfate. The conversion of uracil within the array is achieved through the utilization of polymerase chain reaction (PCR) (Figure 3). These transformed residues are then interpreted as thymine using PCR-amplification and subsequent Sanger sequencing analysis (Kurdyukov & Bullock 2016; Ince & Karaca, 2021; Karaca & Ince, 2023).

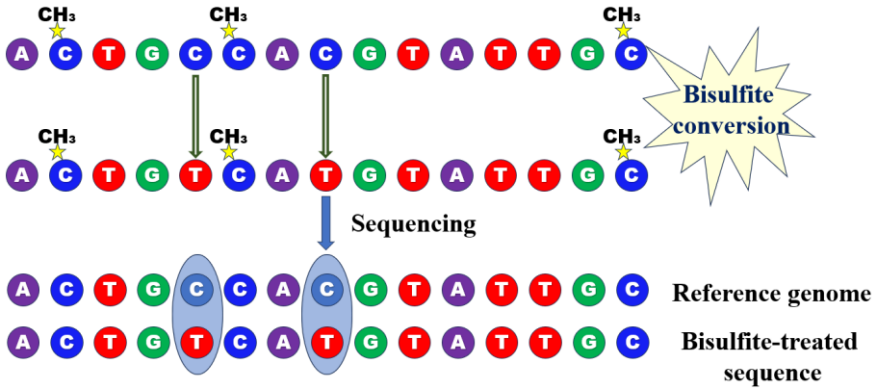

Figure 3. Bisulfite sequencing overview.

In this method, bisulfite application is made after genomic DNA isolation. PCR is performed using bisulfite specific primers. After the PCR process, agarose gel purification is performed. Purified amplicons are transformed and cloned. Finally, DNA sequence is determined (Figure 3). There are several programs such as, KisMeth, CyMATE, etc., for methylation analysis in bisulfite sequencing methods (Ince & Karaca, 2021).

Whole Genome Bisulfite Sequencing (WGBS)

Whole-genome bisulfite sequencing (WGBS), also known as MethylC-seq, is a technique that has the potential to examine every cytosine in the genome at the individual nucleotide level. The WGBS approach allows for the analysis of methylation in all CG, CHG, and CHH context sequences in a genome by examining all the cytosines. WGBS is analogous to whole genome sequencing, except for the bisulfite conversion step. This method is the most thorough among all the ways now in existence. The sole constraints lie in the expenses and challenges associated with the analysis of NGS data. As previously stated, cytosine nucleotides that are not methylated are converted to thymine nucleotides following bisulfite treatment, and assembling DNA consisting of only three bases is extremely challenging.

This procedure entails the extraction of genomic DNA, followed by enzymatic or physical fragmentation (such as sonication or passage through microscopic pores) into segments measuring 200-300 nucleotides in length. Subsequently, the process of bisulfite conversion and cleaning can be carried out. After treating with bisulfite, the fragments are cleaved at the ends, and a single adenine (deoxyadenine) nucleotide is appended and linked to the fragment ends using specific adapters and index sequences. The selection technique relies on the lengths of the fragments, exclusively choosing fragments that possess distinct adapters at both ends. Subsequently, bridge PCR can be performed. The libraries produced are then analyzed using an appropriate next-generation DNA sequencing technique (Figure 4) (Gong et al., 2022; Agius et al., 2023). Recently, this method has been employed in applications such as Adaptase, TruSeq, and SLAT methods.

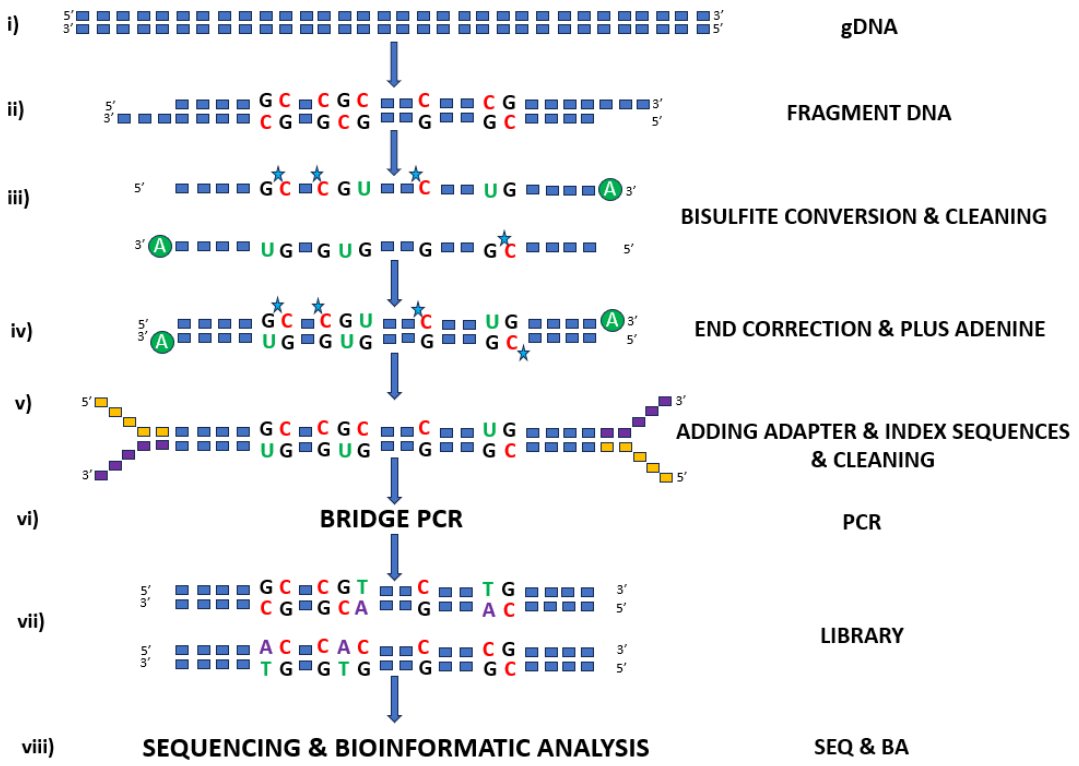

Figure 4. Whole Genome Bisulfite Sequencing steps.

Various programs, including B-SOLONA, BatMeth, BiQ Analyzer HT, BiSeq, BISMA, Bismark, Bis-SNP, Bisulfighter, BRAT, BSMAP, BS-Seeker, DMAP, GSNAP, GBSA, Last, MOABS, MethylExtract, MethylSig, RMAP, SAAP-RRBS, etc., are available for methylation analysis in whole genome bisulfite sequencing (Olkhov-Mitsel & Bapat, 2012; Kurdyukov & Bullock, 2016; Gong et al., 2022; Agius et al., 2023).

CONTRASTING WGBS WITH BISEQ

Bisulfite sequencing method compared to whole genome bisulfite sequencing method, bisulfite sequencing offers the benefit of furnishing more comprehensive and intricate data pertaining to gene body and regulator sequences. Conversely, NGS-based techniques often prioritize depth, coverage, and accuracy. Whole genome bisulfite sequencing method exhibits superior coverage compared to other techniques. In the WGBS method, it is optimal to have a depth of 30 times or greater (Olkhov-Mitsel & Bapat, 2012; Kurdyukov & Bullock, 2016; Gong et al., 2022; Agius et al., 2023).

When the bisulfite sequencing method is examined, the utilization of bisulfite sequencing can present difficulties. Bisulfite PCR leads to challenges in the functioning of target areas, resulting in difficulty caused by BiSeq. Bisulfite conversion decreases the complexity of the genome to only three nucleotides, making post sequence alignment more challenging. Furthermore, the process of bisulfite conversion causes DNA to break apart, which, together with reduced complexity, hinders the amplification of large fragments and may potentially produce hybrid products. Ensuring the full conversion of non-methylated cytosines is of utmost importance, as the predicted degree of DNA methylation relies on it. Hence, it is crucial to include measures to regulate bisulfite reactions and to closely monitor the presence of cytosines in non-CpG locations during sequencing, as this serves as an indication of inadequate conversion. The BiSeq method exhibits greater sensitivity to errors caused by PCR compared to the WGBS method. For a technological standpoint, the BiSeq approach is appropriate for research and laboratories of a smaller scale. Due to the use of purification, transformation, cloning, Sanger DNA sequencing method in the BiSeq method, the study of a low number of genome regions increases the cost of this method (Olkhov-Mitsel & Bapat, 2012; Kurdyukov & Bullock, 2016; Gong et al., 2022; Agius et al., 2023).

The WGBS method is well-suited for laboratories that are both large in scale and complex in nature. The WGBS is a technique that incurs a rather substantial financial investment. Nevertheless, the utilization of WGBS techniques enables the accurate determination of the methylation status of both DNA strands at a resolution of individual bases inside a particular cell or genome, pertaining to a certain stage of development or physiological condition. Furthermore, the utilization of this approach is favoured owing to the ample availability of bioinformatic tools that may aid in the analysis and understanding of WGBS data (Crary-Dooley et al., 2017; Yaari et al., 2019; Shepherd et al., 2022). A previous constraint of WGBS was the need for a substantial quantity of DNA. However, a modification to the protocol, which involved delaying the adaptor ligation step until after bisulfite treatment, enabled the routine use of WGBS with approximately 30 ng of DNA, and in certain instances, as little as 125 pg. Nevertheless, due to the limited proportion of the genome that can undergo differential methylation, WGBS is typically unnecessary. Sequencing the part of the genome enriched with 5-methylcytosine (5 mC) is not only a cost-effective method, but it also enables the

enhancement of sequencing coverage and, consequently, improves the accuracy in identifying differentially methylated areas. Sequencing can be performed using any available NGS technology. Illumina and Life Technologies provide kits specifically designed for this type of study (Tse et al., 2021; Agius et al., 2023).

Compared to the BiSeq method, WGBS method requires a bioinformatics expert and appropriate software programs for its work. While both WGBS and BiSeq post-sequencing analysis share similarities, WGBS analysis necessitates a significant demand for in silico storage capacity due to the exceptionally large volume of data. The utilization of infrastructure and bioinformatics expertise, as well as the storage and transfer of data, contribute to the elevated cost of the WGBS sequencing method. The presence of repeated genomic regions and an abundance of paralogous and analogous sequences diminishes the precision of analysis in WGBS. The abundance of samples with diverse origins poses additional technical challenges in the WGBS method. Moreover, the feasibility of WGBS in small-scale studies is exceedingly limited (Olkhov-Mitsel & Bapat, 2012; Kurdyukov & Bullock, 2016; Gong et al., 2022; Agius et al., 2023).

In the single-molecule real-time sequencing (SMRT) method, the sequence of a single DNA molecule can be extracted using fluorescently labelled nucleotides. Some advantages of the SMRT method in methylation analysis are (i) no need for chemical modification, (ii) no need for DNA amplification, (iii) the amount of DNA required is small, and (iv) the DNA sequence of very long DNA molecules can be extracted.

Nanopore Sequencing is the method in which DNA sequencing is performed by utilizing the ion current strength specific to each nucleotide while passing single-stranded DNA through pores formed from proteins with the help of phage DNA polymerase enzyme, without the need for PCR application. With this method, normal cytosine can be separated from 5-methyl cytosine, as well as other types of modifications (for example, 5-hydroxymethyl cytosine) can be determined. However, this method needs a little more time to be established and reduce the cost.

Two types of algorithms are commonly used in the analysis of bisulfite converted DNA sequences. These algorithms are free card and three-character algorithms. In free card alignment, all "C"s in the sample sequence is replaced by "Y"s. Despite achieving high genomic coverage, high methylation rate error can be achieved. In the three-character algorithm alignment method, all "C"s in the reference genome is read as "T". In this case, genomic coverage decreases (lower capability of mapping). Determining new bioinformatics algorithms for analyses can increase the effectiveness of the methods.

CONCLUSION

Although some next generation sequencing methods such as DNA methylation analyses, single-molecule real-time sequencing and Nanopore technologies offer new opportunities for the identification of new epigenetic markers, they are currently used due to high error rates, high costs and low volumes. Their use is quite limited compared to second generation sequencing technologies due to their processing power (lower throughput). Bisulfite based

methods are still the gold standard in DNA cytosine methylation studies. BiSeq method is the choice of the validation studies of WGBS studies for whole genome sequencing studies. BiSeq studies are also useful for small projects with lower financial supports.

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METHYLATION OF SMALL NUCLEOLAR RNAS IN PIMA-UPLAND COTTON GRAFT

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ABSTRACT

Small nucleolar RNAs (snoRNAs) are widely present in the nucleoli of eukaryotic cells. There are several important processes that snoRNAs are involved in RNA processing, regulation of alternative splicing and performing miRNA-like functions in some transcripts. In one of our ongoing works, we have noted that DNA methylation levels of some snoRNAs were altered in upland-upland grafting of cotton. This study was undertaken to reveal DNA methylation levels of snoRNAs in cotton grafts made using the rootstock of Pima and the scion of upland cotton. Genomic DNA samples of Pima 3-79 (Pima cotton) and TM-1 (upland cotton) were extracted, sequencing libraries were prepared after fragmentation of DNA by sonication and bisulfite treatment. Cluster sequencing analysis was performed on an Illumina NovaSeq 6000 with 150 Gb of 151 bp paired-end sequencing. After processing the raw data, a total of 10,935 snoRNAs, 5,382 of which were located on the forward (+) strand and 5553 of which were located on the reverse (-) strand, were studied between TM-1 (ungraft) and PT, which was a graft of Pima-Upland cotton. Cytosine methylation status of the three contents (CG, CHG, and CHH, where H refers to A, C, or T) of snoRNAs was compared, and studies showed that among the three cytosine contents, there were CG methylation differences between the ungrafted TM-1 and heterografted Pima-Upland, while there were similar CHH and CHG methylation levels. Differently methylated cytosine between ungrafted and Pima-upland graft were also studied. In the present study, the altered methylation status was identified on the mature seeds that were obtained from the mature grafted plants; therefore, these alterations were considered transgenerational methylations.

Keywords: cotton, heterografting, methylation, snoRNAs, transgenerational methylations

INTRODUCTION

Cotton is a soft staple fiber that grows around the seeds of the cotton plants in the genus Gossypium L. The cotton fiber is rich in pure cellulose and contains minor percentages of waxes, fats, pectins, and water in comparison to some other plant fibers. The genus Gossypium has more than 50 diploid and tetraploid species, four of which are cultivated around the world. G. hirsutum L. and G. barbadense L. are tetraploid species that originated in the New World. G. herbaceum L. and G. arboreum L. are diploid species native to Asia and Africa, respectively. Among the four cultivated cotton species, G. hirsutum, upland cotton, is the main cotton species producing more than 95% of cotton fibers. Unlike some other plant species, growing cotton requires multiple management and material inputs with high costs, including seed, pesticide, fertilizer, and irrigation applications. To reduce some of the input of managements, grafting has been suggested for cotton growing (Karaca & Ince, 2023a).

The plant genome has varying kinds of RNAs. Among these RNAs, non-coding RNAs (ncRNAs) are getting more and more attention. Although ncRNA molecules are transcribed molecules from DNA, they are not translated into amino acid sequences. It is well documented in the literature that ncRNAs are one of the key players in post-transcriptional gene regulation (Huang et al., 2022). ncRNAs are generally grouped into small non-coding RNAs (sncRNAs), long noncoding RNAs (lncRNAs), and small nucleolar RNAs (snoRNAs) (Bhattacharya et al., 2016). Apart from snoRNAs, sncRNAs are usually 22 nucleotides long and lncRNAs are greater than 200 nucleotide-long RNA molecules. snoRNAs form an abundant group of ncRNAs, some of which are localized in the cytosol rather than in the nucleus. The presence of some snoRNAs in the cytoplasm suggested that they have some tissue-specific functions. snoRNAs can range from 60 to 120 nucleotides in length and are mainly encoded by intronic regions of both protein coding and non-protein coding genes in genomes.

snoRNAs widely present in the nucleoli of eukaryotic cells can be mainly divided into three types: H/ACA box snoRNAs, C/D box snoRNAs, and small Cajal body specific RNAs (scaRNAs). C/D and H/ACA boxes of snoRNAs are conserved sequence motifs and are used in the classifications of snoRNAs (Bhattacharya et al., 2016; Huang et al., 2022).

Although there have been many studies regarding the function of snoRNA, the methylation status of these RNAs has not been deeply studied in heterografted cotton. The methylation status of an organism is important since DNA and RNA methylation affect housekeeping and the regulatory functions of living organisms. In this study, we made heterograft cotton plants by combining rootstocks of Gossypium barbadense accession Pima 3-79 and scions of G. hirsutum accession TM-1 using a grafting technique previously established in our unit. After whole genome bisulfite sequencing studies, we compared the cytosine methylation status of snoRNAs. Comparative studies showed that among the three cytosine contents (CG, CHG, and CHH, where H refers to any base other than guanine), there were no differently methylated cytosines (dmc) for CHH, while a considerable number of CG and CHG were differently methylated due to heterografting. These findings agreed with the results of methylation differences between homograft and ungrafted cotton (Karaca & Ince, 2023b).

MATERIAL METHODS

Plant Materials

Plant materials consisted of "Texas Marker-1" (TM-1), belongs to Gossypium hirsutum L. and "Pima 3-79", belongs to Gossypium barbadense L. This study was conducted in a greenhouse located in Antalya, on the Mediterranean coast of Turkey. Two weeks after seed sowing, seedlings with two-leaf stage were transferred into a laboratory, where they were acclimated for three days before grafting studies.

Grafting Experiments

Heterografting between Pima 3-79 and TM-1 (Pima 3-79—TM-1) was made using a grafting method described in Karaca et al. (2020). Each plot had 15 heterografted and ungrafted seedlings with three replications.

DNA Extraction

Six randomly selected seeds from TM-1 (control) and heterografts (Pima 3-79—TM-1) were ground to a powder with a mortar and pestle. A DNA extraction protocol previously described in Karaca et al. (2005) was used to extract genomic DNA samples.

Whole Genome Bisulfite Sequencing

Genomic DNA samples were fragmented by sonication to 200–300 bp with a Covaris LE220 sonicator after adding 0.5% (w/w) lambda phage DNA. Fragmented genomic DNA and lambda phage DNA were treated with bisulfite to convert unmethylated cytosines to uracils while retaining those cytosines that are methylated. Reactions were cleaned using the EZ DNA Methylation-Gold kit, and the sequencing libraries were prepared using the Accel-NGS Methyl-Seq DNA library kit (Swift BioSciences, Ann Arbor, MI, USA) according to the library protocol for Illumina platforms. Cluster sequencing analysis was performed by Macrogen Corp. on an Illumina NovaSeq 6000 with 150 Gb of 151 bp paired-end sequencing.

WGBS Data Processing

Raw sequence reads were filtered using Trim Galore (Krueger, 2021). Twenty base pairs were trimmed off from the 3′ ends of R1 and 5′ ends of R2 to eliminate the majority of the adaptase tails after adaptor trimming and reads shorter than 20 bp were discarded. Raw and trimmed sequence reads (forward and reverse) were compared using the FastQC Screen (Wingett and Andrews, 2018) to confirm the quality increase. The bisulfite-treated clean reads in FASTQ format were mapped to the reference genome of G. hirsutum (GCF_007990345.1) using BSMAPz (Zynda, 2018) piped with SAMtools view-bs (Li et al., 2009) to obtain mapped bam files. Bam files contained the number of uniquely mapped reads, non-unique mapped reads, deduplicated reads, and analyzed reads in methylation calling. The evaluation of the quality of the sorted alignment data was performed utilizing Qualimap 2.2 (Okonechnikov et al., 2016). The basic statistics of the alignments (content, mean and standard coverage, insert distribution, etc.) are produced.

In this study, uniquely mapped reads were used in the methyratio.py script within the BSMAPz software to extract methylated and unmethylated cytosines in the three-sequence contexts of CG, CHG, and CHH (where H is any base other than G), along with their coverage profile values. Methylation ratios of every single cytosine satisfying a higher than 1 CT count were called using the methyratio.py program in BSMAPz. During data preprocessing, low

coverage and high coverage bases were filtered using lower and higher cutoff values, 15 and 500, respectively. A lower read cut-off of 10 means that bases with coverage below 10× were discarded because a high enough read coverage will increase the power of the statistical tests.

The bisulfite conversion ratio was calculated using the following formula: Bisulfite conversion rate (%) = # unmethylated read level measurements from the lambda genome/(# methylated and # unmethylated read level measurements from the lambda genome) × 100.

The following conversion rates were obtained: 99.66% for PT and 99.66% for TM-1 (TK) (ungrafted), indicating that a high percentage of unmethylated cytosines were effectively converted (Karaca et al., 2020).

Correlation analyses between samples were obtained through Pearson's coefficient of the MethylRatio values, and it was found that samples had very high correlations. Each cytosine location was annotated using NCBI assembly (GCF_007990345.1 and GCA_008761655.1) data using Linux commands and tools including awk, sed, grep, BEDtools, BEDOPS, deepTools, SeqTK, SeqKit, and SAMtools (Li et al., 2009; Neph et al., 2012; Quinlan & Hall, 2010; Ramirez et al., 2014). Browser extended document (bed) files for further annotated files were made, including the functional location of each snoRNA, gene ID, and strand.

Differently methylated cytosines were identified using Defiant software (Condon et al., 2018). The weighted mean methylation percentage was calculated using the given cut-off of 10% and 10× minimum coverage by utilizing Defiant software (Condon et al., 2018). A p value between samples A and B was calculated by Fisher's exact test using the following formula:

$$p = \frac{(\mathrm{mCA} + \mathrm{mCB})!\,(\mathrm{CA} + \mathrm{CB})!\,(\mathrm{mCA} + \mathrm{CA})!\,(\mathrm{mCB} + \mathrm{CB})!}{\mathrm{mCA!}\,\mathrm{mCB!}\,\mathrm{CA!}\,\mathrm{CB!}\,(\mathrm{mCA} + \mathrm{mCB} + \mathrm{CA} + \mathrm{CB})!}$$

where mC is the number of 5-methyl cytosine and C is the number of cytosine (Condon et al., 2018). After identification of differently methylated cytosines (dmc) as increased or decreased methylation between ungrafted control (TM-1) and heterograft Pima 3-79—TM-1, the GIs were submitted to the Database for Annotation, Visualization, and Integrated Discovery (DAVID) (https://david.ncifcrf.gov/home.jsp) for functional annotation of the gene list (Sherman et al., 2022).

RESULTS AND DISCUSSION

A total of 10,935 snoRNAs were studied, and 5,382 of which were located on the forward (+) strand and 5,553 of which were located on the reverse (-) strand. Results showed that subgenome A had a total of 8,042 snoRNAs, 4,003 of which were located on the forward (+) strand and 4,039 of which were located on the reverse (-) strand. On the other hand, subgenome D had a total of 2,893 snoRNAs, 1,379 of which were located on the forward (+) strand and 1,514 of which were located on the reverse (-) strand. Overall results revealed that subgenome A had more snoRNAs than subgenome D (Figure 1). Studies revealed that the number of snoRNAs was not evenly distributed on the chromosomes of Gossypium hirsutum (Figure 1). The number of snoRNAs in subgenome A was almost 2x greater than the amount in subgenome D. This was not surprising since the genome size of subgenome A is almost twice that of subgenome D.

There were great variations in the number of snoRNAs on chromosomes. For instance, chromosomes A09 and D05 had the lowest number of snoRNAs in subgenomes A and D, respectively. On the other hand, chromosomes A06 and D08 had the highest number of snoRNAs in subgenomes A and D, respectively. The chromosomes A09, D05, A06, and D08 are non-homoeologous; therefore, a higher or lower number of snoRNAs are detected on these chromosomes (Karaca & Ince, 2023b).

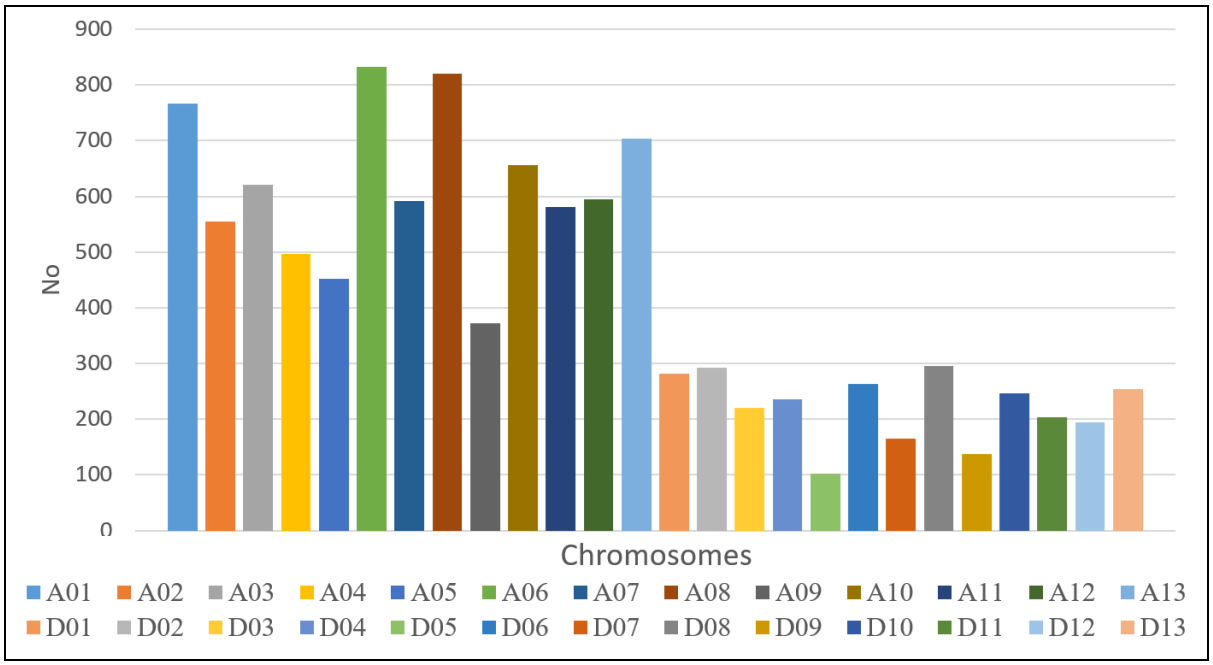

Figure 1. Distribution of snoRNAs on the chromosomes and subgenomes of Gossypium hirsutum.

The methylation alteration of grafting was studied, and the statistics and view of methylation changes between heterograft Pima 3-79—TM-1 and ungrafted TM-1 were showed in Table 2 and Figure 2, respectively.

Table 1. Overall methylation differences between ungrafted and heterografted cotton

Graft	Content	Strand	Methylated (%)
Grafted (Pima 3-79—TM-1)	CG	(+)	75.56
Ungrafted (TM-1 control)	CG	(+)	75.69
Grafted (Pima 3-79—TM-1)	CHG	(+)	**50.81**
Ungrafted (TM-1 control)	CHG	(+)	**48.89**
Grafted (Pima 3-79—TM-1)	CHH	(+)	13.58
Ungrafted (TM-1 control)	CHH	(+)	13.46
Grafted (Pima 3-79—TM-1)	CG	(-)	**78.41**
Ungrafted (TM-1 control)	CG	(-)	**72.85**
Grafted (Pima 3-79—TM-1)	CHG	(-)	**48.69**
Ungrafted (TM-1 control)	CHG	(-)	**51.48**
Grafted (Pima 3-79—TM-1)	CHH	(-)	13.58
Ungrafted (TM-1 control)	CHH	(-)	13.40

Results revealed that there were not statistically significant differences in methylation levels between heterograft and ungraft control for CG and CHH content in forward strands. However, methylation levels in CG content between heterograft and ungraft control for the reverse strand (Table 1). The methylation levels of CHG contents between heterograft and ungrafted control were significant on both strands. Reverse and forward sequences had different methylation levels in CG, CHG, and CHH since they contained different types and numbers of snoRNA genes. All chromosomes had CG, CHG, and CHH methylations in grafted and ungrafted samples. However, CG, CHG, and CHH methylation levels of D11 showed greater variations in comparison to other chromosomes.

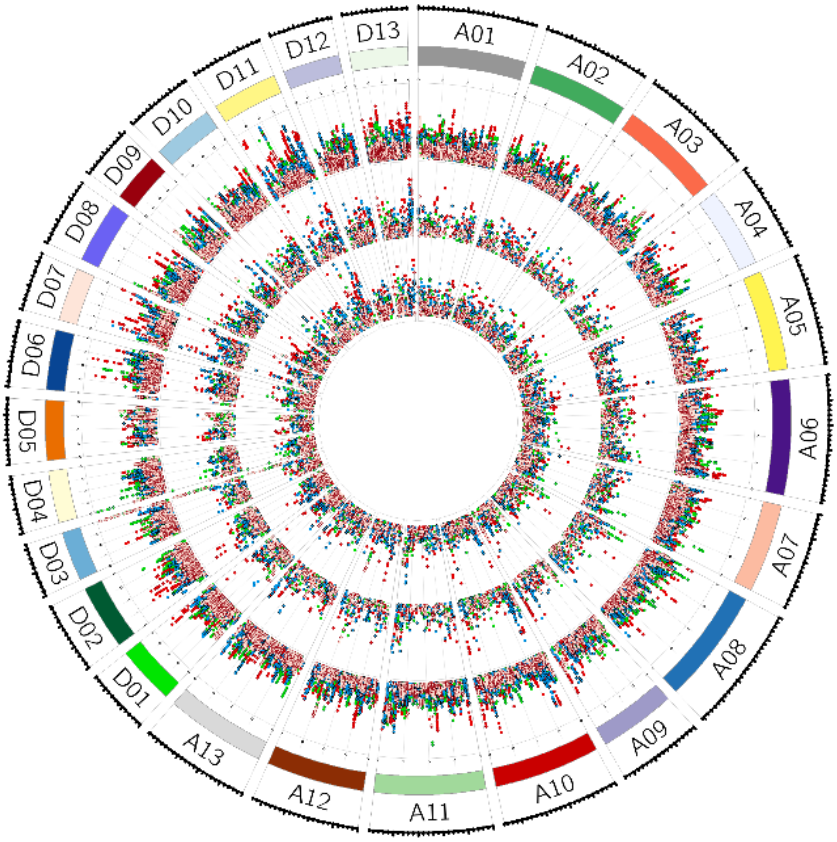

Figure 2. Methylation differences in snoRNA genes between heterograft Pima 3-79—TM-1 and ungrafted TM-1. Circles from inner to outer represented the methylation status of CG, CHG, and CHH, respectively. The colors red and green represented methylations of Pima 3-79—TM-1 on the forward and reverse strands. The colors blue and pink represented methylations of TM-1—TM-1 on forward and reverse strands.

To reveal differently methylated cytosines (DMCs), the method of Condon et al. (2018) was used. Agreeing with the results shown in Table 1, DMC results also revealed that the CG and CHG content of heterograft and ungrafted samples differed. There were 106 DMCs in CG and CHG content between heterograft and ungrafted samples, as shown in Table 2. Among the DMCs, the majority (73.5%) were in CHG content. The number of DMC on each chromosome varied from 1 to 9, but there was at least one DMC on each chromosome (Table 2).

Table 2. Differently methylated cytosines (DMCs) in CG and CHG content between heterograft and ungrafted G. hirsutum TM-1.

Con	Ch	Start	End	Str	Met (%)
CG	A01	43845120	43845121	+	-33.3
CHG	A01	19173630	19173632	-	36.5
CHG	A01	104007146	104007148	-	-48.3
CG	A02	30447502	30447503	+	21.4
CG	A02	95490446	95490447	+	-22.2
CHG	A02	47502542	47502544	+	-31.7
CHG	A02	58001538	58001540	+	-33.7
CHG	A02	18324334	18324336	-	-34.5
CHG	A02	21371899	21371901	-	-29.4
CHG	A02	68029344	68029346	-	-25
CHG	A02	88205838	88205840	-	-37
CHG	A03	15953999	15954001	+	30.7
CG	A04	23380433	23380434	+	33.3
CHG	A04	67294396	67294398	+	41.7
CHG	A04	80210225	80210227	-	25
CG	A05	14824058	14824059	+	27.3
CHG	A05	62593611	62593613	+	-29.4
CG	A06	5151867	5151868	+	21.4
CHG	A06	22651503	22651505	+	-61.8
CHG	A06	58467609	58467611	+	37.1
CG	A07	69519599	69519600	+	33.3
CHG	A07	36358475	36358477	+	39.3
CHG	A07	70755471	70755473	+	35.3
CHG	A07	49450720	49450722	-	-44
CHG	A08	13504848	13504850	+	-38.5
CHG	A08	18476135	18476137	+	43.3
CHG	A08	13758392	13758394	-	-26.7
CHG	A08	114234847	114234849	-	-31.7
CHG	A09	34712572	34712574	-	-40.1
CG	A10	85317064	85317065	+	26.7
CHG	A10	15285983	15285985	+	50
CHG	A10	94020345	94020347	+	-44.2
CHG	A10	21713665	21713667	-	60.3
CHG	A10	65321746	65321748	-	-25
CHG	A11	24332306	24332308	+	-28.6
CHG	A11	40876175	40876177	+	-35.2
CHG	A11	45849682	45849684	+	-44.6
CHG	A11	108788395	108788397	+	-30
CHG	A12	74317368	74317370	+	33.3
CHG	A13	70284292	70284294	+	-36.8
CHG	A13	10993810	10993812	-	-26.7
CHG	A13	58446754	58446756	-	32.5
CHG	D01	17817753	17817755	+	28.7

Table 2. (Continued).

Con	Ch	Start	End	Str	Met (%)
CHG	D01	17820931	17820933	+	-35.7
CHG	D01	26350699	26350701	+	23.5
CHG	D01	29141534	29141536	+	31.8
CHG	D01	59239426	59239428	+	-23.8
CHG	D01	14191187	14191189	-	-18.2
CHG	D01	22007413	22007415	-	-25
CHG	D01	40815295	40815297	-	42.3
CHG	D01	47382748	47382750	-	-39.8
CG	D02	40653659	40653660	-	36.4
CHG	D02	23284890	23284892	-	47.8
CHG	D02	41995422	41995424	-	37.4
CHG	D02	52255818	52255820	-	-23.5
CHG	D02	58753977	58753979	-	30.4
CG	D03	10441435	10441436	-	-27.3
CHG	D03	19601886	19601888	-	27.8
CHG	D03	35624282	35624284	-	-27.9
CHG	D03	54940913	54940915	-	13.3
CG	D04	19476572	19476573	+	-28.6
CG	D04	34867190	34867191	+	28
CG	D04	42178109	42178110	+	-35.7
CG	D04	2744475	2744476	-	25
CHG	D04	1960555	1960557	-	-16.7
CHG	D04	19708639	19708641	-	-28.6
CHG	D05	34851951	34851953	-	-38.9
CHG	D05	37200591	37200593	-	36.7
CHG	D06	40925892	40925894	+	-39.2
CHG	D06	32202952	32202954	-	43.3
CG	D07	32350949	32350950	+	-28.6
CHG	D07	50661057	50661059	+	36
CHG	D07	51029917	51029919	+	-21.1
CG	D08	19513465	19513466	+	-19
CHG	D08	19513365	19513367	+	23.9
CHG	D08	19513464	19513466	+	-39.7
CHG	D08	33013947	33013949	+	36.1
CG	D09	29203816	29203817	+	25
CG	D09	51857139	51857140	+	20
CG	D09	51857208	51857209	+	45.2
CG	D09	6992933	6992934	-	35
CG	D09	9741468	9741469	-	21.1
CG	D10	44960140	44960141	+	-29.4
CG	D10	38313207	38313208	-	-30
CHG	D10	13705237	13705239	+	-22.2
CHG	D10	19329596	19329598	+	-26.6
CHG	D10	48956826	48956828	-	-25

Table 2. (Continued).

Con	Ch	Start	End	Str	Met (%)
CG	D11	41760838	41760839	+	-23.1
CG	D11	53098344	53098345	-	-25
CG	D11	72220220	72220221	-	-30.4
CHG	D11	28125778	28125780	+	-21.4
CHG	D11	32362556	32362558	+	28.9
CHG	D11	37187706	37187708	+	-61.7
CHG	D11	46108079	46108081	-	33.9
CHG	D12	21105778	21105780	+	-29
CHG	D12	34992412	34992414	+	-45.5
CHG	D12	36903063	36903065	+	34.2
CHG	D12	5256592	5256594	-	-30.9
CHG	D12	20529062	20529064	-	-28.2
CHG	D12	24278163	24278165	-	34.5
CG	D13	9716510	9716511	-	-18.8
CG	D13	21416841	21416842	-	-43.3
CHG	D13	9441204	9441206	+	27.7
CHG	D13	50235813	50235815	+	-21.4
CHG	D13	51978932	51978934	+	-53.8
CHG	D13	9716023	9716025	-	30.8

Ch: Chromosome, Met: methylation, Str: strand.

The methylation state of the DNA regions encoding snoRNAs can impact the functionality of snoRNAs. Methylation levels of different classes of snoRNAs showed differences. This is important since methylation of snoRNAs would affect their expression levels. Although there is limited number of studies in the methylation status of snoRNAs, it is known that the snoRNAs establish a binding with target rRNAs by means of these antisense elements (Kiss, 2001; Bratkovic et al., 2020). Thus, methylation status of antisense elements would affect the binding efficiency (Ramakrishnan et al., 2022). Methylation events of snoRNAs are known, for instance Nop1p, functioning as a methyltransferase, plays a crucial role in small nucleolar ribonuclear proteins (snoRNPs) (Filipowicz et al., 1999). The process involves the transfer of a methyl group from S-adenosylmethionine (SAM) to the 2′-hydroxyl group of ribose molecules in the specific RNA target (Stepanov et al., 2015). The addition of the methyl group alters the spatial conformation of the target RNA and enhances its hydrophobic nature, so shielding the RNA molecule from nucleolytic degradation (Sproat et al., 1989). Further studies specifically focused on the methylation status of DNA regions encoding the snoRNAs would reveal the effects of DNA methylation of snoRNAs. In the present study, it was clearly revealed that heterografting caused alteration levels of methylation in the DNA sequences of snoRNAs.

CONCLUSION

Cytosine methylation contents CG had the highest methylated content, followed by CHG and CHH within and between ungrafted and heterografted samples. Results revealed that the methylated CG and CHG of heterograft Pima 3-79—TM-1 were statistically higher than the ungrafted TM-1 (control). A total of 106 DMCs were identified wetween heterograft and

ungrafted samples. 78 of DMCs were in CHG content and 28 DMCs were in CG content. Among the methylation context, there were significant changes in the number of DMCs with CHG cytosine methylations between heterograft Pima 3-79—TM-1 and ungrafted TM-1.

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CELLULOSE SYNTHASES SPECIFIC MICROSATELLITE PRIMERS IN GOSSYPIUM HIRSUTUM L.

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ABSTRACT

Cellulose is the most abundant biological molecule on earth, synthesized in about 180 billion tons by vascular plants, algae, protists, and bacteria. Cellulose is one of the main components of cell walls (primary and secondary cell walls), microfibrils, and many other important biological macromolecules. Cellulose and hemicellulose are synthesized by the cellulose synthase gene superfamily, which includes the cellulose synthase (CesA) and cellulose synthase-like (Csl) families, involved in the synthesis of cellulose. Cotton fibers are more than 90% cellulose, making them different from other fiber crops. Microsatellites, also referred to as simple sequence repeats (SSR) or short tandem repeats (STR), are common in both eukaryotic and prokaryotic genomes. Their extensive polymorphism among closely related species has made them valuable for tasks such as species identification, investigating genetic diversity, and examining evolutionary connections. The aim of this study was to identify microsatellite motifs and design microsatellite primer pairs suitable for marker assisted selection for cotton breeding studies. A total of 82 CesA and Csl DNA sequences were extracted from the Gossypium hirsutum reference genome. Microsatellite definition criteria were set to 12 repeats for di, 8 repeats for tri-, 6 repeats for tetra, 5 repeats for penta-, and 4 repeats for hexa-nucleotides and identified using GMATA software, and primer pairs were identified using Primer3 software. We identified and characterized 17 primer pairs specific to upstream, downstream, or gene body regions of several CesA and Csl genes located on A08, A11, D03, D05, D06, D11, and D13. The utilization and aspects of microsatellite primer pairs were discussed.

Keywords: Cellulose, Cellulose synthase, Cotton, MAS, Microsatellite, SSR

INTRODUCTION

Cellulose is the most abundant biological molecule on earth, synthesized in about 180 billion tons by vascular plants, algae, protists, and bacteria. Cellulose is one of the main components of cell walls (primary and secondary cell walls), microfibrils, and many other important biological macromolecules. Cellulose and hemicellulose are synthesized by the cellulose synthase gene superfamily, which includes the cellulose synthase (CesA) and cellulose synthase-like (Csl) families involved in the synthesis of cellulose. Cotton fibers are more than 90% cellulose, making them different from other fiber crops (Delhom et al., 2022). Cotton plants are cultivated worldwide for fiber and oil. Raw cotton fiber is composed of a polysaccharide that consists of glucose linked by beta-1,4-glycosidic bonds and is synthesized by multimeric protein complexes that form rosette-like structures in the plasma membrane (Zou et al., 2018; Wen et al., 2022; Zhang et al., 2021; Pedersen et al., 2023). The hexamer components were identified as cellulose synthase A (CesA), which is distinguished from other cellulose synthases based on the catalytic subunit (i.e., indicated by the letter A). The Csl genes encoding cellulose synthase-like (Csl) proteins form a gene family with sequences that are similar to CesA sequences. It is known that the Csl genes are involved in the synthesis of hemicellulose, which associates with cellulose microfibrils to form a cross-linked matrix in cell walls. The CesA and Csl proteins belong to the glycosidic transferase family (GT2) and consist of conserved and variable regions (Zou et al., 2018; Wen et al., 2022; Zhang et al., 2021; Pedersen et al., 2023). The textile properties of cotton, such as fiber strength, fiber length, and fiber elongation, are directly affected by the type and the amount of cellulose, which is synthesized by plasma membrane-associated multimeric protein complexes called cellulose synthase. It is a large multiunit enzyme utilizing uridine diphosphate-glucose (UDP-Glc) as a substrate (Zhang et al., 2021; Wen et al., 2022).

Microsatellites, also known as simple sequence repeats, short tandem repeats or simple sequence length polymorphisms, have been extensively used in genetic diversity analysis and marker-assisted selection (MAS) because of their high reproducibility, abundant polymorphisms, co-dominant inheritance, multi-allelic nature (Figure 1), high genome coverage, and simple analysis methods (Karaca & Ince, 2011; Zhang et al., 2020; Zeng et al., 2022). It is known that two mechanisms cause the occurrence and the polymorphism of microsatellites. Replication slippage of DNA polymerase and unequal crossing-over are believed to create microsatellites and polymorphism (Karaca & Ince, 2011). Microsatellite markers have been extensively applied to genetic diversity, genetic structure analysis, paternity testing, and breeding studies on many plant species (Wang et al., 2017; Zhang et al., 2020; Shrestha et al., 2023). However, there are no reports on the development of the cellulose synthase (CesA) and cellulose synthase-like (Csl) families derived microsatellite markers in Gossypium. MAS can make great use of the valuable genetic resources in cotton by precisely selecting genes for cellulose synthase related products, therefore producing superior germplasm. This study was undertaken to study the presence and distribution of microsatellites in 82 cellulose synthase (CesA) and cellulose synthase-like (Csl) gene sequences obtained from the reference genome of Gossypium hirsutum available in NCBI databases.

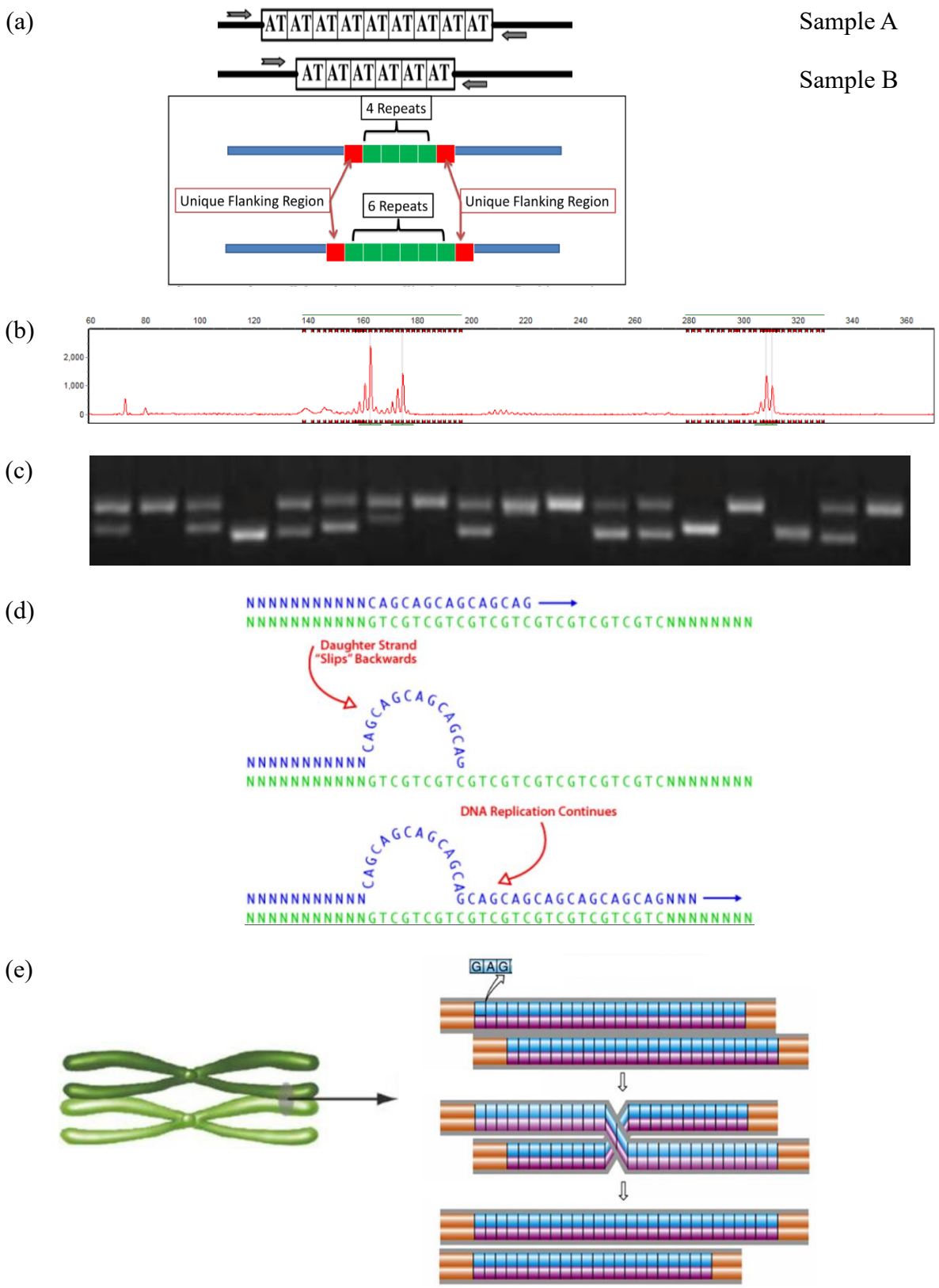

Figure 1. Feature of microsatellites. Panel (a): Arrows indicated forward, and reverse primer pair conserved between two samples, A and B. Panel (b): Multi-allelic microsatellites. Panel

(c) co-dominant nature of microsatellites. Panel (d): Creation of microsatellites by polymerase slippage. Panel (e): Creation of microsatellites via unequal cross-over.

MATERIAL METHODS

Material

G. hirsutum reference genome sequences (GCF_007990345.1) (Table 1) were downloaded from GenBank (https://www.ncbi.nlm.nih.gov) in fasta format (.fa) and General Feature Format (.gff). Based on the information provided in gff, we extracted DNA sequence using coordination information of cellulose synthase (CesA) and cellulose synthase-like (Csl) genes on (+) and (-) strands (Table 2) by the Seqtk 1.4 program on Ubuntu. Some basic features of the reference genes used in the present study were shown in Table 1.

Table 1. Features of reference genome Gossypium hirsutum v2.1

Feature	RefSeq	GenBank
No	GCF_007990345.1	GCA_007990345.1
Genome size	2.3 Gb	2.3 Gb
Total ungapped length	2.3 Gb	2.3 Gb
Gaps between scaffolds	6	6
Number of chromosomes	26	26
Number of organelles	2	0
Number of scaffolds	1031	1031
Scaffold N50	108.1 Mb	108.1 Mb
Scaffold L50	10	10
Number of contigs	6733	6733
Contig N50	783.9 kb	783.9 kb
Contig L50	789	789
GC percent	34	34
Genome coverage	94.1x	94.1x
Assembly level	Chromosome	Chromosome

Extraction of Microsatellites and Analysis

DNA sequences of cellulose synthase A and cellulose synthase like genes listed in Table 2 were used to search for and identify microsatellite primer pairs. In the literature, there existed differences in the definition of microsatellites. In this study, microsatellites were defined as repeating motifs of DNA stretches consisting of 2 to 6 nucleotide repeats. Defined microsatellites were extracted using GMATA software tools using the DNA sequences in the Fasta file obtained from the reference genome.

Microsatellites were considered to have 12 repeats for di-, 8 repeats for tri-, 6 repeats for tetra-, 5 repeats for penta-, and 4 repeats for hexa-nucleotides. Microsatellite coordinates were used to map the reference genome using BedTools and programs within BedTools software (Karaca & Ince, 2023a; 2023b).

Microsatellite primer pairs were identified using Primer3 software using the following criteria: primer length: 18-24, amplicon size range: 160–300, Tm: range from 48 °C to 60 °C and GC content greater than 40%. Primer pairs were confirmed using grep function of Linux to locate the primer pairs in the reference genome. Table 2 showed the whole 82 loci of cellulose synthase A and cellulose synthase like genes used to search for microsatellites.

Table 2. Cellulose synthase A and cellulose synthase like genes used to search for microsatellites.

Locus	Gene	Enzyme/protein
107912646	CslH1	Cellulose synthase-like protein H1
107907453	CesA1	Cellulose synthase A catalytic subunit 1
107958687	CesA1	Cellulose synthase A catalytic subunit 1
107898377	CslI	Cellulose synthase interactive 1
107898894	CslD4	Cellulose synthase-like protein D4
107928590	CslG2	Cellulose synthase-like protein G2
107907451	CesA7	Cellulose synthase A catalytic subunit 7
107955410	CesA4	Cellulose synthase A catalytic subunit 4
107902682	CesA8	Cellulose synthase A catalytic subunit 8
107945371	Prob-CesA8	Probable cellulose synthase A catalytic subunit 8
107929047	CslG3	Cellulose synthase-like protein G3
107916923	CslE6	Cellulose synthase-like protein E6
107925040	CesA2	Cellulose synthase A catalytic subunit 2
107961131	CesA4-like	Cellulose synthase A catalytic subunit 4
107924712	CslD3	Cellulose synthase-like protein D3
107894409	Prob-CesA5	Probable cellulose synthase A catalytic subunit 5
107918220	CslE1	Cellulose synthase-like protein E1
107927704	CslG2	Cellulose synthase-like protein G2
107946664	CslD2	Cellulose synthase-like protein D2
107900907	CslI1	Cellulose synthase interactive 1
121212539	CslE6	Cellulose synthase-like protein E6
107950561	CslD3	Cellulose synthase-like protein D3
121203053	CslE6	Cellulose synthase-like protein E6
107958681	CesA1-like	Cellulose synthase A catalytic subunit 1-like
107958683	CesA7	Cellulose synthase A catalytic subunit 7
107900748	CesA3	Cellulose synthase A catalytic subunit 3
121220991	CslD1	cellulose synthase-like protein D1
107909647	CseA8-like	Cellulose synthase A catalytic subunit 8-like
107937655	CseA4-like	Cellulose synthase A catalytic subunit 4-like
107962315	CseA5-like	Cellulose synthase A catalytic subunit 5-like
107925233	CseA8	Cellulose synthase A catalytic subunit 8
107928422	CslE1	Cellulose synthase-like protein E1
107894422	CslE1	Cellulose synthase-like protein E1
107928982	CslE1	Cellulose synthase-like protein E1
107951817	Prob CseA8	Probable cellulose synthase A catalytic subunit8
107892837	CslG3	cellulose synthase-like protein G3
107924700	CslB4	Cellulose synthase-like protein B4
107949226	CslD4	Cellulose synthase-like protein D4
107949942	CseA6-like	Cellulose synthase A catalytic subunit 6-like
107927657	CslG2	Cellulose synthase-like protein G2
107942314	CslD1	Cellulose synthase-like protein D1

Table 2 (continued)

Locus	Gene	Enzyme/protein
107915763	CseA3	Cellulose synthase A catalytic subunit 3
107902334	CseA2-like	Cellulose synthase A catalytic subunit 2-like
107901762	CseA5	Cellulose synthase A catalytic subunit 5
107942877	CseA1	Cellulose synthase A catalytic subunit 1
107938343	CseA3	Cellulose synthase A catalytic subunit 3
121229536	CseA5-like	Cellulose synthase A catalytic subunit 5-like
107911480	CseA2	Cellulose synthase A catalytic subunit 2
107916051	CslG3	Cellulose synthase-like protein G3
107953681	CseA7-like	Cellulose synthase A catalytic subunit 7-like
107896452	CslG3	Cellulose synthase-like protein G3
107913679	CslI1-like	Cellulose synthase interactive 1-like
107935224	CslE1	Cellulose synthase-like protein E1
121217085	CseA8-like	Cellulose synthase A catalytic subunit 8-like
107935226	CslE1	Cellulose synthase-like protein E1
107896451	CslG2	Cellulose synthase-like protein G2
107916504	CseA4-like	Cellulose synthase A catalytic subunit 4-like
107909056	CslD3	Cellulose synthase-like protein D3
107928458	CslG2	Cellulose synthase-like protein G2
107890709	CslG3	Cellulose synthase-like protein G3
107935220	CslE1	Cellulose synthase-like protein E1
121207998	CslE1	Cellulose synthase-like protein E1
107935218	CslE1	Cellulose synthase-like protein E1
107947180	CslG3	Cellulose synthase-like protein G3
107940246	CslD3	Cellulose synthase-like protein D3
107915502	CslG2	Cellulose synthase-like protein G2
107892464	CslG3	Cellulose synthase-like protein G3
107946051	CslD5	Cellulose synthase-like protein D5
107929134	CslG2	Cellulose synthase-like protein G2
107901428	CslI3	Cellulose synthase interactive 3
107925659	CslD5	Cellulose synthase-like protein D5
107922547	Prob CseA5	Probable cellulose synthase A catalytic subunit 5
107923673	CslI1-like	Cellulose synthase interactive 1-like
107945523	CslI1	Cellulose synthase interactive 1
107940554	CslI3	Cellulose synthase interactive 3
121203141	CseA7-like	Cellulose synthase A catalytic subunit 7-like
107914099	CseA5	Cellulose synthase A catalytic subunit 5
107950592	CseA2	Cellulose synthase A catalytic subunit 2
107951165	CslE1	Cellulose synthase-like protein E1
107947909	CslG2	Cellulose synthase-like protein G2
107937198	CslE1	Cellulose synthase-like protein E1
121229512	CslI3-like	Cellulose synthase interactive 3-like

RESULTS AND DISCUSSION

The content and type of microsatellites in 82 cellulose synthase A (CesA) and cellulose synthase like genes (Csl) listed in Table 2 were studied. Among 82 genes, 32 were CseA, CseA-like, and probable CesA genes. There were 50 cellulose synthase like genes (Csl) studied in the present research. Based on the microsatellite defining criteria, a total of 17 microsatellites with genes were identified (Table 3 and Table 4).

Table 3. List of microsatellites containing CseA and Csl genes, regions and strand information

ID	Gene ID	Chr*	Genes	Region	Str*
D3-1	107940246	A08	Cellulose Synthase-like Protein D3	Upstream	+
I1-1	107898377	A11	Protein Cellulose Synthase Interactive 1	Upstream	+
2l-1	107902334	A11	Cellulose Synthase A Catalytic Subunit 2-like	Upstream	+
2l-2	107902334	A11	Cellulose Synthase A Catalytic Subunit 2-like	Downstream	+
E1-1	107951165	A11	Cellulose Synthase-like Protein E1	Downstream	+
D3-2	107909056	D08	Cellulose Synthase-like Protein D3	Upstream	+
E1-2	107928982	D09	Cellulose Synthase-like Protein E1	Down stream	+
G3	107929047	D09	Cellulose Synthase-like Protein G3	Down stream	+
I1-2	107945523	D12	Protein Cellulose Synthase Interactive 1	Upstream	+
S2	107950592	D03	Cellulose Synthase A Catalytic Subunit 2	Gene Body	-
S1	107907453	D05	Cellulose Synthase A Catalytic Subunit 1	Gene Body	-
S7	107907451	D05	Cellulose Synthase A Catalytic Subunit 7	Gene Body	-
I3	107901428	D06	Protein Cellulose Synthase Interactive 3	Upstream	-
S5-1	107901762	D06	Cellulose Synthase A Catalytic Subunit 5	Upstream	-
S5-2	107901762	D06	Cellulose Synthase A Catalytic Subunit 5	Gene Body	-
H1	107912646	D11	Cellulose Synthase-like Protein H1	Gene Body	-
D5	107946051	D12	Cellulose Synthase-like Protein D5	Upstream	-

ID: Primer id, Chr*: chromosome names, Str*: strand

As can be seen from Table 3, among 17 microsatellites, eight were located in upstream regions, 5 were on gene body and 4 were in downstream regions in CseA and Csl genes. CesA7, CesA1, CesA5, and ClsH1 genes had microsatellites in their gene body regions. Among these genes CesA7 and CesA5 are known to express more in cotton fiber cells. Therefore, these microsatellite primer pairs (Table 4) could be used in MAS cotton breeding studies.

Table 4. Microsatellite primer pairs and related information.

ID	Genes	5' ➔3' Forward and reverse sequences of primers	Motif	Size (bp)	TM
D3-1	Cellulose Synthase-like Protein D3	F: ACCAACACCTAACAAGCCTT	$[ATA]_{10}$	265	57.25
		R: ATACACCGCCCATTCAAACC			58.53
I1-1	Protein Cellulose Synthase Interactive 1	F: TCTCAAAACCCTTCACACACA	$[AC]_{17}$	248	57.64
		R: AGTATTGTGCTACTTGGGTTGT			57.63
2l-1	Cellulose Synthase A Catalytic Subunit 2-like	F: ACTGTTTAACCAAATTCATGCT	$[TA]_{12}$	292	54.80
		R: GGTTGTCCAGATACACTTAAATC			55.07
2l-2	Cellulose Synthase A Catalytic Subunit 2-like	F: ATCCATCGACGTGACTGTTC	$[TTA]_{9}$	356	57.72
		R: ACGTTAGAGGGAAAGTTGAAGG			58.00
E1-1	Cellulose Synthase-like Protein E1	F: TTTGCAAATGTCGGGAAGGG	$[TTTC]_{6}$	238	59.03
		R: ACGAAAGGAAGTTGCAACAGA			58.36
D3-2	Cellulose Synthase-like Protein D3	F: AAACCAACACCGAACAAGCC	$[ATA]_{10}$	267	59.54
		R: AATGCACCGTCCATCCAAAC			59.11
E1-2	Cellulose Synthase-like Protein E1	F: AATGGTAGGAATAAACACAA	$[AAAT]_{7}$	239	49.81
		R: TCGTATTGTTATTGTAGTTC			48.23
G3	Cellulose Synthase-like Protein G3	F: GAGAGTTGAAGTTGCAGGTGA	$[AT]_{14}$	195	58.16
		R: TGAATTTGGTGTATTACGATGGATT			57.13
I1-2	Protein Cellulose Synthase Interactive 1	F: TGTCATGTTGGTTGCGTTGT	$[TAATTT]_{5}$	243	58.90
		R: ACGGAGAGTGGTGTCAACTT			58.88
S2	Cellulose Synthase A Catalytic Subunit 2	F: ACCCACCAACTGAGAGCAAT	$[AAAAG]_{5}$	160	59.23
		R: GCTCCCACTCCATTACACCT			59.09
S1	Cellulose Synthase A Catalytic Subunit 1	F: ACATGTAAAGGAAGCAAGACCA	$[TAA]_{9}$	227	57.90
		R: GTGCAGATCATAGACTACATTGCT			58.70
S7	Cellulose Synthase A Catalytic Subunit 7	F: AGGTCCTATTTAATTATACGCTTTGT	$[TA]_{12}$	240	56.80
		R: ACAACGCAAAGTGATAATTCGT			57.26
I3	Protein Cellulose Synthase Interactive 3	F: GGTTGGGGAGAGGCTATAGG	$[TTTTCT]_{4}$	366	58.65
		R: ACCACAGCTTAGCGAGTTTG			58.49
S5-1	Cellulose Synthase A Catalytic Subunit 5	F: TGTCACACGGCTTGAATAACA	$[ATATC]_{5}$	203	58.16
		R: ACGGGCTGTTACACCTCTAC			59.11
S5-2	Cellulose Synthase A Catalytic Subunit 5	F: TCTGAATGACTCGTACAAGCA	$[TTA]_{8}$	257	57.07
		R: CACGGACTACTAATTGTGCCA			58.03
H1	Cellulose Synthase-like Protein H1	F: CCAATGAGGCGAGGCAGT	$[CCATGC]_{4}$	244	59.73
		R: GCACTCTCTCACTTGATTCATCTC			59.19
D5	Cellulose Synthase-like Protein D5	F: GCAAATTCCCAGCCCAATCA	$[TTTA]_{6}$	184	59.10
		R: TCGGTCAAAGGTCATTTTATCTGG			59.06

ID: Primer Id, TM: melting temperature (°C)

Two A subgenome chromosomes (A01 and A11) and 7 D subgenome chromosomes (D03, D05, D06, D08, D09, D11, and D12) contained CesA and Csl genes with microsatellites (Table 3). Among the chromosomes, A11 had the highest number of CesA and Csl genes with microsatellites.

Among the motifs, $[AC]_{17}$ had the highest number of repeats while motifs $[TTTTCT]_4$ and $[CCATGC]_4$ were the lowest repeats (Table 4). Among the 17 motifs, the highest number were trinucleotides, and the lowest were tetranucleotides. There were no specific motif types for the upstream, gene body, or downstream region.

CONCLUSION

In this study, 82 CesA and Csl genes were searched for microsatellites, and 17 microsatellite primer pairs flanking 12 different CesA and Csl genes were identified. Microsatellites including genes are cellulose synthase A catalytic subunit 1, cellulose synthase A catalytic subunit 2, cellulose synthase A catalytic subunit 2-like, cellulose synthase A catalytic subunit 5, cellulose synthase A catalytic subunit 7, cellulose synthase-like protein D3, cellulose synthase-like protein D5, cellulose synthase-like protein E1, cellulose synthase-like protein G3, cellulose synthase-like protein H1, cellulose synthase Interactive protein 1 and 3. These primer pairs could be used in breeding programs utilizing the marker assisted selection and genetic studies of cotton. We also noted that 14.63% of CesA and Csl genes contained microsatellites indicating that the occurrence of microsatellites in gene body and flanking regions such as upstream and downstream contain microsatellites. Further studies regarding the utilization of these primer pairs are required by using these primer pairs in the segregation population of fiber related alleles.

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GRAFTING INDUCED DIFFERENTLY METHYLATED CYTOSINES IN LONG NON-CODING RNAS OF COTTON

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ABSTRACT

Non-coding RNAs (ncRNAs) are more than 200 nucleotides in length and do not encode proteins. The majority of lncRNAs are transcribed by RNA polymerase II and are subject to post-transcription processes such as 5'-end capping, alternative splicing, and the addition of 3'-poly-A tails. It is known that some lncRNAs are involved in gene expression regulation during the process of regulatory networks with miRNAs and mRNAs. Some others function as blockers of miRNA cleavage, which greatly affect the regulation of plant cell differentiation and the development process; they positively regulate target genes involved in stress response, signal transduction, early somatic embryonic development, fertility, seed germination, seedling root growth, alternative splicing, and flowering. However, there is limited study on the methylation responses of lncRNAs to plant grafting in cotton. This study was undertaken to reveal differently methylated cytosines (DMCs) of heterografted cotton made of Gossypium barbadense and G. hirsutum. Seed genomic DNAs of grafted and ungrafted samples were bisulfite treated, and the sequencing libraries were prepared and sequenced according to the library protocol for Illumina platforms. Comparison analyses between ungrafted Upland cotton (TM-1) and heterografted cotton with Pima rootstock revealed 26700 differently methylated cytosines (DMCs), 13630 of which were in the increased methylation regions and 13070 of which were in the decreased methylation regions. Methylation level differences were also studied at cytosine content levels such as CG, CHG, and CHH. Methylation levels of CG and CHG were decreased by grafting, while CHH type methylation levels were increased by grafting.

Keywords: Cotton, DMC, Cytosine Methylation, lncRNAs

INTRODUCTION

The genomes of eukaryotic cells contain a considerable number of RNA species, differing in their biogenesis and function (Waititu et al., 2020; Cordeiro et al., 2022). Messenger RNAs (mRNAs) are the main intermediates for protein synthesis. However, mRNAs represent a very low amount of the eukaryotic genome transcribed into RNA molecules (Rai et al., 2019). Transcriptomes other than mRNAs can be grouped into two main classes of non-coding RNAs (ncRNAs) (Waititu et al., 2020): (i) housekeeping ncRNAs and (ii) regulatory ncRNAs. The transcriptome in the housekeeping category is also called infrastructural or constitutive ncRNAs. They are abundant in all cell types and include ribosomal RNAs (rRNAs), transfer RNAs (tRNAs), small nuclear RNAs (snRNAs), and small nucleolar RNAs (snoRNAs) (Zhang et al., 2019). On the other hand, ncRNAs in the second category, regulatory ncRNAs, modulate gene expression at transcriptional, post-transcriptional, and epigenetic levels (Zhang et al., 2019). The second category includes the long non-coding RNAs (lncRNAs) with transcripts longer than 200 nucleotides, small RNAs (sRNAs) that are shorter than 30 nucleotides, such as microRNAs (miRNAs), small-interfering RNAs (siRNAs), and phased siRNAs (phasiRNAs) (Borges & Martienssen, 2015).

The majority of lncRNAs are subject to post-transcription processes such as 5'-end capping, alternative splicing, and the addition of 3'-poly-A tails (Chekanova, 2015). lncRNAs of plants are transcribed by two additional polymerases: RNA Pol IV or RNA Pol V (Wierzbicki et al., 2008). These lncRNAs are less characterized and have some structural differences, such as a lack of poly-A tails (Zhou & Law, 2015; Rai et al., 2019), and are the major players driving RNA-mediated DNA methylation (RdDM) (Matzke & Mosher, 2014).

lncRNAs transcribed by Pol II can be grouped into linear and circular lncRNAs (lin-lncRNAs and circ-lncRNAs, respectively). lncRNAs of Pol II could be sub-grouped according to the genome region from which they were encoded, i.e., intergenic, intronic, and coding regions (Yu et al., 2019). It is known that some lncRNAs function as precursors of miRNAs and other sRNAs, and participate as signals, decoys, guides, and regulate chromatin remodelling in cell functions at the epigenetic, transcription, and post-transcription levels (Datta & Paul, 2019; Zhang et al., 2019; Yu et al., 2019; Bhogireddy et al., 2021; Song et al., 2021). Also, some cis or trans acting modes of lncRNAs could regulate the expression of neighbouring or distant genes during different plant developmental processes (Yu et al., 2019). An increasing number of studies suggested the contributions of lncRNAs as essential modulators in plant growth and development, including plant responses to abiotic stresses (Chen et al., 2018; Urquiaga et al., 2021). For instance, some lncRNAs function as blockers of miRNA cleavage, while others involve alternative splicing and flowering (Chen & Penfield, 2018). However, there existed limited studies dealing with the DNA methylation status of lncRNAs between grafted and ungrafted cotton species. Therefore, this study was undertaken to reveal different methylated cytosines between homografted and heterografted cotton species. Results revealed that methylation levels of CG and CHG contents were decreased by grafting, while CHH type methylation levels were increased by grafting. Further studies revealed that there was a great difference in the graft responses in 16,333 cotton lncRNAs.

MATERIAL METHODS

Plant Materials

Plant materials consisted of "Texas Marker-1" (TM-1), belongs to Gossypium hirsutum L., and "Pima 3-79", belongs to Gossypium barbadense L. This study was conducted in a greenhouse located in Antalya, on the Mediterranean coast of Turkey. Two weeks after seed sowing, seedlings with two-leaf stage were transferred into a laboratory, where they were acclimated for three days.

Grafting Experiments

Grafting experiments between Pima 3-79 and TM-1 (Pima 3-79—TM-1) and between TM-1 and Pima 3-79 (Pima 3-79—TM-1) were made using a grafting method described in Karaca et al. (2020). Each plot had 15 seedlings with three replications.

DNA Extraction

Six randomly selected seeds from ungrafted TM-1 (control) and heterograft (Pima 3-79—TM-1) were ground to a powder with a mortar and pestle. A DNA extraction protocol previously described in Karaca et al. (2005) was used to extract genomic DNA samples.

Whole Genome Bisulfite Sequencing

Genomic DNA samples were fragmented by sonication to 200–300 bp with a Covaris LE220 sonicator after adding 0.5% (w/w) lambda phage DNA. Fragmented genomic DNA and lambda phage DNA were treated with bisulfite to convert unmethylated cytosines to uracils while retaining those cytosines that are methylated. Reactions were cleaned using the EZ DNA Methylation-Gold kit, and the sequencing libraries were prepared using the Accel-NGS Methyl-Seq DNA library kit (Swift BioSciences, Ann Arbor, MI, USA) according to the library protocol for Illumina platforms. Cluster sequencing analysis was performed by Macrogen Corp. on an Illumina NovaSeq 6000 with 150 Gb of 151 bp paired-end sequencing.

WGBS Data Processing

Raw sequence reads were filtered using Trim Galore (Krueger, 2021). Twenty base pairs were trimmed off from the 3′ ends of R1 and 5′ ends of R2 to eliminate the majority of the adaptase tails after adaptor trimming and reads shorter than 20 bp were discarded. Raw and trimmed sequence reads (forward and reverse) were compared using the FastQC Screen (Wingett & Andrews, 2018) to confirm the quality increase. The bisulfite-treated clean reads in FASTQ format were mapped to the reference genome of G. hirsutum (GCF_007990345.1) using BSMAPz (Zynda, 2018). BSMAPz was piped with SAMtools view-bs (Li et al., 2009) to obtain mapped bam files.

Bam files contained the number of uniquely mapped reads, non-unique mapped reads, deduplicated reads, and analyzed reads in methylation calling. The evaluation of the quality of the sorted alignment data was performed utilizing Qualimap 2.2 (Okonechnikov et al., 2016). The basic statistics of the alignments (content, mean and standard coverage, insert distribution, etc.) are produced.

In this study, uniquely mapped reads were used in the methyratio.py script within the BSMAPz software to extract methylated and unmethylated cytosines in the three-sequence contexts of CG, CHG, and CHH (where H is any base other than G), along with their coverage profile values. Methylation ratios of every single cytosine satisfying a higher than 1 CT count were called using the methyratio.py program in BSMAPz. During data preprocessing, low coverage and high coverage bases were filtered using lower and higher cutoff values, 15 and

500, respectively. A lower read cut-off of 10 means that bases with coverage below 10× were discarded because a high enough read coverage will increase the power of the statistical tests.

The bisulfite conversion ratio was calculated using the following formula: Bisulfite conversion rate (%) = # unmethylated read level measurements from the lambda genome/(# methylated and # unmethylated read level measurements from the lambda genome) × 100.

The bisulfite conversion rates estimated were 99.6592%–99.6645% across samples using lambda phage DNA as a spike-in control. The following conversion rates were obtained: 99.66% for PP, 99.66% for TP, 99.66% for PK, 99.65% for TT, 99.66% for PT, and 99.66% for TK, indicating that a high percentage of unmethylated cytosines were effectively converted (Karaca et al. 2020).

Correlation analyses between samples were obtained through Pearson's coefficient of the MethylRatio values, and it was found that samples had very high correlations. Each cytosine location was annotated using NCBI assembly (GCF_007990345.1 and GCA_008761655.1) data using Linux commands and tools including awk, sed, grep, BEDtools, BEDOPS, deepTools, SeqTK, SeqKit, and SAMtools (Li et al., 2009; Neph et al., 2012; Quinlan & Hall, 2010; Ramirez et al., 2014). Browser extended document (bed) files for further annotated files were made, including the functional location of each snoRNA, gene ID, and strand.

Differently methylated cytosines were identified using Defiant software (Condon et al., 2018). The weighted mean methylation percentage was calculated using the given cut-off of 10% and 10× minimum coverage by utilizing Defiant software (Condon et al., 2018). A p value between samples A and B was calculated by Fisher's exact test using the following formula:

$$p = \frac{(\mathrm{mCA} + \mathrm{mCB})!\,(\mathrm{CA} + \mathrm{CB})!\,(\mathrm{mCA} + \mathrm{CA})!\,(\mathrm{mCB} + \mathrm{CB})!}{\mathrm{mCA!}\,\mathrm{mCB!}\,\mathrm{CA!}\,\mathrm{CB!}\,(\mathrm{mCA} + \mathrm{mCB} + \mathrm{CA} + \mathrm{CB})!}$$

where mC is the number of 5-methyl cytosine and C is the number of cytosine (Condon et al., 2018). After identification of differently methylated cytosines (dmc) as increased or decreased methylation between ungrafted control (TM-1) and heterograft Pima 3-79—TM-1, the GIs were submitted to the Database for Annotation, Visualization, and Integrated Discovery (DAVID) (https://david.ncifcrf.gov/home.jsp) for functional annotation of the gene list (Sherman et al., 2022).

RESULTS AND DISCUSSION

The reference genome of the Upland genome contained a total of 16333 long noncoding RNAs (lncRNAs), 8485 of which were on the plus (+) strand and 7848 of which were on the minus (-). The chromosome and subgenome distribution of lncRNAs were shown in Figure 1. Apart from chromosomes A11, A13, D03, D07, D09, and D12, the (+) strand contained more lncRNAs than the (-) strand (Figure 1). On the other hand, chromosome A04 had the lowest number of lncRNAs. As it can be seen in Figure 1, there were a considerable number of differences in the presence of lncRNAs among the cotton chromosomes and between the A and B subgenomes. The occurrence of lncRNAs on chromosomes seems independent of chromosome and subgenome sizes (Karaca & Ince, 2023).

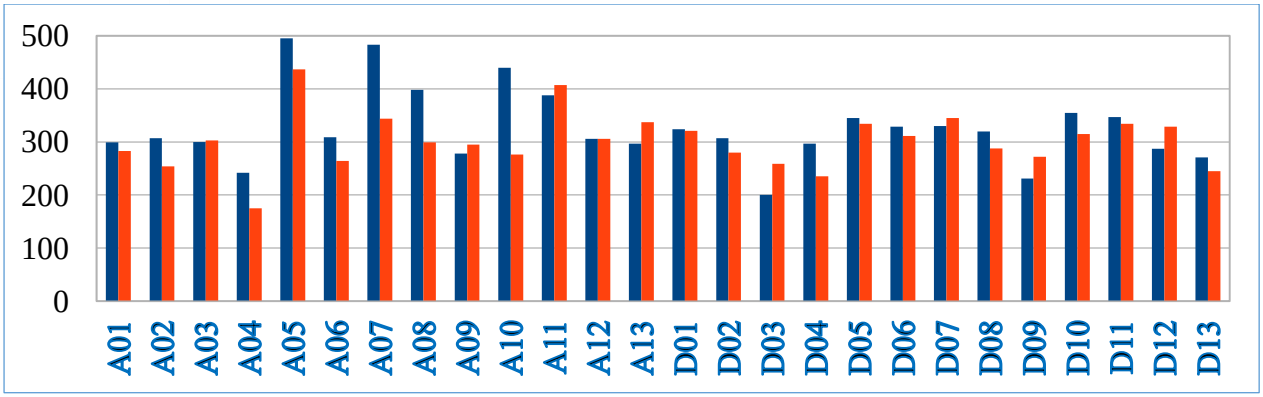

Figure 1. Distribution of lncRNAs on G. hirsutum chromosomes. Blue bars show lncRNAs on the (+) strand, while red bars show lncRNA on the (-) strand (Karaca and Ince 2023).

Results revealed that lncRNAs contained more methylation in CG and CHG, while CHH methylation levels were the lowest (Figure 2). It was noted that there were no differences in methylation between the strands ((+) and (-)). On the other hand, homograft (TM-1—TM-1) had the lowest lncRNAs methylations. The level of methylation in ungrafted control and heterograft (Pima 3-79—TM-1) was higher than homograft (Figure 2). To see the whole picture of methylation, a Circos graph was constructed (Figure 3), and the graph showed differences in methylation between chromosomes and subgenomes.

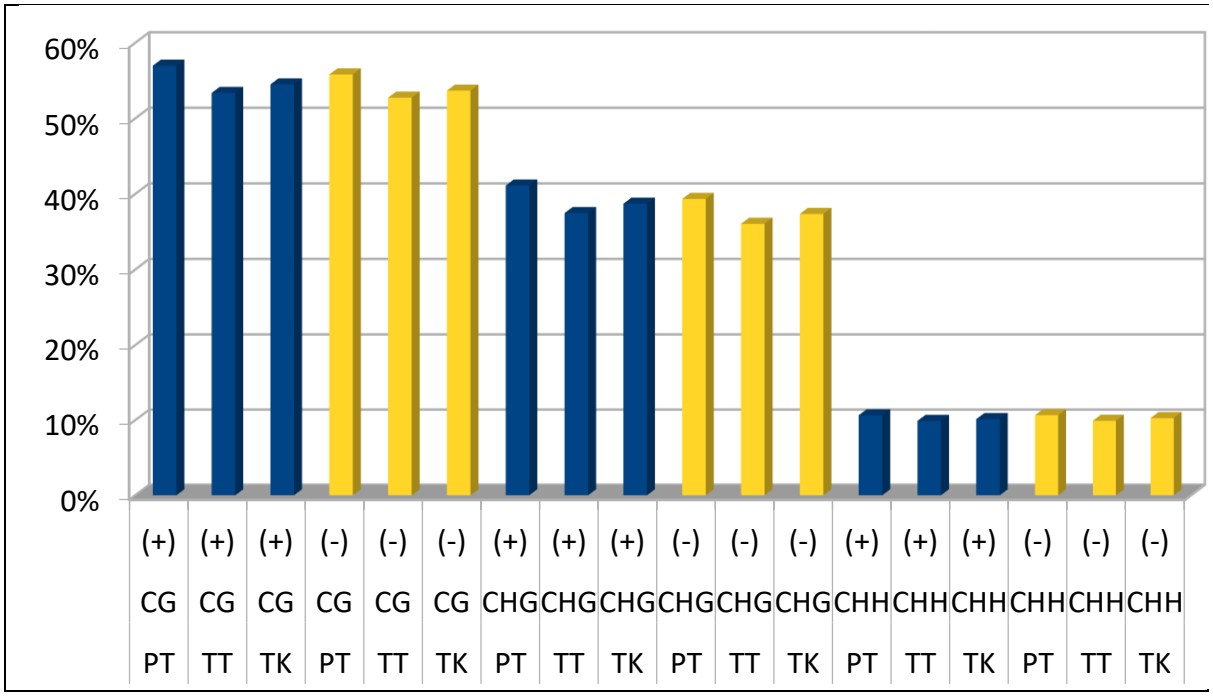

Figure 2. Methylation levels of lncRNAs between grafts. The Y axis shows methylation levels (%), and X axis shows strands, methylation contents, and grafts, respectively. PT: Pima 3-79—TM-1, TT: TM-1—TM-1, and TK: ungrafted TM-1.

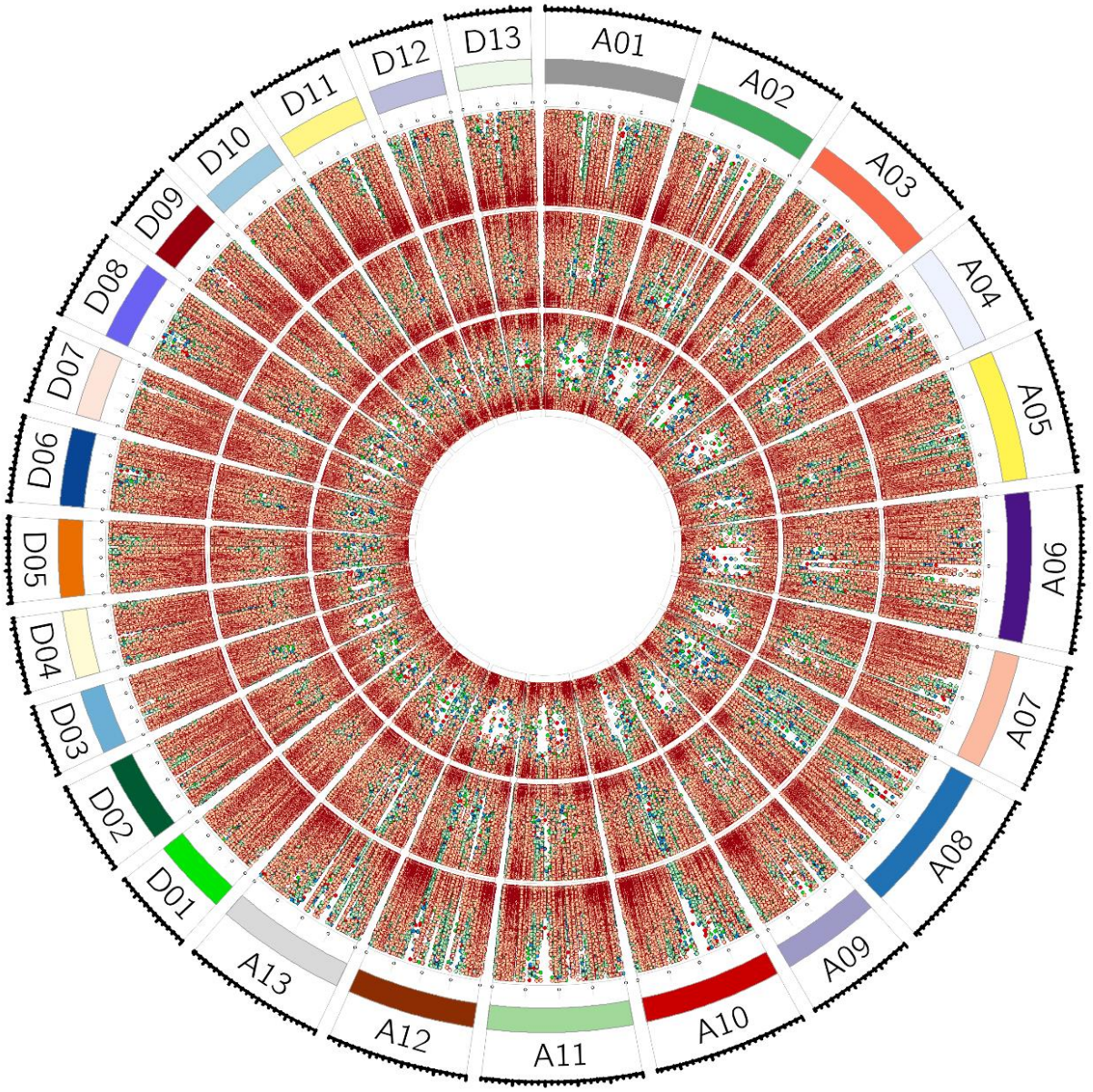

Figure 3. Methylation differences in snoRNA genes between heterograft Pima 3-79—TM-1 and ungrafted TM-1, and homograft TM-1—TM-1 and ungrafted TM-1. Circles from inner to outer represent the methylation status of CG, CHG, and CHH, respectively. The colors blue and light pink represent methylations of ungrafted TM-1 on the forward and reverse strands. The colors red and green represent methylations of Pima 3-79—TM on forward and reverse strands. The colors light green and orange represent methylations of TM-1—TM-1 on forward and reverse strands.

As can be seen in Figures 2 and 3, there existed methylation differences between grafts. However, a statistical method would tell us the real differences. In the present study, differently methylated cytosines were assessed between grafts using the statistical method (Condon et al., 2018). Compared to ungrafted TM-1, CG and CHG methylation levels of Pima 3-79—TM-1 were decreased (Table 1). It was also noted that methylation levels of TM-1—TM-1 were also

decreased, indicating that lncRNA genes in mature cotton seeds were demethylated upon grafting experiments. There were CHH methylation differences between heterograft Pima 3-79—TM-1 and homograft TM-1—TM-1. Although there was increased methylation of CHH in Pima 3-79—TM-1, the level of CHH methylation was decreased in TM-1—TM-1. Comparisons of methylation differences between homograft and heterograft were also assessed. Results showed that homograft TM-1—TM-1 had lower CHG demethylation than Pima 3-79—TM-1, but CG and CHH methylation levels were higher in Pima 3-79—TM-1 compared to TM-1—TM-1.

Table 1. Differently Methylated Cytosines of long non-coding RNAs in grafted and ungrafted upland cotton accessions

Graft	Increased methylation	Decreased methylation	Differences	Total Sites
TM-1 vs Pima 3-79—TM-1	13627	13072	555	26699
CG	745	848	-103	1593
CHG	2079	2275	-196	4354
CHH	10803	9949	854	20752
TM-1 vs TM-1—TM-1	8140	8440	-300	16580
CG	837	981	-144	1818
CHG	2151	2250	-99	4401
CHH	5152	5209	-57	10361
TM-1—TM-1 vs Pima 3-79—TM-1	12834	12166	668	25000
CG	773	704	69	1477
CHG	2011	2112	-101	4123
CHH	10050	9350	700	19400

CONCLUSION

It is known that the genomes of eukaryotic cells contain a considerable number of noncoding RNA species, including long non-coding RNAs (lncRNAs). lncRNAs have a significant function in gene expression. There was a limited study of level of DNA methylation of lncRNAs in cotton. Furthermore, there were no studies dealing with lncRNA methylation and grafting in cotton. In the present study, a total of 16333 lncRNAs were studied between homograft and ungrafted samples and between heterografted and ungrafted samples. Results revealed that the CG and CHG contents of lncRNAs were more methylated than the CHH content in ungrafted and grafted samples. In homograft TM-1—TM-1, all the 3 contents (CG, CHG, and CHH) had significantly lower methylations. On the other hand, heterograft Pima 3-79—TM-1 had higher CHH methylation than ungraft control. The overall findings of this study

suggested that grafting causes methylation levels in scions, lowering the methylation of some lncRNAs. Further research is needed into the biological consequences of altered methylation in mature seed of Gossypium hirsutum.

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3D-QSAR, ADME-TOX IN SILICO PREDICTION AND MOLECULAR DOCKING STUDIES FOR MODELING THE ANALGESIC ACTIVITY AGAINST NEUROPATHIC PAIN OF NOVEL NR2B-SELECTIVE NMDA RECEPTOR ANTAGONISTS

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A new class of selective antagonists of the N-Methyl-D-Aspartate (NMDA) receptor subunit 2B have been developed using molecular modeling techniques. The three-dimensional quantitative structure–activity relationship (3D-QSAR) study, based on comparative molecular field analysis (CoMFA) and comparative molecular similarity index analysis (CoMSIA) models, indicate that steric, electrostatic and hydrogen bond acceptor fields have a key function in the analgesic activity against neuropathic pain. The predictive accuracy of the developed CoMFA model (Q2 = 0.540, R 2 = 0.980, R 2 pred = 0.613) and the best CoMSIA model (Q2 = 0.665, R 2 = 0.916, R 2 pred = 0.701) has been successfully examined through external and internal validation. Based on ADMET in silico properties, L1, L2 and L3 ligands are non-toxic inhibitors of 1A2, 2C19 and 2C9 cytochromes, predicted to passively cross the blood–brain barrier (BBB) and have the highest probability to penetrate the central nervous system (CNS). Molecular docking results indicate that the active ligands (L1, L2 and L3) interact specifically with Phe176, Glu235, Glu236, Gln110, Asp136 and Glu178 amino acids of the transport protein encoded as 3QEL. Therefore, they could be used as analgesic drugs for the treatment of neuropathic pain.

AN ANALYSIS OF GROWTH AND INSTABILITY IN AREA, PRODUCTION AND PRODUCTIVITY OF MINOR MILLETS IN INDIA

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Abstract

This analysis examines the growth and instability patterns in the area, production, and productivity of minor millets in India. While India has excelled in producing major cereals like rice and wheat, the cultivation of minor millets, which hold higher nutritional value, has been overshadowed. The analysis is based on secondary data collected from various government publications and websites. The study spans from 1950-51 to 2021-22, categorizing the periods into four segments. Compound Annual Growth Rates (CAGRs) were employed to assess trends, revealing a consistent decline in land area dedicated to minor millets cultivation, with an overall negative CAGR of -3.64%. Production exhibited a similar downward trajectory, reflecting a negative CAGR of -2.88%, indicating a notable decrease in total production over the years. In contrast, productivity experienced fluctuations, with an overall positive CAGR of 0.78%, signifying moderate growth in yield per unit area. Instability indices highlighted a rising trend in uncertainties across area, production, and productivity. These findings underscore the need for measures to promote sustainable cultivation and raise awareness about the nutritional benefits of minor millets. The study provides valuable insights for policymakers and agricultural stakeholders in shaping the future of minor millet cultivation in India.

Keywords: CAGR, Instability, Minor millets, Area, Production and Productivity

AGRICULTURAL DEVELOPMENT AND GOOD GOVERNANCE IN NIGERIA

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Abstract

There has always been the cry for agricultural development from of old especially after independence when Nigeria wanted to do her things in her own way; taken and implementing decisions by herself. Then, on board we had different leaders with their different programmes on agriculture such as Operation Feed the Nation, Green Revolution, Agricultural Development Projects, to mention a few. Till date, Nigerian agriculture is yet to meet up with her visions; when no one knows. The paper takes a brief look at the Nigerian agriculture with particular reference to Ogun-state agriculture under the present dispensation with a view to making some suggestions for Improvement. Good governance demands that both the governing and the governed work together to achieve targets. Putting up policies is good, but what about the implementation of such policies. Nigerian agriculture deserves good policy implementation that will get the nation out of persistent poverty. Going back to the land is not enough, the support services must be there, provided by good governance. Government must provide the enabling environment for investments in agriculture to thrive.

Key words: Agricultural development, implementation, Agricultural programmes, Mismanagement

Introduction

Nigeria entered the first republic in 1960, since gaining independence she has witnessed about seven military ruler-ships. The goal of the military governance then, was to make all other arms government to depend on the central government, with orders from above a power structure that enforces rules and regulations. The second and third republics were interrupted by the military followed by the fourth republic under the ruler-ship of President Olusegun Obasanjo,

who ruled successfully both as a military and civilian president. His regime introduced Operation Feed the Nation (OFN) as a military government and handed over to Alhaji Shehu Shagari in 1981. Credence was lent to Shehu Shagari's Second Republic led regime which introduced the Green Revolution programme, the present Nigerian Economic Empowerment Development Strategy (NEEDS) is another programme introduced by President Olusegun Obasanjo that encompassed agriculture and other skill-development programmes. The first two agricultural programmes (OFN and Green Revolution) had their problems and were not successful the NEEDS 1 is an on going programme that is yet to be evaluated for 2007 while we enter NEEDS II.

The question is how has agriculture faired during these regimes, most especially with the nation relying more on oil-revenues rather than developing agriculture; with the fund being diverted to other uses, to the extent of having such funds in foreign individual pockets. Gone were the days of the groundnut and cocoa pyramids in Nigeria.

Talking about governance, it is the total ability to organized, synthesis and direct the various actions of the working parts of government machinery in order for such a government to perform meaningfully, creditably and acceptability (Ikpi, 1997). Governance involves popular participation by the people for the people; it must be democratic, accountable and ensure freedom. It involves responsibility and responsiveness in leadership, accountability; and efficient- and effective- allocation and utilization of the country's resources.

Good Governance and Agricultural Development

The era of military government in the Nigeria seems to have gone forever; but what we seemed to find were military leaders in civilian robes. They have either ruled as military and back on the hot-seat of government or they were retired military officers trying to seek political positions which they either got through elections or nominations. Ikpi (1997) reviewed past governments in West Africa as civilian, democratic or quasi-democratic i.e. military rulers changing cloth or wholly military as it was in Nigeria until 1999. Between 1973 and 1983 according to him almost all Africa countries were ruled by military dictatorships. Immediately after taking independence for their people they settle down to rule their people as though they were inventors of the past colonial masters that they separated themselves from the suffering of their people, while they engage in self-aggrandizement. These rulers became insensitive to the yearnings of their people for basic economic and social amenities. They enrich themselves

with the nation's wealth while they undertake colossal worthless development programme (Ikpi, 1997). According to Lawal (2004), Nigeria has been characterized profoundly by irresponsibility, indiscipline, and inadequate accountability kin leadership and governance especially the past regimes

The situation in Nigeria is such that ruler-ship immediately after Agricultural Development and Good Governance in Nigeria military regime because a family/friendship issue as if to say the seat of government is an inheritance, a source of wealth and power to the family. A\ nation where we have father and son ruling an arm of government. A nation where once we are there, we call on friends to join our government not minding their capability. This state of ruler-ship has left agriculture been less attended to, while majority of the people of the people live in poverty. The people are left without food, shelter, good water and inadequate education that resulted in blown-up population; creating unemployment and joblessness among youths. This paper seeks to highlight the effect of poor governance on agricultural development in Nigeria using indices of agricultural performance.

The Nigerian economy was basically agrarian in the 1970s when the GNP per capital was about $90. Then the country was a major exporter of cocoa, cotton, groundnut (the groundnut pyramids of the North) and palm products (Todaro and Smith 2004).

With the advert of oil, this growth was reversed, Nigeria now relied more on petroleum oil for more than 90% of its exports earnings. Then GNP\ per capital rose to $1000. With dwindling in oil prices and the neglect of the agricultural of the resources. The Nigerian foreign borrowing, corruption and mismanagement of the resources. The Nigeria economy now experiences a period of economic stagnation and decline (Todaro, 2004). With this, the GNP began to go down from US$244 as it was in 1970 (Nemedia, 2001; Tadaro and Smith 2004). With the rapid population growth of 140 million, which is very near the 150millon projected for year 2010 and the neglect of agriculture: it beholds that we review agriculture development in Nigeria and the roles played by past government either as developing the sector or jeopardizing sector. While Todaro and Smith (2004) suggested that if Nigeria is to turn the tide of its economics forturnand mismanagement, there is the need to raise domestic food production and labour productivity.

According to Okuneye (2004), a development economist was said to have attributed the present economic situation in Nigeria to the poor performance of the agricultural sector. The need to

raise food productivity requires that the sector be revitalized. The vision of 2nd Nigeria Economic summit held in 1995 was that by year 2005 agriculture should be profitable and sustainable in the provision of food and fibre while exports should be a major source of foreign exchange earnings for Nigeria. In achieving this vision it was proposed that the following objectives should be attainable by 2005:

I. Implementation of the use of modern agriculture practices.
II. Increased economics power for the farmer
III. Conservation of environment natural resources and the protection of the
IV. Efficient funding and marketing systems
V. Improving rural infrastructural and maintenance

Suggested programmes for achieving the objectives were:

Revitalization and maintenance of existing infrastructure rationalization of the land ownership scheme that seeks for freehold and tenement right for farmers. Here, we are saying that the farmer should be given the right to free land or that they can access land\ easily through lease. Hence, land will not be a factor that will limit their production. We also had (c)the removal of bureaucracy from sea and air ports for the export of agriculture products, and lastly (d) improved extension education for the farmers.

The above objectives and suggested programmer are achievable, but how much success has Nigeria been able to make by the year 2005. What were the hindrances to developing agriculture in Nigeria and Ogun State in particular?

Ikpi (1997), said 'the poor performance of the agricultural sector has been a great concern for all, while the problem was attributed to many causes as fellow: policy framework and low policy relevance. Komarwa(2007) attributed the poor performance to poor infrastructure, inadequate human intervention and poor institutional frame work. While Aribisala(1983), put the blame on the small Nigerian farmer for their poor performance in resource allocation; while a host of other factors were listed which hinder the Nigerian small farmer from performing very well. All these factors were classified by Ikpi (1997) into five viz: technological, socio-economic, organization climate and institutions problem. Of these, the most serious problem that has not helped the small farmer is the setting up of various institutions for agriculture which has not really helped the sector; due to poor coordination, gross mismanagement and duplication of efforts. Also, there is the problem of getting at the target group; inputs meant for

the farmers never get to their reach. The farmers are even expected to bride their way before they can access some assistance at times. Experience has indicated that some government officials in charge of delivery of agricultural assistance to farmers see the programme as a way of enriching themselves. In some cases they enlist their immediate families as beneficiary farmers, where they can not even plant a grain. At times, they sell some of the inputs in the open market

There is also the problem of not placing of not agriculture on the priority list, budget allocation to the sector has been very poor, citing Ogun state as example Okuneye (2004) put it that the state placed a high priority to funding education than to agriculture. That what Ogun state budgeted on education even surpassed that of him the federal government leaving agriculture in shambles. In 1997, according to him the budgetary provision for agriculture was put at 15.34%; this was reduced in 2002 to 3.7%. Also, mentioned was the fact that the bulk of the fund for agriculture was put in the hands of the ministry of Agriculture rather than the institutions that are in close contact with the farmers (e.g. Ogun-State Agriculture Development Project OGADEP) such allocations are squandered on overhead. This view was also shared by Komarwa (2007). No doubt the state of poor funding of agriculture culminates into the general low level output especially for arable crops. The necessary service provisions that will support the farmers are grossly inadequate. Where they are available it is politicilized; if you do not belong you may get it. Politics is seen glaringly affecting agriculture.

Various programmes have been put in place and used in Nigeria to develop agriculture, each arm of government followed federal government's policy on agriculture and possibly in addition to their own internally generated policies. Of the policies apart from those mentioned earlier we have: National Agricultural Land Development Programme, Agricultural Credit Guarantee Scheme, Research Institutes, National Agricultural Land Development Programme, Agricultural Development Programme, Establishment of Agricultural Universities or Faculties of Agricultural Insurance, River Basin Development Authorities, Back to Land Programme, National Directorate for Employment, National Economic Empowerment Development strategy (NEEDS).

They Ogun State government as part of the NEEDS programme embarked upon SEEDS State Economic Empowerment development strategy, while agriculture was enlisted as one of the programmes for achieving 50,000 job generation among the youths. Kudus to the initiator,

but the programmecan not go without some programme design and knowledge of the initiator. The target group was not well defined as indicted by selection procedure. Selection criteria for the programme were not well publicized, if at all they did so, Some of the beneficiaries are evenup till now practicing, the cause of which are yet to be determined. Thetarget group is good, but there is the need to include some vulnerable groups in the programme; above all, it require appropriate monitoring and evaluation until we get good result with good governance, that is the government of the people for the people some of these problems would not have arisen. The needs of the rural and general populace would have been determined following the due process i.e. involving the people in the decisions made on their behalf, placing agriculture on the priority list (i.e. food first) while agriculture is funded appropriately. Agriculture programmes that have been executed must be well accounted for, with all transparency, while efficient utilization of the scarce resources must be all and sundries' watch word.

Steps for Agricultural Revitalization

As agriculture is looked as one of the ways of getting country out of poverty; the targets that we have under the NEEDS programme if followed to the letter will help in moving agriculture forward. The reason being that agriculture is all encompassing. Every National policy affects agriculture either directly or indirectly, more so that these policies enable agriculture to achieving its targets. Empowering people in agriculture may involve having to get them started in agriculture as well as moving the forward; this require some interventions in the area of health, education, appropriate technology, creation of enabling environment, integrated rural development, urban and part-time agriculture, etc.

Health: As pointed out by Pinstrup, Rajul, and Suresh (2004) HIV/AIDS and malaria are the most rampart diseases affecting developing nations. The figure for affected persons in Nigeria was put at 50,000 in 1999 while the figure rose to about 300,000 in 2003/2004. In 2003, the United Nations estimated that the population of Nigeria was 124,009,000 and 5.8 percent of adults between age group of 15 to 49 years were living with HIV/AIDS. With the issue of HIV/AIDS in the country, affected farmers are getting out of farming. Individual with the disease cannot get in to farming because it is energy sapping and strenuous doing the Nigerian/Africa way. There is the need to combat the disease; the nation should find ways of stopping it and /or reducing the number of those affected, because of the devastating affect of the disease on agriculture.

Education: This is very important, aside teaching the farmers improved cultivation practices there is the need to increase the number of field extension workers. Monthly meeting can be organized for all farmers enterprises by enterprise. Also the UBE programme can not but affect agriculture indirectly, children often times get home to tell stories of what their teachers said in the each day. Farmers can learn indirectly from their children/wards, Agricultural science and gardening must stay in the schools' curriculum and should be compulsory for all.

Provision of Enabling Environment: Provision of adequate infrastructure is very crucial to increasing productivity. Such infrastructures include road net-working that will agricultural products, construction of good brigdes where necessary also go along with road provision. For example, we have cases of farm households especially during the rains; example can be cited of Ogun water-side of that are cut away by broken/bad brigdes. Some are not even accessible Ogun state; where we have arrears that are not accessible during raining season due to excessive water logging that debars vehicular movement. The mismanagement and neglect of roads contributed to high farms gate prices. Other infrastructure that are necessary for agriculture are banking transportation marketing services, water provision, hospitals and schools for farms' children. With the presence of FADAMA 11 in Ogun state covering ten local government areas, some these areas now enjoy some of the programmes' laudable projects with the support of their community development associations (CDAS), and state government in conjunction with the World Bank.

Integrated Rural Infrastructure: Neglected rural areas should be attended to with regards to the provision of rural infrastructure. This should be paramount as this will attract investors and prevent migration to cities. Others: User-rights for farmers over some natural-resources e.g. land, water, forest-resources. Diversification in agriculture all farmers should diversify in order to reduce risks. Capacity building for extension workers and other key officers as well as provision of adequate extension officers, at the ratio of 30 farmers to 1 extension agent; and adequate financial support for farmers. Above all, leaders should accept their responsibilities, accept criticisms for correction and amend the past. Political leaders should refrain from their offices / position for selfish ends. Let not government/ruler-ship be that we have come to have our share of the 'goody'.

Conclusion

This paper has presented just a bit of the happenings in government and agricultural development. It is important that governance in Nigeria be remodeled, it should be viewed as coming to serve and revitalize not making more money at the expense of the citizenry.Agriculture deserves good policy and implemetation that will get the nation out of the persistent poverty. Going back to the land is not enough, the support services must be there, to be provided by good governance. Government must provide the enabling environment for investments (both private and public) in agriculture to thrive. Nigeria deserves better governance

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ORGANİK ELMA SİRKESİNİN TOPLAM FENOL MADDE MİKTARI, ANTİOKSİDAN KAPASİTESİ VE ANTİDİYABETİK AKTİVİTESİ

TOTAL PHENOL, ANTIOXIDANT CAPACITY AND ANTIDIABETIC ACTIVITY OF ORGANIC APPLE VINEGAR

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ÖZET

Sirke karbonhidrat içerikli hammaddelerden etil alkol ve asetik asit fermantasyonu ile üretilen geleneksel bir gıdadır. Sirke turşu, konserve ve salata gibi birçok gıdanın üretiminde kullanılmanın yanı sıra antioksidan, antimikrobiyal, antikarsinojen etkileri sayesinde de dikkat çekmektedir. Bu çalışmada, ticari olarak üretilen organik elma sirkesinin çeşitli kalite ve biyoaktif özelliklerinin yanında duyusal değerlendirilmesi amaçlanmıştır. Sirkenin toplam fenolik madde miktarı (Folin Ciocalteu), antioksidan kapasitesi (DPPH), Diabetes mellitus'ta anahtar konumundaki enzimlerin inhibisyonu (pankreatik α-amilaz, α-glikozidaz) ve duyusal özellikleri belirlenmiştir. Enzimlerin inhibisyonunda standart olarak akarboz kullanılmıştır. Sirkenin titrasyon asitliği asetik asit cinsinden %3.26 bulunurken, kurumadde değeri %2.71 ve su aktivitesi değeri ise 0.968 olarak tespit edilmiştir. Organik elma sirkesinin toplam fenol madde miktarı 204.02 mg GAE/L ve DPPH antioksidan kapasitesi 288.66 µmol TE/L belirlenmiştir. Sirke hem pankreatik α-amilaz hem de α-glikozidaz inhibisyonunda etkili olmuştur. Duyusal özellikler arasında elma sirkesinin renk ve görünüş puanları, keskinlik, tat ve koku puanlarına göre daha düşük değerlendirilmiştir. Sirkenin genel beğeni puanı ise 5 puanlı skala üzerinden 3.50 olmuştur. Çalışma ile organik elma sirkesinin yüksek biyoaktif özellik içermesinden dolayı fonksiyonel özellik gösterdiğini söylemek mümkündür. Sağlık üzerine olumlu etkileri bulunan sirkelerin (özellikle elma ve organik) özelliklerinin ortaya konulmasıyla tüketicilerin bu ürünlere daha fazla ilgi göstereceği düşünülmektedir.

Anahtar Kelimeler: Sirke, Elma, Antioksidan, Enzim İnhibisyonu, Duyusal Özellikler.

ABSTRACT

Vinegar is a traditional food produced from carbohydrate-containing raw materials by ethyl alcohol and acetic acid fermentation. In addition to being used in the production of many foods such as pickles, canned foods and salads, vinegar attracts attention with its antioxidant,

antimicrobial and anticarcinogenic effects. This study aimed to evaluate the various quality and bioactive properties of commercially produced organic apple cider vinegar as well as its sensory evaluation. Total phenolic substance amount (Folin Ciocalteu), antioxidant capacity (DPPH), inhibition of key enzymes in Diabetes mellitus (pancreatic α-amylase, α-glucosidase) and sensory properties of vinegar were determined. Acarbose was used as standard in the inhibition of enzymes. While the titratable acidity of vinegar was found to be 3.26% in terms of acetic acid, its dry matter value was 2.71% and its water activity value was 0.968. The total phenol content of organic apple cider vinegar was determined to be 204.02 mg GAE/L and the DPPH antioxidant capacity was 288.66 µmol TE/L. Vinegar was effective in inhibiting both pancreatic α-amylase and α-glucosidase. Among the sensory properties, color and appearance scores of apple cider vinegar were evaluated lower than pungency, taste and smell scores. The overall appreciation score of vinegar was 3.50 on a 5-point scale. With the study, it is possible to say that organic apple cider vinegar has functional properties due to its high bioactive properties. It is thought that consumers will show more interest in these products as the properties of vinegars (especially apple and organic) that have positive effects on health are revealed.

Keywords: Vinegar, Apple, Antioxidant, Enzyme Inhibition, Sensory Properties.

GİRİŞ

Sirke, berrak ve hammaddeye göre değişen renge sahip sulu bir ürün olup, üretimi gıda muhafazasında kullanılan en eski yöntemlerden biridir (Aktan ve Kalkan, 2011; Dıraman ve ark., 2023). Sirke, karbonhidrat kaynaklı hammaddelerden (meyveler, hububatlar, sebzeler, şaraplar gibi) mayalar ve asetik asit bakterileri yardımıyla etil alkol ve asetik asit fermantasyonu sonucunda üretilen geleneksel bir üründür (Karabiyikli ve Sengun, 2017). TSE 1880 EN 13188 standardına göre ise sirke; "Tarım kökenli sıvılar veya diğer maddelerden, iki aşamalı alkol ve asetik asit fermantasyonuyla, biyolojik yolla üretilen kendine özgü ürün" ve sirke çeşitleri ise şarap sirkesi, meyve sirkesi, meyve şarabı sirkesi, elma şarabı sirkesi, beyaz sirke, tahıl sirkesi, malt sirkesi, aromalı sirke ve diğer sirkeler olarak bildirilmiştir.

Meyve artıkları ve sofralık olarak kullanılmayan meyveler üretimde kullanıldığı için sirke aynı zamanda bir değerlendirme ürünüdür. Sirke üretiminde kullanılacak olan hammaddenin yüksek şeker oranına ve düşük pH değerine sahip olması istenmektedir (Yücel Şengün ve Kılıç, 2019). Sirkenin kalite ve kimyasal bileşimi; hammadde çeşidi, hammaddenin yetiştirilme koşulu ve üretim tekniğinden (yüzey kültür, hızlı ve derin kültür) etkilenmektedir (Morales ve ark., 2004).

Sirke de %80 oranında su bulunurken, %20 oranında ise mineraller, vitaminler, organik asitler, alkoller, aminoasitler, fenolik ve uçucu bileşikler oluşturmaktadır. Bu bileşikler sayesinde sirke kendine has tat, kokuya sahip olmasının yanında biyoaktif özelliklerde kazanır (Dıraman ve ark., 2023). Meyve ve sebzeler kullanılarak üretilen sirkelerde bulunan biyokatif bileşikler, antimikrobiyal, antitümor, antiobezite gibi sağlık üzerine olumlu etkiler yapmaktadır (da Silva ve ark., 2016; Hafzan ve ark., 2017; Xia ve ark., 2020).

Elma, dünyada muzdan sonra en fazla üretilen yumuşak çekirdekli bir meyvedir. Türkiye'nin hemen hemen her bölgesinde yetiştirilen elma taze tüketilebildiği gibi reçel, marmelat, meyve suyu, şarap, sirke gibi farklı ürünlere de işlenmektedir (Tangüler ve ark., 2021).

Bu çalışmada, ticari olarak üretilen organik elma sirkesinin çeşitli kalite (kurumadde, kül, su aktivitesi, suda çözünür kurumadde, pH, titrasyon asitliği), biyoaktif (toplam fenol madde

miktarı, antioksidan kapasite, enzim inhibisyonu) ve duyusal özelliklerinin değerlendirilmesi amaçlanmıştır. Böylece organik elma sirkesinin kalite parametrelerinin yanında fizyolojik etkileri de literatüre kazandırılacaktır.

MATERYAL VE METOT

Materyal

Organik elma sirkesi (koruyucu kullanılmadan üretilmiş) piyasadan temin edildikten sonra analizler yapılıncaya kadar +4˚C'de muhafaza edilmiştir. Analizler 3 tekerrürlü olarak gerçekleştirilmiştir.

Kurumadde ve Kül Miktarı

Sirkeden 3-5 g tartılarak 105±2°C'de sabit hale getirilmiş ve kurumadde miktarları gravimetrik olarak belirlenmiştir. Krozelere 3-5 g sirke örneği tartılmış ve 550 ºC kül fırınında beyaz kül oluncaya kadar yakılmıştır. Kül miktarları % olarak belirlenmiştir (Cemeroğlu, 2013).

pH Değeri ve Titrasyon Asitliği

Elma sirkesinden 10 ml alınıp 20 ml distile su ile karıştırılarak homojenize edilmiş ve cam elektrotlu dijital pH-metre (Mettler Toledo, İsviçre) ile pH değerleri belirlenmiştir. pH değeri belirlendikten sonra karışım 0.1 N NaOH ile 8.1 pH değerine kadar titre edilmiştir. Sonuçlar asetik asit cinsinden % olarak hesaplanmıştır (Cemeroğlu, 2013).

Suda Çözünür Kurumadde Miktarı

Sirke örneğinin briks değerleri saf su ile kalibre edilen abbe refraktometresi cihazı (SOIF WYA-2S, Çin) kullanılarak belirlenmiştir (Cemeroğlu, 2013).

Su Aktivitesi Tayini

Sirkeden su aktivitesi cihazının kaplarına konulmuş ve cihaz (Novasina AG LabTouch-aw, CH-8853 Lachen, Switzerland) yardımıyla a_w değerleri belirlenmiştir (Konar, 2013).

Toplam Fenol Madde Miktarı ve Antioksidan Kapasite

Sirkenin toplam fenolik madde miktarı Folin Ciocalteu kolorimetrik yöntemine göre tespit edilmiştir. Örnekten farklı konsantrasyonlarda 1 ml alınarak, 60 ml saf su ve 5 ml %10'luk Folin Ciocalteu reaktifi üzerine eklenmiş ve 8 dk sonra 15 ml %20'lik sodyum karbonat eklenmiş ve 100 ml hacme kadar saf su ile tamamlanmıştır. 2 saat karanlıkta bekletildikten sonra numunelerin 760 nm'de absorbansları UV-spektrofotometre (Shimadzu UV-1700, Japonya) ile ölçülmüştür. Toplam fenol madde içeriği mg GAE/L olarak hesaplanmıştır (Singleton ve ark., 1999). DPPH*(2,2- diphenyl-1-picrylhydrazyl) radikal yakalama kapasitesi için 24 mg DPPH* 100 mL metanolde çözündürülerek stok solüsyon hazırlanmıştır. Farklı konsantrasyonlarda 150 µL sirke ve 2850 µL DPPH solüsyonu 24 saat karanlıkta bekletildikten sonra 515 nm'deki absorbansları ölçülmüştür. Sonuçlar standart olarak kullanılan troloksun eşdeğeri (µmolTE/g) olarak hesaplanmıştır (Thaipong ve ark., 2006).

Pankreatik α-amilaz inhibisyonu

6 ünite/mL'lik α-amilaz (40 µL, 0.006 M NaCI içeren 0.1 M, pH 6.9 fosfat tamponu), 560 µL pH 6.9 fosfat tamponu ve 100 µL sirke tüplere alınıp su banyosunda 37°C'de 20 dk bekletilmiştir. Daha sonra nişasta çözeltisi (300 µL %1'lik) ilave edilip tekrar su banyosunda 37°C'de 20 dk bekletilmiştir. Su banyosundan alınan tüplere DNS çözeltisinden 750 µL eklenmiş ve 5 dk kaynar suda kaynatıldıktan sonra soğutulup 6 mL saf su eklenerek UV-spektrofotometrede absorbans 540 nm dalga boyunda köre karşı ölçülmüştür. Kör aynı reaksiyon karışımında enzim yerine enzimin çözündürüldüğü tampon eklenerek hazırlanmıştır. 1 ünite enzim aktivitesi dakikada 1 mmol maltoz oluşturan enzim miktarı olarak tanımlanmıştır (Liu ve ark., 2013).

α-Glikozidaz İnhibisyonu

50 µL 2 ünite/mL α-glikozidaz ve 1.15 mL 0.1 M pH 6.8 fosfat tamponu ile karıştırılmıştır. Karışım üzerine 50 µL sirke eklenerek 37°C'de 10 dk su banyosunda bekletilmiştir. Bekleme süresi ardından karışım üzerine 5 mmol 50 µL substrat (p-nitrofenil-α-D-glikopiranozit) eklendikten sonra 37°C'de 30 dk su banyosunda inkübasyona bırakılmıştır. Süre sonunda 2 mL 0.2 M sodyum karbonat ve 4.7 mL saf su eklenerek reaksiyon durdurulmuştur ve UV-spektrofotometrede absorbans 405 nm dalga boyunda köre karşı ölçüm yapılmıştır. Kör aynı reaksiyon karışımında enzim yerine enzimin çözündürüldüğü tampon eklenerek hazırlanmıştır. 1 ünite enzim aktivitesi dakikada 1 µM p-nitrofenol oluşturan enzim miktarı olarak tanımlanmıştır (Liu ve ark., 2013).

% inhibisyon değeri $[(A_0-A_i)/A_0]\times100$ formülü ile hesaplanmıştır. Burada inhibitörsüz enzim aktivitesi A_0 ve inhibitör varlığında enzim aktivitesi A_i olarak belirtilmiştir. Enzimi %50 inhibe (IC_{50}) etmek için gerekli sirke miktarları hesaplanmıştır. Akarboz enzim inhibisyonu için pozitif kontrol olarak kullanılmıştır.

Duyusal Analiz

Elma sirkesinin duyusal analizi örneklerin renk, koku, keskinlik, tat, görünüş ve genel beğeni açısından durumu 5 puanlı hedonik skala kullanılarak belirlenmiştir.

BULGULAR VE TARTIŞMA

Organik elma sirkesine ait kalite özellikleri Tablo 1'de verilmiştir. Sirkenin titrasyon asitliği, TSE 1880 EN 13188 standardına göre 1000 ml'de 40 g'dan az olmamalıdır. Ancak sirkenin titrasyon asitliği asetik asit cinsinden standardın altında kalmıştır. İlgili standartta pH değeri ile ilgili bir sınırlama yoktur. Elma sirkelerinin titrasyon asitliğini; Aykın ve ark. (2015) %4.05, Gerbi ve ark. (1998) %5.40-6.60, Tangüler ve ark. (2021) %1.53-2.31, Kobya (2018) %2.71-3.50, Chang ve ark. (2005) %1.17-5.28 olarak ve pH değerleri ise 2.36-4.40 aralığında bildirilmiştir (Gerbi ve ark., 1998; Chang ve ark., 2005; Aykın ve ark., 2015; Tangüler ve ark., 2021).

Organik elma sirkesinin kurumadde miktarının büyük bir oranını suda çözünür kurumadde oluştururken kül miktarı düşük bulunmuştur. Sirkenin genel kimyasal bileşimi kullanılan hammaddenin çeşidi, cinsi, yetiştirme koşulları ve kullanılan üretim tekniğine göre değişiklik gösterdiği bilinmektedir.

Tablo 1. Organik elma sirkesinin kalite özellikleri

pH	3.23±0.08
Titrasyon asitliği*	3.26±0.12
Kurumadde (%)	2.71±0.09
Kül (%)	0.15±0.00
Briks	2.29±0.30
a_w	0.968±0.15

* %asetik asit cinsinden

Diğer çalışmalara bakıldığında elma sirkesinin kurumadde oranını Aykın ve ark. (2015) %2.14, Tangüler ve ark. (2021) %1.71 olarak belirlerken, % kül miktarını Gerbi ve ark. (1998) %0.20-0.23, Akbaş ve Cabaroğlu (2010) %0.07-0.35 aralığında tespit etmişlerdir. Farklı hammaddelerden üretilen sirkelerin briks değeri literatürde 2.50-9.10 aralığında (Ünal ve Canbaş, 2008; Cavdaroglu ve Ozen, 2022; Öztürk, 2022), elma sirkesinden ise briks 2.60 (Chang ve ark., 2005) olarak bildirilmiştir.

Toplam fenol içeriği ile antioksidan kapasitesi Tablo 2'de verilmiştir. Elma sirkelerinin toplam fenolik madde miktarı diğer çalışmalarda 40.44-4684.50 mg GAE/L aralığında bildirmiştir (Aykın ve ark., 2015; Öztürk ve ark., 2015; Bayram ve ark., 2018; Ousaaid ve ark., 2020; Tangüler ve ark., 2021). Elma sirkesinin DPHH antioksidan kapasitesini Pinsirodom ve ark. (2008) 71 µg TE/ml olarak bildirirken, Ousaaid ve ark. (2020) IC50 DPHH değerini 0.74 µl/ml

olarak tespit etmişlerdir. Çalışma konusu olan organik elma sirkesinin yüksek antioksidan kapasiteye sahip olduğunu söylemek mümkündür.

Tablo 2. Organik elma sirkesinin toplam fenol madde miktarı ve antioksidan kapasitesi

Toplam Fenol (mg GAE/L)	204.02±0.02
DPPH (µmol TE/L)	288.66±0.95

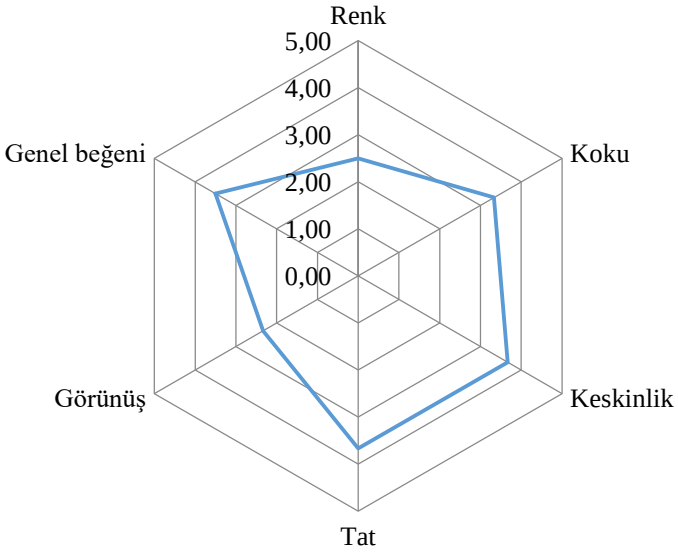
Elma sirkesinin α-glikozidaz ve α-amilaz enzimleri üzerine inhibisyon etkisi, standart olarak kullanılan akarboza yakın olarak tespit edilmiştir. Sirkenin hammaddesine ve üretimine bağlı olarak diyabette etkili olmaktadır. Sirkenin organik elmadan yapılması ve katkı maddesi kullanılmaması enzim inhibisyonuna katkı sağlamıştır.

Tablo 3. Enzim inhibisyonunun IC_{50} sonuçları (mg/L)

	α-Glikozidaz inhibisyonu	**α-Amilaz inhibisyonu**
Akarboz	11.91±1.02	13.59±1.13
Elma suyu sirkesi	14.65±1.21	14.12±2.10

Sirkenin in vivo/in vitro çalışmalarda insülin hassasiyetini geliştirerek kan şekeri seviyesini olumlu yönde etkilediği ve postprandiyal glisemiyi düşürdüğü bildirilmiştir. Bundan dolayı diyabet hastalarında sirke tüketimi önerilmektedir (Leeman ve ark., 2005; Öztürk ve ark., 2009; Yücel Şengün ve Kılıç, 2019).

Elma sirkesinin duyusal analizinde panelistlerden aldığı ortalama puanlar Şekil 1' de verilmiştir. Panelde 5 puanlık skala kullanılmış olup elma sirkesi renk ve görünüş açısından ortalamanın altında kalmıştır. Ancak koku, keskinlik, tat ve genel beğeni bakımından elma sirkeleri beğeni görmüştür.



Şekil 1. Duyusal analiz sonuçlarına ait örümcek ağı grafiği

SONUÇ

Bu çalışmada ülkemizde en fazla tercih edilen sirkelerden biri olan elma sirkesi konu alınmıştır. Ticari organik elma sirkesinin kalite özellikleri, toplam fenolik madde miktarı, antioksidan kapasitesi, α-glikozidaz ve α-amilaz enzimleri üzerine inhibisyon etkisi ve duyusal özellikleri belirlenmiştir. Kalite analizleri sonucuna bakıldığında sirkeden beklenilen pH ve asitlik

değerine ulaştığını, sirkede bulunan kurumaddenin büyük bir oranının suda çözünür kurumadde olduğunu ve kül oranının düşük bulunduğunu söylemek mümkündür. Organik elma sirkesi yüksek toplam fenolik madde ve buna paralel olarak da yüksek antioksidan kapasiteye sahip olmuştur. Sirkenin hem α-glikozidaz hem de α-amilaz enzimlerine karşı standarda yakın bir inhibe etkisinin bulunduğu tespit edilmiştir. Duyusal olarak koku, keskinlik, tat ve genel beğeni kriterlerinden yüksek puan almıştır. Ülkemizde üretilen sirkeler üzerine yapılmış çalışmalar bulunmasına karşın hem organik hammadde kullanılarak üretilen hem de sirkelerin enzim inhibisyonu ile ilgili yapılmış çalışmalar sınırlıdır. Yapılan çalışmanın literatürdeki bu boşluğun doldurulmasına yardımcı olacağı düşünülmektedir.

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SLOW RELEASE MECHANISM OF COATED FERTILIZERS AND AFFECTING FACTORS

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ABSTRACT

Coated fertilizers are a type of fertilizers designed with a controlled-release mechanism to deliver nutrients to plants over an extended period. The coating on these fertilizers plays a crucial role in regulating nutrient release. Coated fertilizers contain small, granular particles of conventional fertilizers such as nitrogen, phosphorus, or potassium encapsulated within a protective coating. The coating material is typically made of polymers or other materials that can be semi-permeable or impermeable. The primary purpose of the coating is to slow down the release of nutrients from the fertilizer granules. This slow-release feature helps provide a continuous and steady supply of nutrients to plants, which can be particularly beneficial for crops requiring nutrients over an extended growth period. The release of nutrients from the coated fertilizers is influenced by various environmental factors such as temperature, moisture, and microbial activity in the soil, which can affect the coating's permeability and the rate at which nutrients are released. Coated fertilizers are designed to match the nutrient release rate with the plant's nutrient uptake requirements. This helps to prevent nutrient leaching into groundwater and reduces the risk of over-fertilization, which can protect the environment. These fertilizers can be formulated to provide nutrient release over a specific duration, ranging from a few weeks to several months or even years. The controlled-release mechanism in coated fertilizers offers several advantages, including improved nutrient use efficiency, reduced fertilizer application frequency, decreased risk of nutrient runoff and pollution, and enhanced crop yield and quality. There are different types of coatings used in coated fertilizers, such as sulfur, polymer, resin, or wax-based materials, each with its own specific characteristics and release patterns. Releasing of the nutrients from the coated fertilizer is mostly related with water penetration into the sistem. After water, which has an important role in release, penetrates into the covered fertilizer granule, the gradual release of nutrients occurs. As the osmotic pressure in the coated fertilizer core gradually increases, the coating on the fertilizer begins to swell. This causes two possible mechanisms depending on the osmotic pressure. First, if the osmotic pressure value is greater than the resistance created by the covering material, the material coating begins to crack and all the nutrients begin to be released from the fertilizer. The second is; If the coating resistance is strong enough to carry out the pressure, the coated fertilizer releases the nutrients very slowly. In summary, the release mechanism in coated fertilizers involves encapsulating conventional fertilizers within a protective coating that regulates the gradual release of nutrients to plants. This technology helps optimize nutrient delivery, minimize environmental impact, and improve overall crop performance.

Keywords: Coated fertilizers, slow-release mechanism, effectiveness, fertilizer technology.

IMPACT STUDY OF LOCALIZED IRRIGATION ON SOIL SALINIZATION IN THE REGIONS OF AL HAOUZ AND KELAA DES SRAGHNA

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Summary

The El Haouz and El Kelaa Des Sraghna region has a well-known agricultural reputation, and on the other hand, salinization is a problem in these perimeters, given the aridity of the area and the unfavorable climatic conditions for soils and plants. For this reason, irrigation activities have been organized through the installation of localized irrigation systems, on the one hand, to supply crops with water and, on the other, to guarantee maximum crop yields. In the present work, we will approach this subject from another angle to investigate the traces and footprint of these irrigation systems in the region while comparing the upstream and downstream parts of the area. In this respect, the work requires an overview of remote sensing, to verify areas with high salinity potential, followed by a field visit and collection of samples reserved for the process of physical and chemical analysis of agricultural soil. These analyses are used to monitor changes in salinization and determine whether localized irrigation has been successful in the areas concerned.

Keywords: Al Haouz, Kelaa des Sragna, salinization, localized irrigation, and soil

THE ANALYSIS OF THE RELATIONSHIP BETWEEN DIESEL OIL PRICES AND FOOD INFLATION IN TURKIYE

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ABSTRACT

Increasing drought concerns due to environmental degradations, disruptions in the global supply chain during the pandemic and increases in oil prices have led to significant increases in food prices, especially in recent times. Food prices are one of the important elements for food security. In this context, the aim of this study is to analyze the causal relation between diesel oil prices and food inflation in Türkiye for the period of 2002-2023 by using the Fourier Toda Yamamoto Causality Test. Monthly data was used in the study. The results show that there is a bidirectional causality between diesel oil prices and food inflation. This finding proves that policies decreasing agricultural input costs are important to reduce food inflation.

Keywords: Diesel oil prices, food inflation, Fourier Toda Yamamoto Causality Test

1.INTRODUCTION

Climate changes occurring due to environmental degradation, increase in logistic and production costs because of rise in oil and natural gas prices, disruption in the global supply chain owing to COVID-19 and the Russia and Ukrania War, high marketing margin trigger food safety concerns by increasing food prices (Yavuz 2021: 24). Table 1shows that in the changes global food prices during 2005-2022.

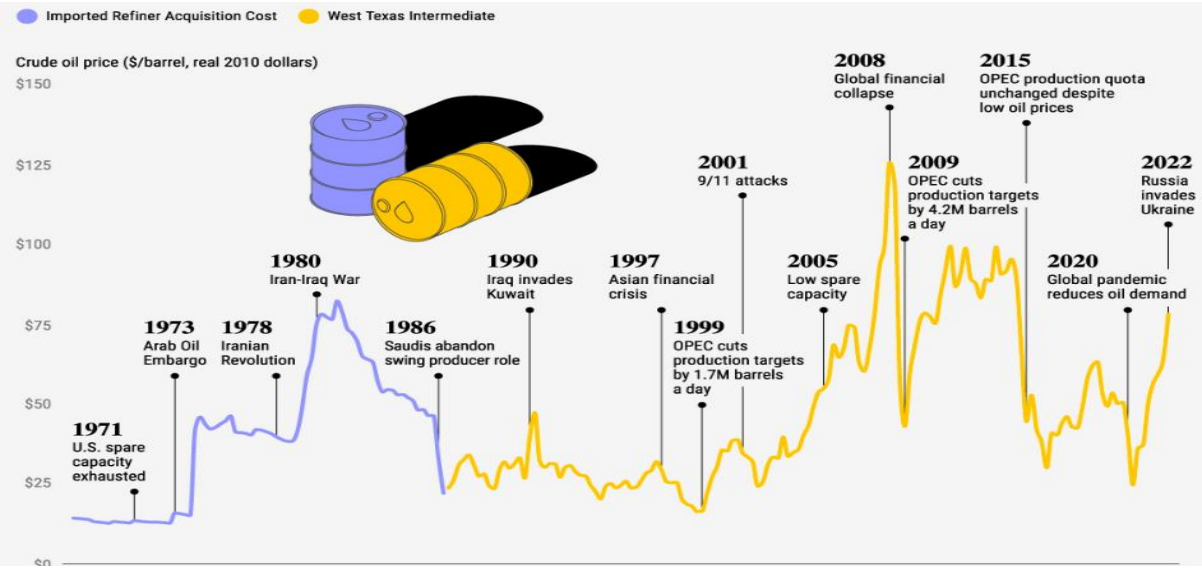
Table 1: Global Food Price Index

	Food Price Index	Meat	Dairy	Cereals	Vegetables oils	Sugar
2005	67.4	71.8	77.2	60.8	64.4	61.2
2006	72.6	70.5	73.1	71.2	70.5	91.4
2007	94.3	76.9	122.4	100.9	107.3	62.4
2008	117.5	90.2	132.3	137.6	141.1	79.2
2009	91.7	81.2	91.4	97.2	94.4	112.2
2010	106.7	91	111.9	107.5	122	131.7
2011	131.9	105.3	129.9	142.2	156.5	160.9
2012	122.8	105	111.7	137.4	138.3	133.3
2013	120.1	106.2	140.9	129.1	119.5	109.5
2014	115	112.2	130.2	115.8	110.6	105.2
2015	93	96.7	87.1	95.9	89.9	83.2
2016	91.9	91	82.6	88.3	99.4	111.6
2017	98	97.7	108	91	101.9	99.1
2018	95.9	94.9	107.3	100.8	87.8	77.4
2019	95.1	100	102.8	96.6	83.2	78.6
2020	98.1	95.5	101.8	103.1	99.4	79.5
2021	125.7	107.7	119.1	131.2	164.9	109.3
2022	143.7	118.8	142.4	154.7	187.8	114.5

Source: FAO

Since 2006, global food prices have increased by about 70 % within a few months. When the table is examined, it is seen that global food prices rose significantly in 2007 and 2008. Increasing oil prices due to the 2008 global economic crisis are the main reason for the increase in food prices in this period. Figure 1 shows the change in oil prices.

Figure 1: Historical oil Prices



Source: [Visualizing Historical Oil Prices (1968-2022) (visualcapitalist.com)]

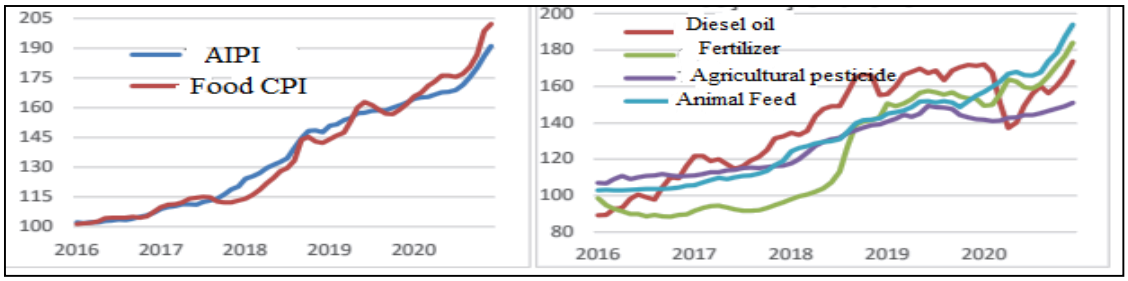
In addition, Since the end of 2007, financial uncertainties have increased and speculative investments in the agriculture, energy, and food sectors increased. This process led

to an increase in the prices of food products such as wheat, rice, corn, and soybeans and the formation of price bubbles in the food market (UN, 2011: 67).

COVID-19 and the Russia-Ukrania War are other factors triggering food inflation. Covid 19 reduced oil demand. Therefore, oil prices decreased during the pandemic. But, After pandemic, a huge increase in oil demand led to a rise in oil prices. Economic sanctions imposed on Russia because of the war caused to an increase in oil prices. In addition, Russia and Ukrania plays an important role in the global food supply chain. Russia and Ukraine provide 14% of world wheat production and more than half of sunflower production (FAO, 2022).

In Turkey, Oil prices trigger food inflation by increasing diesel oil prices, which is an important agricultural input, Figure 2 illustrates the changes in agricultural input prices in Turkey.

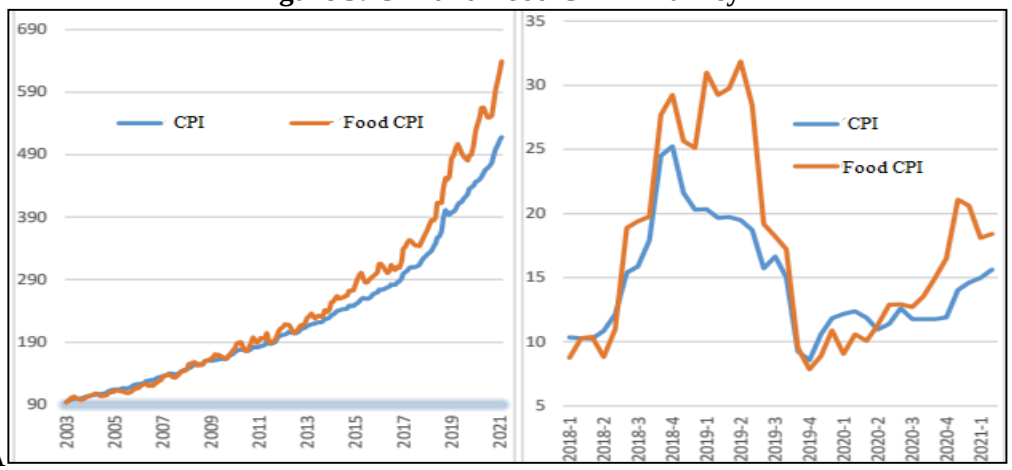
Figure 2: Agricultural input prices



AIPI represents the agricultural input price index while the producer price ındex of agricultural products
Source: Yavuz, 2021:17.

When Figure 2 is examined, it is seen that agriculture input prices increased about by twice in Turkey. Diesel oils vary in parallel with oil prices.

Figure 3: CPI and Food CPI in Turkey



A
Source: Yavuz, 2021:17

Figure 3 shows the change in CPI and Food CPI in Turkey for the period of 2003-2021. According to Figure 3, Food CPI is higher than food CPI in Turkey. Reducing food prices is important for food security both at the level national and international.

2. DATA SET AND METHODOLOGY

The aim of this study is to investigate the causality relationship between diesel oil prices and food prices. Diesel oil prices were compiled from the Republic of Turkey Ministry of Agriculture and Forestry and food prices were compiled from TURKSTAT.

Table 2: Data Set and Database

Variables	Notation	Database
Diesel Oil prices	LNINF	Ministry of Agriculture and Forestry
Food Price Index	LNDIESELOIL	TURKSTAT

2.1.Fourier Toda Yamamoto Causality Test

In the study, the Fourier Toda Yamamoto Causality Test was applied Fourier Toda Yamamoto Causality test developed by Nazlıoğlu et al. (2016). Fourier Toda Yamamoto Causality test was adapted from the Toda Yamamoto causality test developed by Toda & Yamamoto (1995). Fourier Toda Yamamoto test considers structural breaks. Structural breaks were included in the Toda Yamamoto causality test by using trigonometric functions. The model is formulated as follows;

$$y_t = a_0 + \gamma_1 sin\left(\frac{2\pi kt}{T}\right) + \gamma_2 cos\left(\frac{2\pi kt}{T}\right) + \beta_1 y_{t-1} + \cdots + \beta_{p+d} y_{t-(p+d)} + \varepsilon_t \quad (1)$$

The null hypothesis indicates there is no causality from one variable to another variable. The existence of a causality relationship shows that past period values of the independent variable can be used to estimate the next period values of the dependent variable

2.2.Econometric Tahmin

The degrees of the variables must be determined in causality tests. In this study, the Fourier ADF unit root test developed by Enders & Lee (2012) was used to decide the degree of the stationary of the variables. Table 3 indicates the results of the Fourier ADF Unit Root Test.

Table 3: Fourier ADF Unit Root Test

	Frequency	Min. KKT	F	Optimal Lag	FADF Test stat
LNINF	1.000000	0.140559	8.759922	8.000000	4.901937*
LNDIESELOIL	1.000000	0.698697	7.990227	14.00000	4.126102*

Critical values for F statistics are 10.35, 7.58, and 6.15 for 1 %, 5 %, and 10 % significance levels., respectively. Critical Values for FADF test statistics are -4.42, -3.81, and -3.49 for 1 %, 5 %, and 10 % significance levels., respectively.

When estimation results are examined, it is seen that the test statistics calculated for both LNINF and LNDIESEL are higher than critical values as absolute values. The null hypothesis emphasizing that series do not have unit roots is rejected. Table 4 shows the results of the Fourier Toda Yamamoto Causality Test.

Table 4: The results of Fourier Toda Yamamoto

H_0	Wald Stat	f	Prob
There is no causality from diesel oil prices to food inflation.	110.088	1.00	0.000
There is no causality from food inflation to diesel oil prices.	15.733	1.00	0.001

The findings show that there is a bidirectional causality between diesel oil prices and food inflation.

CONCLUSION

Climate change, increase in speculative food investments, rising energy costs, disruption global supply chain due to COVID-19, Russia-Ukrania War are factors rising regional and global food inflation. Since 2006, global food prices have increased by about 70 % within a few months. In Türkiye, the food price index is higher than the general price index. Oil prices trigger food prices by raising logistic and agricultural input costs. In this context, this study investigates the causality relationship between diesel oil prices and food prices. According to the results of the study, there is bidirectional causality between diesel oil prices and food prices. This finding shows that past diesel oil prices can be used to estimate the next food prices. In this context,

In order to reduce the rise in food prices, it is necessary to expand the use of biodiesel by encouraging oilseed plant production and reducing foreign dependency in agriculture with policies that will increase agricultural productivity.

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HIGH-ALTITUDE PASTURES

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Abstract

The high-altitude zones host a range of grasslands and pioneer communities above the ecological limit for woody plants. Climate-related variables, such as the duration of snow cover, prolonged frost, short growing season, stifling heat, and wind, impede their development. Additionally, a wide variety of ethnic communities that have cultivated and transmitted through rich cultural practices, farming methods, and related traditional knowledge homes the mountains. A unique type of free-range grazing known as transhumance is practiced in mountains all over the world. It is a significant source of income for those who live in high-altitude regions and has been developed in response to the poor quality of the land and the seasonality of production. Long-term conservation and development planning for these animal producing zones will require an understanding of the nature of high-altitude ecosystems, their interactions, and how they respond to climatic and non-climatic forces.

Keywords: High altitude, rangelands, pastures, fodder, livestock, grazing

1. Introduction

Rangelands and the interfaces they form with other ecosystems have the potential to play a key role in preserving the most essential services, including as carbon sequestration, water storage and provision, and biodiversity maintenance. Therefore, national and international

organizations are working to protect and restore this ecosystem in order to preserve the carbon reserves already there and to slow down climate change. There is an urgent need to promote in-depth research on high-altitude ecosystem interfaces and to develop sound methodologies for monitoring, restoring, and valuing these interfaces (Ning et al., 2014).

Over 12% of the world's population lives in mountainous areas, which make up almost 24% of the planet's land surface (Sharma et al., 2010). One-fifth of humanity depends on the mountains for a wide range of ecosystem products and services, including freshwater, energy, timber, numerous bioresources, possibilities for recreation, and opportunities for spiritual renewal. Mountains harbor an extremely high level of biological diversity, which results from the compression of eco-climatic zones along sharp altitudinal gradients, the diversity of habitats produced by micro-topographic variation, and the variable directional orientation with rapid changes in aspect (Körner, 2003).

Mountains are home to a staggering amount of biological diversity due to the compression of eco-climatic zones along acute altitudinal gradients, the diversity of habitats caused by micro-topographic variation, and a varied directional orientation with quick changes in aspect. Long-term conservation and development planning will require an understanding of the nature of high-altitude ecosystems, their interactions, and how they respond to climatic and non-climatic forces. Boundaries are now seen as crucial structural and functional elements of landscape mosaics due to the development of landscape ecology. Over the last decade, the term ‘ecosystem interface’ has been used more frequently in a comprehensive context by conservationists and planners, while considering transboundary landscapes and anthropogenic disturbances and considering crosscutting issues related to policy, governance, and regional dataset sharing. The terms ‘ecosystem interface’ and ‘ecotone’ and are virtually synonymous, but ecotone is more commonly used by traditional community ecologists and ecosystem interface by natural resource managers and landscape ecologists (Ning et al., 2014).

At the forest and tree line, cold temperatures are considered to be the main limiting factor. At temperatures below 5 °C, cambial growth, or the development in girth of trees, ceases to occur (Rossi et al., 2007). High-altitude pastures, or alpine summer grazing regions, are hotspots for biodiversity and have significant cultural historical assets. The Flora-Fauna-

Habitat-Directive of the European Union protects low density forests (Alpine Larix decidua and/or Pinus cembra forests) and species-rich open land (Alpine and boreal heaths, siliceous Alpine and boreal grasslands). These habitats are threatened by the accelerated mountain climate warming and the expected upslope shift of vegetation zones (Peringer et al., 2022).

The alpine elevational belts host a range of grasslands and pioneer ecosystems above the biological limit for woody plants. Climate-related variables, such as the duration of snow cover, protracted frost, short growing season, stifling heat, and wind, impede their development. Steep south-facing slopes are taken up by grasslands, forming steppe-like settlements. Because they resemble arctic tundra and are found on flat slopes, these communities are frequently referred to as "Alpine tundra." They are only partially herbaceous. Usually, “Alpine tundra” grows over podzolized soils and is believed to originate from the removal of dwarf-shrub heaths or even from boreal-type forest (Holtmeier, 2009). Warmer, gentle slopes may support highly productive ecosystems including a widespread, Nardus-rich type, commonly related to anthropogenic forest clearance and pasture fertilization. Overall, distinguishing modern natural grasslands from human-shaped pastures is not straightforward (Pini et al., 2017).

Mountainous regions are home to over half of the world's 34 biodiversity hotspots. Many mountainous regions show high levels of endemism and rapid evolutionary processes as a result of their unique biophysical context and geographic isolation. A variety of ethnic communities that have cultivated and transmitted through rich cultural practices, farming methods, and related traditional knowledge live in the highlands. However, mountain ecosystems are among the most fragile in the world and are under severe threat from climate change, invasive alien species, globalization, urbanization, and other anthropogenic pressures (Ning et al., 2014).

Fig. 1. Livestock grazing in a high-altitude rangeland (Ning et al., 2014).

2. Animal husbandry in high altitudes

On the eastern Tibetan Plateau, animal husbandry is carried out by using the local grasslands. Yaks, sheep, and horses make up the herd. Traditional nomadic livestock husbandry has adjusted to the challenging environment. The condition of pastures has always been an issue in conventional herd management. The regeneration of the grasslands depends on basic pasture rotation from summer to winter pastures (Manderscheid, 2001). During the last few decades the number of animals has increased in Dzoge county. In Dzoge the local grassland bureau is concerned about the condition of the pastures. There are signs of overgrazing and pasture degradation. The situation in Dzoge is quite similar to the rest of the western Sichuan province where there have been reports of increasing pressure on pastures by a growing livestock number during recent decades. Over the past five to ten years, there has been an increase in the fencing of pastures. Winter and summer pastures as well as pasture acreage for certain herders have been divided using fencing. Some erosion-prone regions in the Dzoge have been walled off by

the local government to prevent grazing. A sustainable use of pastures is facilitated by reliable data on the quality and quantity of pastures as well as the amount of natural fodder supplies (Price et al., 2001). Remote Sensing and Geographical Information System (GIS) methods combined with conventional pasture mapping provide a methodology to make a cost effective and reliable inventory of large areas (Kumpula et al., 2004).

The primary livelihood of the highland pastoral nomads (Brokpa and Dokpas) of northeast India is yak rearing on alpine pastures. Due to the near absence of agricultural operations in this region, these pastoral nomads who live in the remote mountains are totally dependent on high altitude pastures for their nutritional and economic stability. They rear yaks under transhumance and utilize various pastures while migrating from low land winter pastures to high altitude alpine pastures during summer. Therefore, the temperate and alpine pastures are the major feed resources for the yaks. The indiscriminate use of pastures and impending climate change results in their degradation that may affect the productivity of the animals reared on them (Paul et al., 2020).

A unique type of free-range grazing known as transhumance is practiced in mountains all over the world. Developed in response to low land quality, seasonality in production, and labor shortage, it is a significant source of income for the people who live-in high-altitude regions (Moktan et al., 2008). Cattle grazing is a frequent transhumance activity, but the types of cattle, their migration patterns, and the relative importance of pastoral activities vary from region to region. According to Kreutzmann (2004), transhumance-the vertical, cyclical movement of livestock-is widespread in the Himalayas. In majority of the cases, transhumance in the Himalayas is guided by customary rules and institutions (Dong et al., 2009). Transhumance is being practiced in the Himalayas since the early human civilization and is considered to be one of the important livelihood activities especially for the people living in the high-altitude areas. However, only in recent years this practice has been under a question of debate among conservationists and resource users i.e. herders and other agropastoralists (Kala and Shrivastava, 2004). Herders assess the rangeland condition on the basis of livestock productivity whereas ecologists and conservationists prioritized biodiversity maintenance in the grazing land. Langtang, which lies in the Central Himalayas, has a long history of transhumance

practices. Transhumance is regarded as one of the pasture management strategies in the area. Livestock raring is an integral part of social, religious and agro-economic life. People have been practiced transhumance at least for 300 years (McVeigh, 2004) and the main livestock units in this pastoral landscape are yak and yak cow hybrids. From low to high elevation, herders move their livestock in a specific spatio-temporal manner that is dictated by conventional management principles. The transhumance route and goth (a semi-permanent structure formed of stones that serves as a gathering place for animals and a shelter for herders) are set, and the ownership of these goth is governed by customary laws. In addition to the institutional framework of the state, two groups of local organizations-community committees and community associations-are engaged in rangeland management (Aryal, 2010).

In Gilgit-Baltistan, Pakistan, rangelands and their interface regions encompass around 2.34 million hectares, making them the second-largest land cover after snow-capped mountains. For mountain people, subsistence agriculture, including livestock herding, provides the majority of their income, making up 35-40% of household income and 11% of GDP. The rangelands offer a significant amount of fuelwood to meet home energy demands, cattle feed, and high-value aromatic and medicinal herbs for both traditional purposes and sale, in addition to their usual applications. As an ecosystem, rangelands have been vital for sustained economic growth, regulation of air and water, and ecosystem flows. However, the ever-increasing human population and increased livelihood needs have led to a rapid increase in livestock numbers over the past four decades. This increase, coupled with other factors such as removal of natural vegetation for fuelwood, fodder, food, and medicine, has resulted in degradation of the rangelands. The reasons for the fast depletion of rangelands in the region include lack of adequate regulations and appropriate policies regulating rangeland resource use, and sheer lack of capacity, both human and material, in the custodian departments to enforce and monitor even the available laws. A multi-pronged integrated conservation and development strategy comprising short, medium, and long-term interventions is required to protect, restore, and eventually improve the degraded rangelands in Gilgit-Baltistan (Khan et al., 2013).

Alpine and subalpine pastures in the Jammu and Kashmir region of India are well recognized and locally known as "Margs" or "Bahaks" (Haq et al., 2022). In addition to being

an important biological resource, these pastures also have a big impact on the socioeconomic situation in the Himalayan Valley. According to Singh et al. (2015), Kashmir pasturelands have a total area of about 9595 km^2. In the rural areas where these pasturelands are located, around 97% of the population works in agriculture. The residents' secondary occupation is raising sheep, goats, and cattle. A sizable community of nomadic Bakerwals, Gujjars, Chopans, Changpas, and Gaddies is also reliant on meadow products and pasturelands for their cared-for animal herds (Mugloo et al., 2023). The term “grassland” (also designated by “pastureland”) can be defined as land (and the vegetation growing on it) devoted to the production of introduced or indigenous forage for harvest via grazing, cutting, or both. The grassland’s vegetation includes grasses, legumes, and scantly woody species. Thus, grassland is a highly dynamic ecosystem that supports fauna, flora, and human populations worldwide. It also encloses fodder crops that covered approximately 3.5 billion hectares in 2000 and contains around 20% of the world’s soil carbon stocks. These stocks can be well enriched through the good management of grasslands via Voisin’s rational grazing, resulting in an increased milk production by ruminants. Using this approach, ruminant intake and pasture growth can be maximized while still maintaining a circular, sustainable system. Adopting such a strategy is essential, especially in the Himalayan pasturelands, which for decades and centuries were overgrazed (Apollo et al., 2018).

3. Products of animals fed with forage in highlands

In hilly areas, cows graze on meadows that get higher as the season goes on. Transhumance is the term for the seasonal movement of livestock between permanent summer pastures and lowland areas. This method enables the highest possible valorization of highland pastures. Farmhouse cheese manufacturing is frequently linked to transhumant dairy systems, which adds a noticeable value to systems that must contend with difficult circumstances and low output (Sturaro et al., 2013). In Europe, 18% of the land consists of mountains and a prospering agricultural sector in these areas supports other sectors such as tourism in economy. Moreover, the agricultural and food production linked with tradition and local know-how (terroir) are of great importance to the local culture. Such products are labelled and protected by the European Union. In Aosta Valley (Italy), a semi-hard cheese is traditionally produced

with raw milk from autochthonous cows grazing high alpine pastures in summer, the Fontina PDO (Protected Designation of Origin). Farmers manufacturing the cheese directly in the buildings at the site of the alpine pastures often report facing challenges in cheese production shortly after the transhumance (Koczura et al., 2019).

Environmental changes such as the adjustment of the feed of the animals are known to affect milk composition and specifically fat content (Elgersma et al., 2006), which is playing a significant role in cheese manufacture. Under high altitude grazing conditions, these impacts are much more evident. The amount of carotenoids and unsaturated fatty acids in milk fat from cows eating highland pastures has a significant impact on the cheese's texture and color (Nozière et al., 2006). However, variations in diet quality when changing pasture concern the entire alpine grazing season and are mostly associated with positive cheese quality (more yellowish, for example). Extensive studies on alpine systems with transhumance showed that the milk yield, milk protein content and rennet coagulation properties are impaired on highland pastures especially at very high altitude. In addition, Highland pastures decrease cheese making efficiency with a reduction of cheese yield. There is also a higher percentage of milk samples that do not coagulate in the highlands. The greater somatic cell count in milk accounts for some of these variations. High somatic cell counts are thought to contribute to cheese faults in terms of flavor (rancid taste due to prominent lipolysis and proteolysis, respectively) and texture (reduction in firmness and elasticity, increase in stickiness) (Koczura et al., 2019).

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2. INTERNATIONAL PARIS CONGRESS ON AGRICULTURE AND ANIMAL HUSBANDRY

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12.11.2023

REF: Akademik Teşvik

İlgili makama;

2. Uluslararası Paris Tarım ve Hayvancılık Kongresi, 16-18 Ocak 2023 tarihleri arasında Paris, Fransa'da 11 farklı ülkenin (Türkiye 14 bildiri- Diğer ülkeler 20 bildiri) akademisyen/araştırmacılarının katılımıyla gerçekleşmiştir

Kongre 16 Ocak 2020 Akademik Teşvik Ödeneği Yönetmeliğine getirilen "Tebliğlerin sunulduğu yurt içinde veya yurt dışındaki etkinliğin uluslararası olarak nitelendirilebilmesi için Türkiye dışında en az beş farklı ülkeden sözlü tebliğ sunan konuşmacının katılım sağlaması ve tebliğlerin yarıdan fazlasının Türkiye dışından katılımcılar tarafından sunulması esastır." değişikliğine uygun düzenlenmiştir.

Bilgilerinize arz edilir,

Saygılarımla

Dr. Yusuf Hassan
Committee Member

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İLGİLİ KURUMA

İçişileri Bakanlığı tarafından tahsis edilen 06-146-071 tescil kodu ile Tüzel Kişiliğe sahip olan İKSAD Enstitüsü 5253 sayılı kanuna uygun olarak "Bilimsel araştırmalar ve akademik çalışmalar" alanında ulusal ve uluslararası düzeyde faaliyetlerini yürütmektedir.

Kurumumuzun Yönetim Kurulu 5 Nisan 2023 tarihinde saat 10.30'da "Bilimsel Diplomasi Projesi" görüşmeleri ile "Bilimsel Kongreler Düzenlenmesi" gündemleri ile toplanmış ve alınan (2 numaralı) karara istinaden aşağıda detayları yazılı olan bilimsel etkinliğin düzenlenmesine ve etkinliğe ilişkin resmi görevlendirme konusunda karar vermiştir.

Bilgi ve gereğini rica ederim

Dr. Kaldygul ADİLBEKOVA
Genel Sekreter

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