

**WorldVeg Golden Jubilee Year Student Research Fellowships**

**Suggested Research Topics for BSc, MSc and PhD Students**

April 2023

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# FOOD SCIENCE, NUTRITION, FOOD SYSTEMS RESEARCH

## Nutritional analysis of food preparation methods (MSc/PhD students)

WorldVeg has a well-equipped chemical analysis laboratory for the quantification of minerals, vitamins and phytonutrients. Students are invited to submit innovative research ideas to conduct chemical analysis of vegetables and vegetable dishes that contribute to knowledge on how vegetables contribute to better health. These ideas could, for example, include experiments analyzing variations of key vitamins, minerals, and antioxidants in vegetables by food preparation methods (e.g. duration of washing, size of chopping) or cooking methods (e.g. boiling, blanching, microwaving, deep frying or cooking duration); research on nutrient interactions in composite dishes involving multiple ingredients; or research on the nutritional effects of alternative postharvest management options.

## Nutrition-sensitive and sustainable diets, food environments and food systems (MSc/PhD)

WorldVeg acknowledges the importance of vegetable-rich food systems and conducive food environments in driving healthy diets for all. Students are invited to conduct their research with our food systems researchers on innovative research ideas that are relevant, but not limited, to the following topics: (i) understanding food environments and diets of marginalized populations in different contexts (e.g., physical, economic, political and socio-cultural); (ii) development of tools and metrics; (iii) experimental interventions and pilots; (iv) plant-based or plant-rich diets.

# SEED SCIENCE AND GENETIC RESOURCES

## Seed dormancy and quality of crop wild relatives and traditional vegetables (MSc/PhD)

WorldVeg holds the largest public vegetable genebank in the world with 65,000 seed samples of more than 300 vegetables and their crop wild relatives. In contrast to commercial vegetable crops, the seed behavior of crop wild relatives and traditional vegetables is poorly known. This impedes proper seed storage and use of these species in crop breeding. Research objectives for this topic include**:** i) **un**derstand the seed longevity of these species; ii) **d**evelop seed dormancy and viability tests for these species; and iii) **d**evelop seed treatments to break dormancy and deliver pathogen-free and healthy seeds. The knowledge generated will help to safeguard these species properly at WorldVeg and globally, and secondly will help to promote their use in breeding and cultivation.

## Bring back microbiome diversity from seed banks (MSc/PhD)

Seeds stored at seed banks are time capsules that not only capture the genetic diversity of crops that emerged over time. They also carry the diversity of associated microorganisms that co-evolved with them or were indirectly selected for during domestication. Little research is carried out on this associated crop diversity. At the same time there is a call by practitioners and policy makers for an integrated approach to understand, safeguard, and use agrobiodiversity that links research on seeds and soils. Research objectives for this MSc or PhD could include: i) assess biodiversity of beneficial organisms associated with stored seeds with different levels of crop improvement (improved lines, landraces, wild relatives; ii) assess the relationship between taxonomic, phylogenetic and functional diversity and structure of the microbiome across the domestication gradient of selected crops; and iii) test the performance of these seeds and their microbiome under different environmental conditions. This workwill be jointly supervised by the center’s genetic resource unit and pathology.

## Crop wild relatives to safeguard the history and future of vegetable crops (MSc/PhD)

With the current decline of biodiversity, crop wild relatives are increasingly threatened. Crop wild relatives hold traits related to climate change adaptation and pest and disease resistance that have been lost in modern crop varieties. They are therefore a valuable resource for developing new crop varieties for nutritious and secure food. Their diversity, however, is being lost while they are underrepresented in genebank collections. The objectives of this topic include: i) identify populations of crop wild relatives for germplasm collecting; ii) assess the conservation status of populations by revisiting historic locations of herbarium specimens, describe the status of the populations, and carry out ethnobotanical surveys; and iii) estimate trends and dynamics in distribution range and genetic diversity with methods such as participatory mapping and mutation-area-range modeling.

## Seed health treatments for tropical vegetables (MSc)

Seed health is key to ensure the distribution of vegetable seed. However, for most vegetable species no seed health protocols yet exist, which puts at risk the distribution of the seeds of these species by genebanks and breeding programs. This research consists of a literature review and practical tests to make recommendations on 1) seed health treatments to the genebanks of WorldVeg in Tanzania and Taiwan and to the breeding programs of WorldVeg on Solanaceae, cucurbits, okra, and pulses; 2) identify gaps for further research in seed health treatments for specific vegetable crops.

## Morphological characterization of vegetable germplasm (BSc/MSc)

For four decades, WorldVeg has characterized morphologically the crop diversity held in its genebank, which is the world’s largest public collection of vegetable genetic resources with 65,000 seed samples of more than 300 vegetable species and their crop wild relatives. These phenotypic data are a valuable resource for breeders and researchers to select germplasm for further research and to associate with genotypic data, and helps to understand phenotypic variation.

# VEGETABLE BREEDING AND GENOMICS

## Landscape genomics (MSc/PhD)

Human activity and climate change has transformed the natural environment and thereby the survival of many species. Global effects of climate change are swiftly altering ecosystems in various parts of the world, endangering plant and animal life. Landscape genomics research is essential in understanding populations, local adaptation and ability to adapt to natural, disturbed, or exploited environments. Local adaptation is where local populations develop traits that improve their overall fitness enabling them to survive in their local environment compared to those from other populations from a different environment. To achieve this, researchers evaluate environmental conditions in detail and correlate them with population genomes to understand which genomic regions enhance local adaptation to specific environmental conditions such as heat or salinity.

## Genome wide association studies for bacterial wilt resistance in pepper (MSc/PhD)

Bacterial wilt, caused by *Ralstonia solanacearum* species complex (RSCC), causes extensive losses to smallholder pepper producers worldwide. Management strategies to reduce losses associated with bacterial wilt are limited, because of the wide host range of the pathogen and the ability of the pathogen to survive in the soil for long periods of time, leaving host resistance as the best management strategy. However, we have access to limited genetic resources to breed for resistance to bacterial wilt in pepper. Using a high-throughput method for disease screening, we will evaluate with Capsicum core collection for host resistance to at least three major trains of RSCC. Genome wide association studies will be conducted to identify loci contributing to strain-specific and durable host resistance to RSCC. The significant loci identified will be validated using molecular markers developed in the region and tested in a segrand population for host resistance.

## Recurrent selection and QTL mapping for host resistance to thrips in chilli (PhD)

Chilli thrips are a global problem for pepper producers, not only causing losses through direct damage, but also through vectoring viruses. Efforts to develop host resistance to thrips are limited and producers typically rely on pesticide, which can be detrimental to the farmer, the consumer, and the environment. Recently, outbreaks of thrips have caused significant losses for farmers in South Asia and pesticide applications are largely ineffective to control the pests. The World Vegetable Center has initiated a breeding program for host resistance to thrips; however, no immune accessions have been identified. Therefore, we need to increase the level of resistance to thrips through recurrent selection. The intern in this project will conduct three generations of recurrent selection, and will map the host resistance in the population and identify loci significantly associated with resistance. Molecular markers in identified regions associated with resistance will be developed by the student to support future efforts for marker assisted selection for thrips resistance in chilli.

## Gene identification for photosynthetic capacity under heat stress in pepper (MSc/PhD)

The climate crisis disproportionally affects smallholders farmers in tropical and subtropical regions. These regions are also the major pepper production areas, accounting for more than 65% of global production. Unlike many biotic stresses, there are few management strategies farmers can implement to limit the losses associated with high temperature stress. Therefore, breeding for tolerance to high temperatures is the best strategy to ensure high productivity and quality. The World Vegetable Center has conducted pepper heat stress trials systematically by the high throughput phenotyping facility, Phenospex, for three years. This multi-year experiment revealed the Normalized Difference Vegetation Index, a plant health indicator, changes dramatically above 28 °C. The student involved in this project will conduct a phenotyping experiment to link the photosynthetic capacity and NDVI as well as a RNA experiment in temperature-controlled conditions to identify the gene network responsible for the heat stress.

## Genomic selection for yield and yield component traits in pepper (MSc/PhD)

Crop yield is determined by many genetic and environmental factors, making mapping of genes conditioning yield difficult. Genomic selection produces prediction models based on genotypic profiles and phenotypic data of a training population to develop genomic estimated breeding values for individuals of breeding population that could be used for selecting favorable genotypes. WorldVeg is testing this method to improve yield in a breeding population of pepper, and a graduate student will conduct the analysis for genomic selection in pepper, providing a basis for more efficient breeding. Students involved ingenomics, biostatistics and molecular plant breeding are preferred.

## Improved resistance to insect pests in tomato (MSc/PhD)

Farmers use pesticides to reduce insect populations on vegetable crops, which has undesired effects for the environment and for human health. Insect resistant tomato cultivars reduce pesticide application and make tomato farming more sustainable and environmentally friendly. Insect resistance for tomato is sourced from crop wild relatives brought into tomato by crossing. The resultant tomato materials have variable levels of resistance and often show undesired traits characteristic for wild species. The works for this topic include crossing tomato with wild relatives, measurements of pest resistance such as chemical analysis and determining the survival of insect (larvae) on the plants and genetic mapping of pest resistance genes.

## Identify genetic resources to develop tomato cultivars resistant to ToBRFV (MSc/PhD)

Tomato is grown all over the world and is the second most-consumed vegetable after potato. Tomato brown rugose fruit virus (ToBRFV) was first identified in 2014 on tomato plants and causes significant economic losses due to reduced crop yield and quality. There is an urgent need to find sources of resistance in tomato by screening biodiverse tomato collections for resistant genotypes. The thesis will include training in plant genomics and virus resistance screening.

## The trade-off between heat tolerance and fruit size in tomato (MSc/PhD)

Heat tolerance is an important trait for tomato production in tropical regions. However, heat tolerance is generally carried by small-fruit cultivars or wild tomatoes. Investigating the genetic behavior of this potential trade-off between heat tolerance and fruit size is key to designing a selection strategy for both traits. In this research, we will create a bi-parental population derived from a heat-tolerant and small-fruit parent crossing to a heat-sensitive and big-fruit parent to estimate the heritability and the correlation of these two traits, identify the QTL, and apply genomic selection to predict the progeny. Students will need to collect the phenotypic data, prepare DNA libraries, process the sequencing data to perform QTL mapping and also genomic selection for the heat tolerance and fruit size. This study is designed for students to learn the knowledge of QTL mapping and the bioinforamtic skills.

## Develop genomic tools for okra (MSc/PhD)

Okra is an important economical vegetable in South Asia. Although DNA markers can accelerate breeding programs, lacking genomic resources makes okra marker development challenging. In this research, we will perform genotyping-by-sequencing for diverse okra germplasm and use SNP-based and kmer-based approaches to profile the genetic diversity of this germplasm. This work will provide more genomic information about okra species and develop a strategy for trait mapping. Students will need to prepare DNA libraries and process the sequencing data to perform genetic diversity analyses. This study is designed for students to learn bioinformatic skills for orphan crops.

## CRISPR for crop improvement – Manipulating fruit size in tomato (MSc)

Fruit size is an important determinant for commercial **tomatoes**. Introgression of pest and disease resistance from landraces or wild species can lead to fruit types that are not acceptable for farmers and consumers. World**V**eg is testing whether gene editing can be used to increase fruit size in tomato lines where crosses with wild tomato to improve disease and pest resistance has led to small fruit size. The work involves genetic transformation and regeneration of **tomatoes**, and the identification of and the phenotypic evaluation of gene-edited plants.

# PLANT PATHOLOGY, ENTOMOLOGY

## Metagenomic analysis of the microbial communities in the rhizosphere of susceptible and resistant chili lines to Phytophthora in field conditions (MSc/PhD)

Phytophthora blight caused by Phytophthora capsici is a serious disease that limits chili production worldwide. Some sources of resistance to individual strains of the pathogen have been identified in greenhouse trials, but very few have been validated in field conditions. Rhizosphere microorganisms play a crucial role in plant health and resistance to soil-borne pathogens. We propose to use metagenomic approaches to analyze differences in rhizosphere microbial communities between susceptible and resistant chili lines to Phytophthora under field conditions, and how these differences affect plant health and pathogen resistance? The field trial will be conducted in three farmers’ fields with known Phytophthora disease history (three locations in Taiwan). The field trial study will compare the microbial communities of two groups: one susceptible and one resistant chili line to Phytophthora. Rhizosphere soil samples will be collected at different stages of plant growth and subjected to DNA extraction and metagenomic analysis, including nanopore sequencing. Statistical analysis will compare the microbial communities between the two groups. The study is expected to provide insights into the differences in rhizosphere microbial communities between susceptible and resistant chili lines to Phytophthora. The data generated from the metagenomic analysis will help to identify key microbial taxa associated with resistance to the pathogen. These taxa can be used as potential biocontrol agents against Phytophthora. The study will also provide information on the relationship between rhizosphere microbial communities and plant health and resistance to Phytophthora.

## Nanoparticle pesticides against virus diseases in solanaceous crops (MSc/PhD)

The emergence and re-emerging of viral diseases causing considerable economic losses is a major concern for the agriculture sector in Asia. The lack of practical solutions represents a threat to countries heavily reliant on agricultural production. Several insect-transmitted viral diseases are important for solanaceous crops. Developing tools for priming the plant or generating plant vaccines that provide cross-protection are alternative approaches from a resistance toolbox. We want to explore nanoparticle pesticides, which are virus-like particles packed with dsRNAs, to trigger RNA silencing against the disease. The team will select a model system to build and test the technology.

## Biocontrol agents against major pests and diseases in tomato and pepper (MSc/PhD)

Many agricultural pest and disease problems can be reduced using biological control, and when successful, biocontrol agents provide effective, enduring, environmentally friendly control. The world vegetable center has identified and plans to continue to evaluate biocontrol agents, their mechanism of action (metabolite production and genes associated with the biocontrol agents’ mode of action), and optimize the application variables (time of application, concentration, and formulation) of important diseases such as southern blight, phytophthora blight, fusarium, and bacterial wilt as well as entomopathogenic fungi against the *Thrips palmi* and T*uta absoluta* on tomato and pepper. In addition, use bioinformatics approaches to analyze and characterize the microbiome to identify putative biocontrol agents.The development of new biocontrol agents by Worldveg will serve as a technology to be transferred to stakeholders interested in using and commercializing biopesticides to increase more environmentally friendly options to control pests and diseases.

## Exploring pathogenomics of bacterial wilt and/or bacterial spot (MSc/PhD)

Pathogenomics explores genome-wide association studies to identify putative genes, regulators, and effectors associated with virulence, pathogenicity, and primary and secondary metabolism of Ralstonia solanacerum species complex. The World vegetable center has sequenced and plans to continue to sequence whole genomes of Ralstonia and Xanthomonas species worldwide to compare genes among related pathogens; and identify potential genetic targets for plant resistance to discover and characterize the complex dynamics of host–microbe interactions that lead to disease. One objective is to characterize Transcription Activator-like effectors (TALE) from these pathogens to understand potential host susceptibility targets. The pathogenomics research will identify genes for fast identification and tracking of virulent strains and the pathogenicity genes for breeding programs to develop resistant varieties to control bacterial wilt.

## Use of brassica species as Biofumigation to control bacterial wilt (MSc/PhD)

Bacterial wilt is one of the critical diseases of tomatoes. Reduction of the initial inoculum of the causal agent *Ralstonia solanacearum* can effectively control tomato bacterial wilt. The potential of brassica biofumigant cover crops can be used as an environmental friend alternative to the synthetic fumigants used to control soilborne diseases such as bacterial wilt. The World Vegetable Center has an experimental disease bacterial wilt field, ideal for evaluating different brassica species that can reduce bacterial wilt inoculum. In addition, microbiome and soil change analysis will be conducted to estimate the benefits of soil health. Identifying effective brassica biofumigant species will serve as a practical recommendation for a cultural method to control bacterial wilt while increasing soil health on vegetables.

## Identification of differentially expressed genes using wild tomato germplasm with bacterial spot tolerance (MSc)

Tomato bacterial spot is a disease that has increasingly damaged tomato fruit quality and yield, causing significant economic losses to farmers. Recent studies indicate that the predominant pathogen group of bacterial spot has changed from *Xanthomonas euvesicatoria* to *X. perforans*, creating a new challenge for bacterial spot management. Using resistant varieties is an effective and environmentally friendly strategy to control this disease. However, developing markers from bi-parental populations takes much effort because of the crossing and advancing populations as well as phenotyping disease scores. RNA sequencing analysis has been proven to be an efficient way to identify resistant genes by comparing susceptible with resistant plants. Based on our previous screen of tomato germplasm, we have identified tolerant wild tomato accessions. The purpose of this research is to establish the methodology of using RNA sequencing to identify differentially expressed genes from tolerant material and to develop BS-resistant markers for future use.

## Biological control of Southern Blight (*Sclerotium rolfsii*) on tomato (MSc)

Southern blight of tomato (*Sclerotium rolfsii*) is carried over from crop to crop in the soil and in crop debris. It can cause significant losses as there is little durable resistance to the pathogen and fungicide treatments are generally ineffective and unsustainable. An alternative and promising means of managing the disease is through the use of biocontrol agents such as plant activators and/ or antagonists. This project will continue to assess the efficacy of biological control agents and work with tolerance tomato materials for management of southern blight (*Sclerotium rolfsii*) initially under glasshouse conditions with artificial inoculation, with the possibility of moving later to field trials in hotspot locations.

## Allele mining of Solanaceae germplasm and establishment of screening system and evaluation for resistance to pepper veinal mottle virus (MSc/PhD)

The aphid-transmitted pepper veinal mottle virus (PVMV) is a member of the genus *Potyvirus* in the family *Potyviridae.* It has been reported as causing an epidemic in solanaceous crops, including eggplant, pepper, and tomato in Africa and also reported to infect pepper and tomato in Asia. The PVMV-infected plants expressed symptoms such as mottle, necrotic, leaf distortion, vein-banding, and vein chlorosis, and leaf abscission and fruit distortion were also reported. Though several measures are adopted to control virus diseases on vegetables, cultivating the virus-resistant varieties is generally considered the most effective one. To explore PVMV-resistant sources we would like to develop an allele mining approach using the available genomic sequences from tomato and pepper. We will identify allelic variants of common susceptibility genes and evaluate their performance against the virus. In parallel, WorldVeg will establish a reliable screening system to evaluate the solanaceous germplasm. The components of the screening system such as isolates, inoculation conditions, temperature effect, symptoms observation and virus detection will be investigated to optimize the screening flow. The identified PVMV-resistant sources are able to be used for developing PVMV resistance varieties as well as for the further study of resistance genes in the host genome and its mechanisms against the virus.

## Unraveling the resistance mechanism of soybean anthracnose through RNA sequencing and histochemistry (MSc)

Soybean anthracnose caused by *Colletotrichum truncatum* is a significant threat to soybean production worldwide. Few novel resistance sources to this disease were recently identified through collaboration between WorldVeg & TARI. To utilize such plant materials well in breeding programs for disease control, more understanding related to resistance mechanisms such as genetic and structure/morphology characteristics is needed. Transcriptome profiling or expressed sequence tag (EST) sequencing has been recently used to identify candidate genes or pathways involved in the soybean- *Colletotrichum truncatum* interaction. This study will use RNA sequencing and histochemistry approaches on these resistant soybean lines. This study will provide a better understanding of the molecular basis of the resistance mechanism of soybean anthracnose. The results can be used in selecting resistant germplasm and developing soybean cultivars with improved resistance to the disease, leading to increased crop yield and enhanced food security.

##  Optimizing foliar vs. soil application of neem against insects (MSc)

Azadirachtin extracted from the neem tree (*Azadirachta indica*) inhibits the development of immature insects to adulthood by interfering with molting, it also has repellent and antifeedant properties that are effective deterrents of >200 insect species, and it has been also extensively studied as a safe biopesticide alternative due to low impacts on nontarget beneficial insects. Previous studies conducted on woody and herbaceous plants suggest that systemic applications of azadirachtin extracts affect a variety of pests on different hosts. Furthermore, it has also been suggested that there is no advantage to using neem when applied as a soil (systemic), foliar spray, or in combination in the case of Japanese Beetles on Roses[[1]](#footnote-1). However, as there are many enquiries from farmers on the regions, there is a need to understand how to optimize foliar vs. soil application of neem preparations against diverse insects and on different feeding guilds to generate better and accurate recommendations for farmers located on different agroclimatic conditions.

# AGRONOMY, AGROECOLOGY

## Effect of leguminous green manure crops and microbiome-based nutrient management on production and quality of tomato (MSc/PhD)

In intensive vegetable production systems, excessive amounts of mineral fertilizers and chemical pesticides are often used, increasing human and environmental health risks. Mineral fertilizers do not replenish organic matter, leading to reduced functioning and health of the soil. Moreover, the soaring price of fertilizers poses another challenge for smallholder farmers, calling for alternative and sustainable solutions. Green manure crops are grown in rotation with the main crops to be incorporated into the soil to provide organic matter, nutrients, and phytochemicals. Yet, there is a lack of knowledge on the long-term benefits of green manures on vegetable production systems. It also needs to be quantified to what extent green manures can reduce the use of mineral fertilizers. Therefore, this study will identify the best-performing green manure crops to improve soil nutrient cycling, production and quality of tomato at HQ in Taiwan. The effects of green manure crops, with and without fertilizer, will be compared in a field experiment. The data on soil nutrients, soil microbiome composition, pest and disease incidence, yield, and nutrient composition of tomato will be measured and analyzed.

## Vegetable intercropping for efficient resource use and climate-resilient production (MSc)

Continuous monocropping of cereals contributes to soil degradation and makes farming systems more vulnerable to climate change. Agriculture will have to become more resilient to increasingly common extreme climatic events such as droughts, heat, and floods. Diversification of cropping systems could play an important role in transitioning to more efficient and resilient production systems. Intercropping has the potential to produce a greater yield per area of land through more efficient use of space and resources than solo crops. Including legumes in the cropping systems provides free nitrogen, improves soil health, conserves soil and water, and reduces the incidence of pests, diseases, and weeds. This field trial will identify good intercropping patterns for resource-efficient and resilient vegetable production. It will address knowledge gaps, such as how the spatial (row/strip design) and genetic dimensions (different lines) of intercrops interact and affect the production and agroecosystem. Under this trial, selected soil parameters; incidence of pests and diseases; and various intercropping indices (land equivalent ratio, yield advantages, etc.), will be used to identify a good intercropping pattern for more nature-positive and climate-resilient vegetable production systems.

## Transition to sustainable vegetable production: A system-level comparison of benefits among regenerative, organic and conventional vegetable production systems (PhD)

Conventional vegetable production tends to be productive but may negatively impact human and environmental health. Overusing chemical pesticides negatively impacts the environment, producers and consumers, while continuous use of mineral fertilizers combined with intensive tillage operations increases the emissions of greenhouse gases and degrades the soil. This results in reduced soil health and loss of associated ecosystem services, including carbon storage and water cycling in the soil. New approaches to vegetable production that generate healthy food while regenerating soil are urgently needed. Regenerative agriculture (RA) represents an interesting opportunity to achieve this. Despite receiving much attention, evidence about the benefits of RA is mostly anecdotal, which is limiting its wider adoption. In addition, previous research on RA practices focused mainly on individual practices (e.g., green manures, minimum tillage) and field crops and largely ignored vegetable production systems, creating a knowledge gap. Similarly in Taiwan, where earlier work has focused on rice. This long-term study will address this gap through a system-level field experiment comparing multiple outcomes and costs of regenerative, organic, and conventional approaches on selected vegetable cropping system. This experiment will take a more holistic approach by looking at a comprehensive set of outcomes covering soil health, incidence of pests and diseases, productivity, nutritional value of vegetables, and also economic costs and benefits of each system. It will generate evidence for the benefits and costs of regenerative vegetable production approaches. The results can stimulate the adoption of more sustainable agricultural practices and result in a broader impact in Taiwan and elsewhere.

## Under fertilization vs overfertilization: Evaluation the effect of soil nutrients on the expression of insect resistance in advanced tomato lines (MSc/PhD)

Scientific evidence has demonstrated that high nitrogen levels in plant tissue can decrease resistance and increase susceptibility to pest attacks, including red mite, two-spotted spider mite, aphids, on diverse crops such as tomatoes, beans, Brussels sprouts, sorghum, etc.[[2]](#footnote-2) Therefore, the evidence suggest that the use of conventional synthetic fertilizers can dramatically affect the balance of nutritional elements in plants, as these fertilizers likely create nutritional imbalances with their large pulses of available nitrogen, which in turn compromise crops’ resistance to insect pests. In contrast, other nutrients may have variable effects on enhancing or decreasing the plant susceptibility to insect pest and diseases[[3]](#footnote-3),[[4]](#footnote-4),[[5]](#footnote-5). Therefore, this research intends to provide a better understanding in the role of primary macronutrients, nitrogen (N), phosphorus (P), and potassium (K); as well as secondary macronutrients, calcium (Ca), sulfur (S), and magnesium (Mg); and the micronutrients, boron (B), manganese (Mn), iron (Fe), zinc (Zn), copper (Cu), and silicon (Si), and its effects on the expression of insect resistance on advance tomato lines.

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