

Newe Yaar Students Day
Agricultural Research-
A look to future challenges



Tuesday, April 22th, 2025

Lecture hall, Newe Yaar

Program and
Abstract book

Program:

Time	Lecturing student	Title
08:30		<i>Get-together</i>
09:00		<i>Opening and an Introduction of the judging panel</i>
Session 1- Plant protection, Chair: Dr. Moshe Zagouri		
09:20	Dana Siso	Genomic characterization of sunflower (<i>Helianthus annuus</i>) resistance to sunflower broomrape (<i>Orobanche cumana</i> Wallr.)
09:35	Shlomi Aharon	Using satellite remote sensing for evaluating herbicide efficacy in maize (<i>Zea mays</i>)
09:50	Sahar Malka	Examining the competitive dynamics of <i>Parthenium hysterophorus</i> populations and summer crop species in Israel
10:05	Amit Faran	Characterizing the dynamics of the fungi-vanillin interaction in <i>Vanilla planifolia</i> during bean development
10:20		<i>Coffee break</i>
Session II- Genetic, chemical and physiological characterization, Chair: Dr. Elad Oren		
10:40	Ben Itzchaki	Genetic characterization of variation in sugar accumulation in melon using diverse collections and segregating populations
10:55	Tali Kahane	Chemical variation among <i>Salvia dominica</i> L. natural populations in Israel
11:10	Orr Shemer	Characterizing the physiological diversity between wild and domesticated watermelon under water limitation
11:25	Ori Eisenbach	Identification of physiological factors and genetic linkage of the Stem Photosynthesis Capability (SPC) trait in the wild almond species <i>Prunus arabica</i> and examination of their contribution to almond breeding
11:40		<i>Coffee break</i>
Session III- Environment, Chair: Dr. Uri Hochberg		
12:00	Gal Wodowski	Viruses as hidden players in parasitoid wasps: a new avenue for biological control
12:15	Asaf Salmon	Understanding the role of native beneficial Phosphorus Solubilization Rhizobiome in agroecosystems through the application of environmental and functional genomic approaches
12:30	Amit Sivan	where is it going? Closing the nitrogen cycle of a perennial legume (<i>Calicotome villosa</i>) in water-limited systems
12:45	Itay Shulner	Embracing a life cycle assessment (LCA) approach to analyze the environmental impacts of almonds grown along a climatic gradient in Israel
13:00		<i>Closing remarks</i>
13:10		<i>Lunch!</i>

Genomic characterization of sunflower (*Helianthus annuus*) resistance to sunflower broomrape (*Orobancha cumana* Wallr.)

Dana Sisou

Department of Plant Pathology and Weed Research, Newe Ya'ar Research Center, Agricultural Research Organization, Galilee Research Institute (MIGAL) and The Robert H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University of Jerusalem

Supervised by Prof. Hanan Eizenberg and Dr. Sarel Hübner

The sunflower broomrape (*Orobancha cumana* Wallr.) is considered a major threat for sunflower (*Helianthus annuus*) cultivation across Europe, the Mediterranean region, and Asia, leading to severe yield losses. To control broomrape infestations, several herbicides and crop management approaches are practiced commonly. However, in the long term, breeding for resistance remains the most efficient and environmentally friendly approach. Many resistant sunflower cultivars have been developed over the years, yet broomrape has a remarkable ability to evolve and overcome the resistance mechanisms. Thus, new genetic resources of resistance are necessary. This study focused on the genomic basis of sunflower resistance to broomrape. The sunflower association mapping (SAM) population, comprising of 287 accessions, was screened for resistance against two sunflower broomrape races and egyptian broomrape (*Phelipanche aegyptiaca*) in a high-throughput system based on an image processing procedure, allowing the mode of resistance to be quantified and characterized. A resultant representative panel of 77 accessions which were characterized as susceptible, post haustorial-resistant, and pre-haustorial resistant, were selected for field evaluation, phenotypic traits were recorded during the growing season and indicated that the initial high-throughput system well predicted the response of sunflower to infestation under field conditions. Thus, we conducted Genome-wide association analysis using two approaches: k-mer based GWAS and SNP based GWAS to identify QTLs and candidate genes that underlie broomrape resistance based on the high-throughput screening. Significant associations between genomic regions and the response to broomrape infestation were detected on chromosome 7 which supported by previous findings, and on other chromosomes, providing new candidate QTLs for broomrape resistance in sunflower.

Using satellite remote sensing for evaluating herbicide efficacy in maize (*Zea mays*)

Shlomi Aharon

*Department of Plant Pathology and Weed Research, Newe Ya'ar Research Center,
Agricultural Research Organization and The Robert H. Smith Faculty of Agriculture, Food and
Environment, The Hebrew University of Jerusalem*

Supervised by Dr. Ran Lati, Prof. Hanan Eizenberg and Dr. Yafit Cohen

Evaluating herbicide efficacy using remote sensing satellites can enhance practical weed control management and enable large-scale scientific analysis. Despite advancements in remote sensing for agriculture, satellite imagery's relatively low spatial resolution limits the ability to detect weed damage after herbicide application. This study presents a novel method for estimating weed control efficacy by integrating spatial, spectral, and temporal metrics from satellite imagery. We hypothesize that effective control reduces weed cover and biodiversity, producing more uniform spectral patterns. A maize field experiment was conducted with three treatments: two herbicides with different modes of action (HPPD and ALS inhibitors) and a control with no weed control intervention. UAV-based multispectral imagery was used throughout the study to collect ground-truth data on healthy and damaged weed cover in each treatment using SVM classification model. PlanetScope satellite images, with eight spectral bands and four spectral indexes that calculate from them, were analyzed using the Gray Level Co-occurrence Matrix (GLCM) to derive 8 textural features describing spatial variation. These were evaluated across five-time points post-herbicide application to capture temporal changes. The results show that UAV-based spectral data and the SVM model provided high accurate and reliable ground-truth data. GLCM variance, which reflects spatial texture feature in satellite imagery, exhibit significant differences (Wilcoxon test, $P\text{-value} < 0.05$) between herbicide-treated and control plots in six of these layers already after 3 days following herbicide application. In the dynamic analysis using a Linear Model, GLCM variance values in herbicide treated plots remained relatively stable over time (Slope = 0), indicating spatial uniformity due to effective weed suppression. In contrast, control plots showed an increasing trend in variance, reflecting more significant spectral heterogeneity driven by continued weed growth and spread (Slope = 0.15). Despite these findings, further analysis is needed to understand variations in weed patch reflectance and GLCM texture features across fields based on data from eight commercial sites.

Examining the competitive dynamics of *Parthenium hysterophorus* populations and summer crop species in Israel

Sahar Malka

Department of Plant Pathology and Weed Research, Newe Ya'ar Research Center, Agricultural Research Organization and The Department of Evolutionary and Environmental Biology, Faculty of Natural Sciences, and the Institute of Evolution, University of Haifa
Supervised by Prof. Assaf Distelfeld, and Dr. Maor Matzrafi

The impact of weeds on crop plants is influenced by various factors; weed density, weed type, and the specific crop being cultivated. *Parthenium hysterophorus* (Asteraceae) is a noxious weed species that has invaded over 50 countries globally. This plant has a high seed production potential, and it can grow up to 2m tall. In Israel, it was first detected in 1980 at Tirat-Zvi, located in eastern-northern Israel. In recent years, there has been an increasing concern about the spread of this weed in agricultural regions across the country. Here, we examine the competitive abilities of two *P. hysterophorus* populations, Tirat Zvi (TZ), a well-established population, and Ha'hotrim (HT), which represents a new introduction site. Furthermore, we have compared the competitive dynamics of both populations with two crops, corn (*Zea mays*) and cotton (*Gossypium hirsutum*). The experiments took place in a glasshouse, using 60L Styrofoam boxes. Crop plants were grown with transplanted seedlings at low and high weed density (six or twenty-two plants per 0.25m², accordingly). For the control treatment, weed or crop plants were grown alone. Biomass and height of both weed crop plants were measured at the end of the experiment. Our results show that 92 days after transplanting, weight of cotton plants grown with low density of HT plants was higher than of those grown under low density of TZ plants (t-test, $p=0.0298$). The average weight of cotton plants grown in low density was 50% lower than control and in high density 70% lower than control. However, under high density of *P. hysterophorus* no significant differences were observed between the two populations. Examining the weight of corn plants under competition, no significant differences for both densities and different *P. hysterophorus* populations. Interestingly, corn plants grown with high density of TZ plants were shorter compared to those grown under low density (t- test, $p=1.08e-5$). From these results we can assume TZ population plants are a stronger competitor against both corn and cotton crops. We may also conclude that cotton plants are more sensitive to *P. hysterophorus* competition compared to corn plants. The differential responses of corn and cotton plants to competition highlight the importance of crop selection in areas with high *P. hysterophorus* infestation.

Characterizing the dynamics of the fungi-vanillin interaction in *Vanilla planifolia* during bean development

Amit Faran

*Albert Katz International School for Desert Studies, Ben-Gurion University of the Negev and
Neve Yaar Research Center, Agricultural Research Organization*

Supervised by Prof. Vered Tzin, Prof. Michele Zaccai, and Dr. Mwafaq Ibdah

Vanillin is the main aroma compound in vanilla (*Vanilla planifolia*) bean, known as one of the most popular spices in the world. Traditional post-harvest treatments lead to spoilage problems due to pathogen infection, which may cause a significant yield loss. It is known that vanillin possesses antimicrobial and antifungal properties. However, its biosynthesis and distribution during bean development are not fully known. This work aims to investigate spatial and temporal aspects of fungi-vanillin interaction. For spatial characterization, we measured the vanillin and its storage form of glucose-vanillin along five sections of the green and brown beans.

We isolated two fungi from spoiled vanilla beans, which were mostly colonized in the detached meristem section. To test vanillin anti-fungal activity, we exposed these fungi-infested crops to vanillin-linked compounds and observed their effects on both common and isolated fungi growth rates. Also, these compounds are exposed to other general post-harvest fungi to evaluate the level of crop damage.

By examining the products of the vanillin biochemical pathway, we will identify the active compounds and biosynthesis regulation that prevent the spoilage of vanilla beans. The results of this research will provide farmers with better techniques to improve their crop quality and reduce yield loss.

Genetic characterization of variation in sugar accumulation in melon using diverse collections and segregating populations

Ben Itzhaki

*Cucurbits Section, Agricultural Research Organization, Newe Ya'ar Research Center, and
Department of Evolutionary and Environmental Biology, Faculty of Natural Sciences and the
Institute of Evolution, University of Haifa*

Supervised by Dr. Amit Gur and Prof. Assaf Distelfeld

The sweetness in melons is an important quality factor, primarily dependent on the sugar content in the fruit. Melon (*Cucumis melo*) shows a wide range of sweetness, from 2° Brix in non-sweet varieties to 18° in dessert fruits. During fruit development, the raffinose oligosaccharide is broken down enzymatically into the glucose and fructose monosaccharides. In sweet varieties, a metabolic transition occurs during ripening, the disaccharide sucrose accumulates in the fruit, and sweetness increases. Genetic studies have mapped multiple genomic regions associated with sugar accumulation in melons, but specific genes controlling this trait have not yet been isolated.

This study focused on the genetic characterization of the variation in sugar accumulation in melon fruit. A diverse core collection was used, including three subspecies and thirteen breeding groups, to characterize the dynamics of sugar accumulation through fruit development. In sucrose-accumulating varieties, the decline in monosaccharide levels was synchronized with sucrose accumulation. However, significant differences were found in the sucrose accumulation curves across three different breeding groups. A genetic analysis using BSA-seq (Bulked Segregant Analysis sequencing) of three segregating populations generated from different genetic combinations identified fourteen quantitative trait loci (QTLs) spread across seven chromosomes. In a comparative analysis, a genetic segment on chromosome 3 (qTSS3.1) was associated with sweetness in all three populations.

Chemical variation among *Salvia dominica* L. populations in Israel

Tali Kahane Achinoam

Unit of Aromatic and Medicinal plants, Newe Ya'ar Research Center, Agricultural Research Organization and The Robert H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University of Jerusalem

Supervised by Dr. Itay Gonda and Prof. Nativ Dudai

Sclareol and α -Linolenic acid (ALA) are two plant-sourced compounds with high commercial value. Today, they are obtained from *Salvia sclarea* L. grown commercially for these purposes. Sclareol is a valuable diterpene to the perfumery industry. ALA is an omega-3 fatty acid essential for the human diet that is also available from fish or flax seeds. In this work, different genotypes of a different local *Salvia* species, *Salvia dominica* L., were tested for their chemical composition and variation in order to seek alternative and improved sources. *S. dominica* is a wild species endemic to Israel and its region. We have grown 24 natural populations from various locations in Israel, under equal conditions in the field in Newe-Ya'ar to eliminate the environmental effects. Flowers and leaves were collected from all the plants and evaluated for their metabolites content and composition. Seeds were collected to measure the fatty acids content and composition.

Two of the populations showed up to 20% increase in sclareol levels compared to the current commercial *S. sclarea*. Sclareol was most abundant in the flowers compared to the leaves. Sclareol levels were found to decrease when the flower opens, and rise to the maximum post full bloom. In addition, both flowers and leaves showed two chemical composition patterns (chemotypes) of their essential oil, with or without α -terpinyl acetate. There is a chemotype variation within and among the populations. ALA levels in the seeds among all populations tested were similar to those of the current commercial *S. sclarea* accession.

In conclusion, *S. dominica* has a metabolic profile similar to *S. sclarea* and is possibly better commercially. There are favored accessions with higher levels of sclareol that might improve the yield obtained from the crop. It appears that *S. dominica* might be a potential new source for sclareol and vegan Omega 3. The great variation in sclareol levels found among populations warrants exploration of additional populations.

Characterizing the physiological diversity between wild and domesticated watermelon under water limitation

Or Emma Shemer

*Cucurbits Section, Agricultural Research Organization, Newe Ya'ar Research Center, and
Department of Evolutionary and Environmental Biology, Faculty of Natural Sciences and the
Institute of Evolution, University of Haifa*

Supervisors: *Dr. Amnon Cochavi and Prof. Assaf Distelfeld*

Citrullus spp., originating from Africa, is known for its capacity to thrive in arid regions globally. *Citrullus colocynthis*, in particular, is highly adapted to extreme dry environments. This study aims to compare drought-tolerance traits of *C. colocynthis* to the cultivated *C. lanatus*.

An experiment was set up under two irrigation conditions: drought and control. Both species were grown in one-meter-deep, eight-inch-diameter tubes filled with clean sand. During the experiment, soil water content was measured in four depths (25, 50, 75, and 100 cm) every two-three days. In addition, gas exchanges and fluorescence measurements were done using Li-600 porometer, and leaf samples were taken for osmolarity measurement. In the end of the experiment the foliage was removed, dried and weight. The soil column was dissected to the different depths, the soil was removed and the roots were scanned, and afterward dried and weight.

The results revealed that while the above ground physiological response was similar between the *C. colocynthis* and *C. lanatus*, the below ground response was different. The root system of *C. colocynthis* was found to develop a branched root system in dippiest depth under drought conditions compared to the cultivated watermelon under similar conditions. This response reflects the plant's strategy to cope with water scarcity by seeking water deeper in the soil, contributing to its drought tolerance.

The findings regarding the well-developed root systems highlight their important role in improving drought tolerance. Therefore, this trait can be utilized to enhance cultivated watermelon growth under arid conditions. In the next step of the work we wish to incorporate this trait to cultivated watermelon through planned breeding program.

Identification of physiological factors and genetic linkage of the Stem Photosynthesis Capability (SPC) trait in the wild almond species *Prunus arabica* and examination of their contribution to almond breeding

Ori Eisenbach

*Unit for Fruit Tree, Newe Ya'ar Research Center, Agricultural Research Organization, and the
Faculty of Agriculture, Food and Environment, The Hebrew University
Supervised by Dr. Tamar Azulai-Shamer and Dr. Smadar Saad-Harpaz*

In recent decades, we are experiencing warmer winters due to a trend of climate change. These changes affect the rate of energy reserve utilization in almond trees. Being a deciduous tree, the almond cannot perform photosynthesis during winter, which limits its ability to respond to climate changes. In a study conducted at the Fruit Tree Unit in Newe Ya'ar, a unique trait was identified in the wild almond species, *Prunus arabica*. The branches of the Arab almond remain green throughout the year, even in winter after leaf fall, and perform gas exchange through functional stomata (Stem Photosynthesis Capability - SPC). These stomata regulate CO₂ uptake and water loss through transpiration, enhancing photosynthetic fixation from stem tissue and improving water utilization in response to environmental conditions. The goal of this study is to identify the physiological and genetic factors that provide the wild almond *P. arabica* with this unique trait and to examine their contribution to breeding almond varieties that are more adaptable to climate change. This study investigates several unique traits that were identified solely in the wild *P. arabica* almond species, and their contribution to stem SPC trait. These traits include the delay of stem bark formation, differentiation of the epidermis into a specialized tissue for gas exchange rich in stomata, and their parenchyma to palisade mesophyll-like chloroplast-rich tissue, which also include peripheral vascular bundles for transporting photosynthetic materials. To characterize the genetic factors that provide the *P. arabica* almond with their ability to fix carbon, hybrid populations between the *P. arabica* and commercial almond varieties were established at Newe Ya'ar. These populations are being investigated using various physiological, histological, and genetic methods. The research results obtained so far indicate that SPC is a complex trait composed of several factors, which will be presented at this conference.

Viruses as hidden players in parasitoid wasps: a new avenue for biological control

Gal Wodowski

Supervised by Dr. Einat Zchori-Fein and Dr. Elad Chiel

*Institute of Plant Protection, Agricultural Research Organization, Newe Ya'ar Research Center,
and Department of Evolutionary and Environmental Biology, University of Haifa*

Microbial symbionts shape insect biology in profound ways, influencing reproduction, immunity, and metabolisms. While bacterial and fungal associations are well-documented, nonpathogenic viral interactions remain largely unexplored. Here we study the phenotypic effect of AnvRV, a segmented dsRNA virus, on the parasitoid wasp *Anagyrus vladimiri* a key biological control agent of pest mealybugs. Previous results in the lab found that the virus is maternally vertically transmitted, and horizontally transmitted through superparasitism (laying more than one egg per host). In addition, infected wasps have higher hatching rate than uninfected wasps, although there is no difference in fecundity. Using Transmission electron microscopy (TEM) we uncover the localization of AnvRV in the wasp's reproductive system. Transcriptomic analysis of infected and uninfected wasps reveals the molecular interaction between the virus and the wasp. Transmission electron microscopy (TEM) showed that AnvRV predominantly localizes to the wasp's ovaries, consistent with maternal transmission. However, we did not detect the virus in the venom gland, or venom reservoir. Interestingly, TEM images revealed a previously undescribed group of cells within the female reproductive system, which we term "satellite cells," characterized by a high viral load. Our transcriptomic results indicate significant differential gene expression, particularly in immune-related genes and venom composition. Notably, we observed immune suppression in the ovaries, where the virus is localized, suggesting a potential mechanism for viral persistence. Understanding how RNA viruses shape parasitoid fitness opens new opportunities for enhancing biological control strategies. By leveraging viral symbioses, we could potentially improve parasitoid efficiency, stability, and adaptability in pest management programs. This study highlights the untapped potential of insect specific viruses, paving the way for innovative, virus-focused approaches in agricultural biocontrol.

Understanding the role of native beneficial Phosphorus Solubilization Rhizobiome in agroecosystems through the application of environmental and functional genomic approaches

Asaf salmon

*Newe Ya'ar Research Center, Agricultural Research Organization and The Robert H. Smith
Faculty of Agriculture, Food and Environment, The Hebrew University of Jerusalem*

Supervised by Dr. Shiri Freilich

Nanobubbles (NBs) are tiny gas bubbles with a diameter of less than 1 micron. According to research literature, irrigation with NBs has many advantages, including: increased growth rate of crops, increased plant biomass, improved crop quality, and accelerated germination processes. Additionally, studies have shown that irrigation with NB-enriched water reduces the emission of the greenhouse gas N_2O from the soil. The goals of the research are to isolate factors that may have beneficial effects on the plant and on biochemical processes in the soil, and to understand the mechanisms causing the observed effects. During the research, germination experiments were conducted with various seeds under different conditions (various temperatures, salinities, and pH levels) in different media, using different gases to create the NBs (oxygen, air, and nitrogen). In one of these experiments, the seedlings were transferred to continue growing in the iCore greenhouse under controlled conditions, with continuous measurement of various. Irrigating tomato seeds with oxygen-NB water increased the germination rate while at the same time delaying growth processes. This finding was reflected in the parameters: germination rate, hypocotyl diameter, number of true leaves, stem height, dry shoot weight, and transpiration rate. It was found that acceleration of the germination rate also occurs with a single irrigation of seeds with NB-water, followed by irrigation with regular water. A possible mechanism to explain the high germination rate achieved with irrigation using NB-water, which is extensively described in the literature, is the weakening of the seed coat by reactive oxygen species (ROS) present in the NB-enriched water. In the context of this research, another possible direction to be examined is the physiological effects of NBs on the plant's root zone, by examining oxygen and carbon dioxide concentrations and pH levels in the root zone using an optical sensor system.

לאן הוא הולך? מחזור החנקן של מין קטנית רב שנתי (קידה שעירה) במערכות מוגבלות מים

עמית סיון

המחלקה למדעי צמח וגנטיקה בחקלאות, הפקולטה לחקלאות מזון וסביבה ע"ש רוברט ה. סמית, האוניברסיטה העברית בירושלים, והמחלקה למשאבי טבע, מרכז מחקר נווה יער, מנהל המחקר החקלאי-מכון וולקני.

בהנחיית דר' גיא דוברת ופרופ' אפרת שפר

קידה שעירה היא שיח ממשפחת הקטניות בעל תפוצה נרחבת בחורש בישראל. השיח מקיים סימביוזה עם חיידקים מקבעי חנקן אטמוספרי (ריזוביום), המעניקים לשיח אספקה של חנקן זמין המהווה יתרון בגדילה באזורים מוגבלי חנקן ובהתחדשות לאחר שריפה. במערכות אקולוגיות רבות, קיבוע סימביוטי הוא המקור הטבעי העיקרי לכניסת חנקן חדש ולכן עשוי לכוון את מהלך הסוקצסיה ולעודד התחדשות של המערכת אחרי שריפות. בניגוד למצופה, שני מחקרים שנערכו לאחרונה על קידה שעירה באזורים שונים בארץ הראו שלמרות שהשיח מקבע חנקן, לא נמצאה הצטברות של חנקן בקרקע תחתיו. על מנת לבחון את ההשפעה של שיח הקידה על מאזן החנקן במערכת האקולוגית שסביבו, נוטרו שיחים בחמישה אתרים המייצגים מגוון של תנאי אקלים, סוגי קרקע ותצורות צומח. לאורך שנה שלמה נבדקה ביומסת השיחים וחלוקתה לאיברים השונים, נמדדה תכולת החנקן בחלקי הצמח השונים ובנשר, בוצעה הערכה למידת ההשקעה בקיבוע (יצירת פקעיות) וקצב הקיבוע, ונמדדו מאגרי החנקן האורגני והאנאורגני בקרקע. כמו כן נמדדו ייצור הנשר ע"י השיחים וקצב פירוקו על הקרקע, והוערך ייצור זרעים ע"י השיחים וטריפתם ע"י חיפושיות. בעזרת מדדים אלו, בוצעה הערכה של מאגרי החנקן בשיח ובסביבתו ואת השטפים דרכם חנקן נכנס ויוצא מהשיח למערכת, מכניסתו לצמח דרך הקיבוע הסימביוטי, דרך מעברו בצמח והדרכים בהן הוא עוזב אותו. התוצאות הראשוניות שלי תומכות במחקרים הקודמים שלא מצאו הצטברות של חנקן תחת שיחי הקידה בהשוואה לשטחים הסמוכים. בנוסף, מצאתי שבאתר שבו תכולת החנקן בקרקע היו הגבוהות ביותר משאר האתרים (אלוני אבא), תכולת החנקן בעלים היו הגבוהות ביותר גם כן, ופעילות הקיבוע הייתה הנמוכה ביותר בהשוואה לשאר האתרים. כמות הנשר שהתפרק הייתה דומה בין האתרים, אך פירוק החנקן בנשר היה שונה מאוד בין האתרים. הערכה ראשונית של מאגרי החנקן והשטפים הראתה שבשיח ממוצע, איבוד החנקן דרך פירוק נשר וטריפת זרעים נמוכה מאוד, ורוב החנקן נאגר בענפים בצמח. המחקר מראה כי לשיחי קידה שעירה תרומה נמוכה מאוד למחזור החנקן במערכת בטווח הקצר, אך לאורך חיי השיח יותר ויותר חנקן ישתחרר וייכנס אל המערכת.

Embracing a life cycle assessment (LCA) approach to analyze the environmental impacts of almonds grown along a climatic gradient in Israel

Itai Shulner

Department of Geography and Environmental Development, Ben Gurion University of the Negev and Department of Phytopathology and Weed Research, Agricultural Research Organization, Neve Ya'ar Research Center

Supervised by Dr. Ran Nisim Lati and Prof. Meidad Kissinger

Changing environmental conditions and the need to reduce the environmental impact of food systems highlight the importance of analyzing the direct and indirect environmental impacts of agricultural production systems. This analysis should include different environmental conditions and consider farmers' practices. This paper embraces a Life Cycle Assessment (LCA) approach to analyze a range of environmental interactions of almond production in three climatic regions – Mediterranean, semi-arid, and arid.

Data was collected from 94 farmers across the state of Israel, representing 75% of the country's almond orchard area. We found that producing 1 kg of almond kernel generates an average emission of 4.78 kg CO₂ eq., 0.02 kg SO₂ eq., and 0.02 kg of N eq.

The three main inputs, accounting for over 90% of these emissions, are irrigation, fertilizers, and pest management. Weed management had a small impact. In addition, differences among and within growing regions were observed, allowing exploring the climatic and human factor influence in each studied farm. This study joins a small number of studies that have analyzed the Almonds LCA, and it is among the first to examine the implications of climatic variables in different growing regions. By identifying major hotspots, it provides a foundation for future detailed studies of alternative methods, implementing farmers' best practices, and policy implications for promoting an adaptive and sustainable almond-growing system.