PROCEEDINGS BOOK OF
9. EUROPEAN SUNFLOWER BIOTECHNOLOGY CONFERENCE
SUNBIO 2025

19-21 NOVEMBER, 2025

Megasaray Westbeach Hotel, Antalya, Turkey

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Organized by

Trakya University
International Researchers Association
International Sunflower Association

ISBN #:
978-625-96407-2-3

WELCOME NOTES

You are welcome to our 9th European Sunflower Biotechnology Conference which is organized by International Researchers Association and the in cooperation with Trakya University and International Sunflower Association. The conference will be held in Megasaray Westbeach Hotel, Antalya, Turkey, on November 19-21, 2025 with the support of several national and international partners with normal as well as with online participation. The program will include oral talks by invited prominent scientists and oral and e poster presentations by participants in selected topics. The Conference is intended that the subjects to be kept broad in order to provide opportunity to the science and research community to present their works as oral or poster presentations in a friendly environment of Antalya, Turkey to share their knowledge and experience and benefit from each other.

The 9th conference will gather scientists from around the world, and present their recent achievements. The attendees will have ample opportunities for learning, reconnecting, engaging and networking with colleagues from academia and industry as well as meeting with various exhibitors.

As there have been many different scientific meetings around the world, we aimed to bring three different communities together, namely science, research and private investment groups considering practical information sharing that is of value for researchers and scientists from around the world, in a friendly environment of Antalya, Turkey to share their knowledge and experience and benefit from each other as well as prospects to overcome the limitation for sustainable crop production to feed the world.

There are 40 papers contributed by about 150 authors from 14 different countries from the world. 12 oral and 20 poster presentations existed in the conference program both joining and presenting normal and online presentations by 77 normal and 3 online as total by 90 participants.

With care for our nature and environment, we aim the green conference, meaning that as little as possible papers will be used. Abstract book is published in electronic book and is distributed to the participants by e mail for online participants. All the e-posters are prepared in electronic form and then submit to via the conference e mail and exhibited in electronical poster boards as well as in online e poster hall in our web page during the conference.

The Conference topics will cover on sunflower:

Plant Breeding and Genetics, Molecular Genetics and Biotechnology, Biology and Physiology, Genetic Resources, Plant Protection, Agronomy, Economy, Trade, Quality, etc.

We would like to thank all of you for joining this conference and we would like to give also special thanks to our sponsors and collaborators for giving us a big support to organize this event.

Prof Dr Yalcin KAYA
Head of the Organizing Committee

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SUNFLOWER SEED BASED FAT REPLACERS (FR): THE BIOTECHNOLOGICAL SUSTAINABLE ASSESMENT OF FR MANUFACTURING STRATEGIES ON FOOD QUALITY APPLICATIONS

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ABSTRACT

Sunflower seed is the fourth most important oil crop worldwide, after palm oil, soybean oil and rapeseed oil. Sunflower meal is the most important by-product of sunflower oil production, accounting for 36% of the processed mass of sunflower seeds and the agronomical quality of crop gives the efficiency to the meal product. The protein content of sunflower seeds is approximately 20%, while the protein content of sunflower meal ranges from 30% to 50%. Moreover, to protein, sunflower meal contains other valuable nutrient constituents as vitamins, minerals, and polyphenols. Because of this, sunflower meal is not only mainly utilized as animal feed but also used the potential human consumption agent owing to it has good water holding capacity. Sunflower meal has been biotechnological upgraded to a versatile food-grade defatted sunflower meal (SUN) with a variety of potential food and beverage applications. Phenolic acids (PA), especially quinic acid derivatives of caffeic acid or ferulic acid, have previously been considered the most important phenolic compounds in sunflower seeds and especially in sunflower meal otherwise Pas as hydroxybenzoic acid, vanillic acid, sinapinic acid, quinolactones of caffeic acid, 1,2-diesinaroylgentiobiose, and hydroxyphenylpropionic acid 3,4-dihydroxyphenyl-2-oxopropionic acid. The applied biotechnological manufacturing SUN based fat replacer (FR) has been reported to increase total phenolic content, antioxidant capacity, and improve the nutritional profile. Fat replacers are food additives that provide the benefits of fat to zero-calorie or low-calorie foods. They perform the functions of fat, imparting a soft texture, pleasant mouthfeel, and flavor to foods. Different types of baked goods use different types of fat replacers. Carbohydrate-based fat replacers have been reported to bind water, adding volume, moisture, and a pleasant mouthfeel. FRs are utilized to reduce trans-fat and total fat content while maintaining consumer acceptance. A variety of fat replacers have been explored for use in baked goods, including complex polysaccharides, gums and gels such as cookies, cakes, and crackers can contain high levels of trans fats as whole food matrix structures, and combinations thereof. The application of SUN based FR to popular and frequently consumed gelled/emulsified meat products such as frankfurters is particularly interesting due the obtained technological and nutritional properties of SUN may improve the formulation of these products, resulting in healthier meat products.

Keywords: Sunflower Seed, Fat Replacer, Biotechnology, Agronomical Quality, Food Quality

REVIEW OF THE NUTRITIONAL AND HEALTH BENEFITS OF SUNFLOWER SEEDS

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ABSTRACT

Sunflower (*Helianthus annuus* L.) is a species of the Asteraceae family. Sunflower seeds are edible and have excellent nutritional value due to their richness in nutrients and biological activities. The inclusion of sunflower seeds in the diet may provide health benefits. This review summarizes the currently recognized but understudied nutritional and medical importance of sunflower seeds by highlighting the potential benefits of their phytochemical constituents, including phenolic acids, flavonoids, and tocopherols that act as antioxidants, which help prevent free radical damage. The objective is to provide scientific evidence to improve the food and pharmaceutical applications of this common but popular crop as a functional food. Sunflower seeds have been pharmacologically studied for their anti-inflammatory, antimicrobial, and wound healing properties. They also have cardioprotective, antitumor, antidiabetic, and cholesterol-lowering effects. Although sunflower seeds are a healthy food, there are some risks to be aware of.

Keywords: Sunflower seeds, Nutritional value, Phytochemicals, Medicinal uses

THE EFFECTS OF PRICE AND SUPPORT POLICIES ON SUNFLOWER PRODUCTION IN TURKEY ON THE WELFARE OF PRODUCERS

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ABSTRACT

This study provides an overall assessment of sunflower production, which is important for the Turkish economy and agriculture, in terms of price and agricultural support policies. Oilseed crops are among the strategic products with a supply gap in Turkey's agricultural production. Turkey ranks second after the EU in global sunflower imports. Turkey, which has a significant production gap in oilseed crops and vegetable oil production, is projected to have a total import value of $5.6 billion by 2025. While the current price of sunflower seeds increased by 145% between 2022 and 2025, area-based support increased by 450%. When the product price is adjusted according to the Consumer Price Index (CPI) based on 2003, the highest unit price was observed in 2020 at 0.88 TL. In terms of subsidies, it has been calculated that a sunflower producer receiving a total of 696.50 TL/da in current prices in 2024 will receive 20.03 TL/da in real terms and 20.40 $/da in dollar terms. This figure is expected to be 732 TL/da at current prices, 25.39 TL/da at real prices, and 25.76 $/da in dollar terms under the new support model to be implemented as of 2025. In Turkey, a sunflower producer received total support amounting to 54% of their total income per decare in 2006, whereas this figure has declined to 18% in 2025. Developing price and support policies that will reduce Turkey's dependence on imports in sunflower agriculture is crucial for all stakeholders.

Keywords: Keywords: Agriculture, Sunflower, Agricultural Support

COMBINATIONS FOR AGROFORESTRY PROJECTS OF RURAL HOUSEHOLDS IN BOSNIA AND HERZEGOVINA THAT INCLUDE PLANTING SUNFLOWERS

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ABSTRACT

One way to include sunflowers more in the production processes in Bosnia and Herzegovina is to start planting them more intensively on private farms of farmers in Bosnia and Herzegovina. Private farms are fragmented to a certain (relatively high) percentage in Bosnia and Herzegovina, especially in those areas where the processes of land consolidation and arondation during the former state system (Socialist Federal Republic of Yugoslavia) were complicated or incomplete. Certain cantons (for example, the Sarajevo Canton) are characterized by a high degree of underutilization of agricultural land, but this is the case in many parts of the country. One way to intensify agricultural production is to encourage local rural households to grow sunflowers and to inform them about the possibility of starting their own business and agroforestry-oriented production. Agroforestry projects enable the population to grow plants for private production, including plant species whose parts are used for human food, animal feed, for breeding and feeding bees, for the production of basketry (baskets, wicker furniture for personal use), timber for personal use (fences, roofing material, livestock houses) and for the purpose of improving the quality of air, water and microclimate on private property (greenery, shade, water filtration on private property, noise reduction). Agroforestry projects in Bosnia and Herzegovina could be supported (logistically and financially) by the competent ministries and municipal structures (local and agricultural development offices), which could be an additional help for the population inhabiting rural areas in Bosnia and Herzegovina. Sunflower is one of the plants grown on agricultural plots in the country, and is widely used in oil production. It is necessary to investigate what other crops and tree species can be combined on private properties. Some of the proposals are certainly growing together with soybeans, clover, linden, acacia, willow, poplar, tobacco (where permitted) and on more compact land plots characterized by a wealth of diversifiable micro-localities with mosaic soils and brown soils. This paper could serve as the first such review of the above-mentioned plant species for Bosnia and Herzegovina. There are indications that the cultivation of acacia and linden would help feed bees, while the creation of a good climate for sunflower growth could eventually affect the health of sunflower plants in the area and abundant pollination. This is very important from the perspective of climate change, which threatens populations of insects that are important for pollination.

Keywords: Sunflower, lime, Agroforestry, rural households, Bosnia and Herzegovina, climate change, bees populations

EFFECTIVENESS OF A STATIONARY FIELD INFECTIOUS BACKGROUND FOR ASSESSING SUNFLOWER RESISTANCE TO ALTERNARIA LEAF BLIGHT IN THE NORTHERN STEPPE OF UKRAINE

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ABSTRACT

A stationary field infectious background was created at the Institute of Oilseed Crops of NAAS (IOC NAAS) (Zaporizhzhia, Ukraine) in 2005. High infectivity of the background was ensured by constant sowing of sunflower in the same field (monocrop) and deliberate inoculation of infectious agents of the most harmful diseases that are common in the northern steppe of Ukraine. Sunflower fallen seed is managed annually in accordance with the methodology developed at the Institute. In the first three years after the artificial infectious background organization, a pure culture of the pathogen, Alternaria helianthi (Hansford) Tubaki, which was isolated in the laboratory from a local population of the pathogen, was inoculated into the soil of the experimental field. Subsequently, sunflower plant residues collected from the fields of the study region that were significantly affected by Alternaria leaf blight and other pathogens were dispensed into the soil annually. On plants grown on the stationary infectious background, Alternaria parasitized alone or in a combination with three other foliar fungal pathogens - Plasmopara halstedii (Farl.) Berl. et. de Tony, Embellisia helianthi (Hansf.) Pidolp and Phoma macdonaldii Boerema. There were 30% of plants affected by Alternaria leaf blight and downy mildew simultaneously, 35% of plants affected by Alternaria leaf blight and Embellisia simultaneously, and 75.9% of plants affected by Alternaria leaf blight and black stem disease simultaneously. In accessions susceptible to Alternaria leaf blight, the number of plants simultaneously infected with two pathogens amounted up to 83.4%, while in accessions that were more resistant to Alternaria leaf blight, there were up to 41.2% of plants infected with two pathogens. In 2024–2025, 15 accessions (self-pollinated lines, hybrids) bred at the Yuriev Plant Production Institute of NAAS (YPPI NAAS) (Kharkiv) and 17 accessions bred at the IOC NAAS were examined on the stationary infectious background. The accessions were evaluated using a nine-point scale. Five relatively resistant accessions bred at the IOC NAAS and six accessions bred at the YPPI NAAS were identified. The maximum resistance score to Alternaria blight disease in combination with resistance to Plasmopara halstedii and Phoma macdonaldii was shown by hybrids ‘Ahent’, ‘Ahronomichnyi’, ‘Vilnyi’, and ‘Serpanok’, which had been bred at the IOC NAAS.

Keywords: Sunflower, monocrop, infectious background, Alternaria leaf blight, resistance, self-pollinated lines, hybrids

RESOURCES FOR SUNFLOWER BREEDING FOR BIOTIC AND ABIOTIC FACTORS

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ABSTRACT

Sunflower seed yield is limiting by abiotic and biotic factors and an important pool gene is represented by sunflower wild species. Helianthus argophyllus is annual wild specie used in sunflower breeding programs, especially for drought resistance. For resistance/tolerance at parasite broomrape (Orobanche cumana Wallr), in our breeding program at National Agricultural Research and Development Institute Fundulea, Romania, we use perennial wild species Helianthus maximiliani, Helianthus mollis and annual wild species Helianthus neglectus, Helianthus praecox. In year 2023, in Braila, in natural infested field with broomrape, sunflower genotypes 10B x Helianthus maximiliani, 15C x Helianthus neglectus and 17C x Helianthus mollis has 0% attack degree with Orobanche cumana. In year 2024, in Braila, in natural infested field with broomrape only sunflower genotype 15C x Helianthus neglectus has 0% attack degree, that means virulence of Orobanche cumana increase.

Keywords: Sunflower, breeding, wild species

NEW SUNFLOWER STARTING MATERIAL OF THE NATIONAL PLANT GENE BANK OF UKRAINE

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ABSTRACT

Expansion of the genetic diversity of starting materials is critically important in sunflower breeding to increase yield, product quality, resistance to diseases, pests and tolerance to adverse environmental conditions, which is especially vital in the context of climate change. Gene banks play an important role in such expansion; their activities are aimed at forming collections, introducing, and preserving accessions of domestic plants and wild species. The National Center for Plant Genetic Resources of Ukraine of the Yuriev Plant Production Institute of NAAS has built up a sunflower collection, which comprises 802 accessions, including 175 breeding cultivars, 19 landraces, 463 self-pollinated lines, 72 genetic lines, and 73 related wild species from 22 countries worldwide. In 2020-2025, 173 new sunflower lines created at the Yuriev Plant Production Institute of NAAS were added to the National Plant Gene Bank of Ukraine. The new sunflower lines were evaluated for a set of economic and biological characteristics and described by distinctness traits in accordance with guidelines. These lines are included in the European Search Catalogue for Plant Genetic Resources (EURISCO) and available on requests under authors' terms (http://EURISCO.ipk-gatersleben). Based on examination results, 23 sunflower lines - pollen fertility restorers (RfRf) have been registered as sources of a set of valuable traits, which combine resistance to biotic and abiotic factors, high quality and valuable economic characteristics. The new lines were selected for early ripeness, cold tolerance at early stages of plant development, resistance to downy mildew, resistance to sunflower broomrape, and altered composition of tocopherol isomers in seeds.

Keywords: Sunflower, genetic resources, cultivar, landrace, line, wild species, valuable trait

XYLEM CHARACTERISTICS OF WILD HELIANTHUS GERMPLASM AS A SOURCE FOR DROUGHT TOLERANCE IN CULTIVATED SUNFLOWER

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ABSTRACT

Cultivated sunflower is moderately drought tolerant crop. However, insufficient water supply during the key stages of its growth and development significantly reduces sunflower seed yield. Considering that wild Helianthus species inhabit different habitats, including desert areas, they can represent a significant source of desirable traits for improving drought tolerance in cultivated sunflower. It is known that xylem architecture in plants is related to drought tolerance. In this regard, our research provides a comparative overview and detailed characterization of the xylem of the vegetative organs and parts of the reproductive region of 19 perennial wild sunflower species. Cross sections were obtained from the middle part of petiole, lamina main vein and peduncle, using cryotechnic procedure. Observations and measurements of the vessels of all vascular bundles in cross sections were carried out using the light microscope with Image Analyzing System. The obtained results of the comparative xylem anatomy revealed significant phenotypic variability among analyzed species. According to the results of the Discriminant Analysis, characteristics of vascular tissue such as size of lumen, number of vessels, as well as the % of vessels with small lumen (leaf < 100 µm2; peduncle < 150 µm2) mostly contributed to the discrimination among the analyzed species. Species H. californicus, H. divaricatus, H. maximiliani, H. nuttalli, H. pauciflorus and H. salicifolius in which the xylem of the leaf and peduncle are predominantly (60-99%) made up of vessels with small lumen may indicate their xeromorphic structure and greater tolerance to drought. The observed differences in xylem characteristics among the analyzed species may be a consequence of their developmental adaptability. These findings hold valuable implications for shaping upcoming breeding approaches aimed at enhancing drought tolerance in sunflower cultivars.

Keywords: anatomy, drought, wild sunflower, xylem.

Acknowledgment: This work is supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, grant number 451-03-136/2025-03/ 200032, by Center of Excellence for Innovations in Breeding of Climate-Resilient Crops - Climate Crops, by BREEDTECH -Building Capacity in Plant Breeding and Biotechnology Education and Research through partnership program in Africa, Middle East and Europe for Agricultural transformation, Funded by Erasmus+ Programme, Capacity Building in the field of Higher Education Grant number: 101128862, by bilateral cooperation project between the Republic of Serbia and Turkey 2024-2026, grant number 0260207, financed by The Ministry of Science, Technological Development and Innovations of the Republic of Serbia (NITRA) and The Scientific and Technological Research Council of Turkey (Tübitak), and based upon work from COST Action RECROP (CA22157)..

ACTIVITY OF ANTIOXIDANT ENZYMES IN SUNFLOWER LEAVES CO-CULTIVATED WITH FUNGAL STRAINS

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ABSTRACT

Sunflower (*Helianthus annuus* L.) is a globally important oilseed crop. Its productivity and seed quality are significantly constrained by both biotic and abiotic stresses, particularly under current climate change conditions. One of the biotic factors affecting the crop is seed-borne fungal strains, including various species of Fusarium, Rhizopus, Alternaria, Penicillium, and Curvularia, which negatively impact seed quality, germination, and plant development. Exposure to biotic and abiotic stresses often leads to an overproduction of reactive oxygen species (ROS), such as superoxide radicals and hydrogen peroxide, which can cause oxidative damage to proteins, lipids, nucleic acids, and other cellular components. To survive and adapt, plants have evolved complex antioxidant defense systems that mitigate ROS accumulation. Key enzymes such as superoxide dismutase (SOD), catalase, and ascorbate peroxidase function synergistically to detoxify ROS, maintaining cellular redox homeostasis. Among these, plays a primary role in enzymatic defense by catalyzing the conversion of superoxide radicals into less harmful hydrogen peroxide, which is subsequently detoxified by other antioxidant enzymes. The efficiency of these adaptive mechanisms is critical for plant resilience under stress conditions, influencing growth, development, and yield stability. Therefore, assessing SOD activity provides valuable insights into the plant's capacity to mitigate oxidative stress and serves as an important indicator of tolerance to biotic stresses, such as fungal infections. In the present study, the activity of SOD was analyzed in various local sunflower genotypes co-cultivated with different fungal strains (Fusarium oxysporum, Rhizopus arrhizus, Alternaria alternata, Aspergillus niger) to assess their oxidative stress response and adaptive capacity. SOD activity was determined spectrophotometrically, based on inhibition of nitro blue tetrazolium reduction. Results showed a significant increase in SOD activity in plants co-cultivated with F. oxysporum and Rh. arrhizus (by 25-35% compared to the control, depending on hybrid). These increases were associated with improved biomass accumulation and root elongation, suggesting an effective and regulated oxidative defense mechanism. In contrast, sunflower plants exposed to Alternaria alternata exhibited only slight, statistically insignificant increases in SOD activity, correlating with pronounced reductions in shoot length and biomass, indicating a less efficient antioxidant response and more severe oxidative damage. Overall, the study highlights the critical role of SOD as an early and sensitive biomarker of oxidative stress in sunflower under biotic stress conditions. Furthermore, it emphasizes genotype-specific variability in antioxidant responses, providing valuable insight into breeding strategies for improved fungal resistance and stress resilience in sunflower crops.

Keywords*:* *Helianthus annuus*, fungal strains, biotic stress, reactive oxygen species, superoxide dismutase

Acknowledgement. This work was supported by the Subprogram 011101 Genetic and biotechnological approaches to agroecosystem management under climate change, financed by the Ministry of Education and Research of the Republic of Moldova.

LIPID PROFILE OF SUNFLOWER POLLEN OIL

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ABSTRACT

Pollen grains are complex structures that contain a wide range of lipid compounds with essential roles in plant biology, including reproductive signaling, protection against environmental stress, and attraction of pollinators. Among the lipid components, fatty acids and their derivatives are especially important due to their multifunctional biological properties. Helianthus annuus L., being an entomophilous species, produces large quantities of pollen that are readily accessible throughout its flowering period. This makes sunflower pollen a promising biomass resource that can be valorized as a byproduct, contributing to more circular and sustainable agricultural practices. Despite this potential, the lipid profile of sunflower pollen remains insufficiently explored. In the present study, fatty oil was extracted from the pollen of a single sunflower genotype collected from three different locations and analyzed using gas chromatography–mass spectrometry (GC-MS). The results revealed a complex and diverse chemical composition. Organic acids, particularly monocarboxylic acids and their methyl esters, dominated the profile (34.77–44.43%) and are known for their antioxidant and anti-inflammatory activities. Diterpenic esters were also abundant (26.12–40.46%), offering potential regenerative and therapeutic effects. Additionally, the oil contained considerable amounts of ketones (9.00–14.16%), which may contribute to fragrance and biological activity, and lipid-soluble vitamins (1.72–3.41%) that support nutritional and skin-protective functions. Minor components such as monoterpene hydrocarbons and oxygenated monoterpenes further enriched the oil's bioactive profile and may contribute to its stability. These findings underscore sunflower pollen as a rich and promising source of bioactive lipids with potential applications in dermatological formulations, functional foods, and natural pharmaceuticals. The integration of pollen-derived lipids into such products represents a novel opportunity to enhance the economic value of sunflower crops while aligning with principles of sustainable resource use.

Keywords: Helianthus annuus, Sunflower pollen, Lipid composition, Fatty acids, Bioactive substances

Acknowledgement. This work was supported by the research project (PN-IV-P8-8.3ROMD-2023-0269) Comprehensive valorization of Helianthus annuus L. by-products for the development of new products with biomedical potential, funded by UEFISCDI, Romania and by the Subprogram 011101 Genetic and biotechnological approaches to agroecosystem management under climate change, financed by the Ministry of Education and Research of the Republic of Moldova.

BY-PRODUCTS FROM SUNFLOWER OIL PRODUCTION AS VALUABLE SOURCES OF BIOACTIVE COMPOUNDS

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ABSTRACT

In the context of global efforts toward sustainable development and resource efficiency, the agri-food sector is under increasing pressure to minimize waste and to maximize the valorization of secondary raw materials. The United Nations 2030 Agenda emphasizes the sustainable management of natural resources through the prevention, reduction, recycling, and reuse of production residues. Within this framework, the vegetable oil industry represents a major source of agro-industrial by-products that remain largely underexploited, despite their significant potential for value addition. Sunflower (Helianthus annuus L.), one of the world's most important oilseed crops cultivated for edible oil and biodiesel production, generates large amounts of residual biomass during industrial processing. Oil extraction results in secondary products that represent approximately 30–35% of the processed seed mass. Although sunflower seed by-products, such as hulls, expelled cakes, or extracted meal, are mainly used in the animal feed industry or as organic fertilizers, their rich composition in bioactive compounds, including phenolic compounds, flavonoids, and tocopherols, has recently attracted growing scientific interest. Particular attention has been directed toward their potential applications in agriculture, where bioactive extracts and derived formulations can act as natural stimulants or antifungal agents, offering alternatives to synthetic agrochemicals. The present study focuses on evaluating the bioactive potential (stimulant and antifungal) of novel products obtained from residues generated by the cold pressing of sunflower seeds. Through this approach, the research aims to explore the possibility of transforming low-value agro-industrial residues into high-value bioresources, thereby contributing to environmental sustainability and the development of innovative bio-based products for agricultural use.

Keywords: sunflower by-products; antifungal activity; biostimulants; sustainable agriculture

Acknowledgement. This work was supported by a grant of the Ministry of Education and Research, CCCDI-UEFISCDI, project number PN-IV-PCB-RO-MD-2024-0406, within PNCDI IV and funded by the Ministry of Education and Research of the Republic of Moldova, project no. 25.80013.5107.27.

APPLICATION OF MINIRHIZOTRONS IN SUNFLOWER ROOT RESEARCH

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ABSTRACT

Unlike humans and animals, plants cannot move and go where the conditions for their life and development are more favorable. Where we saw plants, they stayed there. That is why the adaptation of plants, both the aerial part of the plant and the root system, is extremely important. The aerial part of the plant has been the subject of a large amount of research, but the root has been significantly less researched in comparison to its importance. The reasons should be sought in the more complicated process of such research. However, we have decided that, in addition to more research and phenotyping on the aerial part of sunflowers, we will focus part of our efforts on the roots as well. Our primary task was to observe root growth in early developing sunflower plants using a minirhizotron. This technology has been massively used in research at KWS since 2015, but it has been directed first at sugar beet and later on corn mostly in the study of roots and its connection with drought tolerance. In sunflower, we focused our research more on seed treatments with biostimulators, which does not mean that we will not extend them to other areas in the future. After several years of research, they helped us to decide on a biostimulator that not only has a positive effect on the growth of the aerial part, but also on the growth of the root system. As the development of biostimulators rapidly increases, new biostimulators also come into our research, where the method of using the minirhizotron has become standard in our research. We wanted to present our experiences and results at this conference, so that perhaps this method could be widely introduced in research.

Keywords: Sunflower, Root, minirhizotrons, Drought Tolerance

TISSUE CULTURE AND MICROPROPAGATION TECHNIQUES IN SUNFLOWER (HELIANTHUS ANNUUS L.): TRENDS AND ADVANCES

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ABSTRACT

Between 2020 and 2025, research on in vitro culture of sunflower (Helianthus annuus L.) has led to the refinement of explant use, including cotyledons, cotyledonary nodes, and immature embryos. Murashige and Skoog (MS)-based media, supplemented with specific combinations of auxins (IAA, NAA) and cytokinins (kinetin, 6-BA), have been optimized to enhance organogenesis—the main regeneration pathway. Somatic embryogenesis remains difficult and inconsistent. A major limitation is the genotype-dependent response and the generally low regeneration efficiency. These challenges are being addressed through genotype-specific protocols and by investigating the expression of key genetic regulators of totipotency, such as SERK and BBM. Improved in vitro systems now allow efficient genetic transformation, particularly through Agrobacterium tumefaciens-mediated methods, facilitating the development of transgenic or genome-edited lines. Moreover, these technologies support the conservation of genetic resources from wild Helianthus species and the rapid clonal propagation of elite agronomic genotypes. Overall, these advances underpin the development of cutting-edge biotechnological strategies in sunflower breeding, with applications in sustainable production and improved tolerance to biotic and abiotic stress factors.

Keywords: Explant sources, cotyledon segments, immature embryos, regeneration techniques, genetic transformation

FROM SILENCE TO SIGNAL: REBUILDING THE GENOMIC TOOLBOX FOR SUNFLOWER RESISTANCE TO BROOMRAPE

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ABSTRACT

The development of sunflower resistance to broomrape (*Orobanche cumana* Wallr.) is a critical objective in ongoing breeding programs. In the early stages of establishing a molecular breeding platform for broomrape resistance, two F3 populations were developed by crossing a resistant and a susceptible sunflower line. Phenotypic evaluations were conducted across two environments, Feketić and Lipar, as well as under controlled conditions in a glasshouse. Data were collected over two consecutive growing seasons, and included assessments of O. cumana infection severity and the number of parasitic plants per sunflower individual, recorded separately on roots and stems. All evaluations were performed using broomrape race E, which is predominant in the region and relevant for current resistance breeding efforts. A set of 14 SNP markers previously associated with broomrape resistance in the literature was selected for genotyping. However, the results revealed that four markers failed to amplify, and the remaining ten were predominantly monomorphic—indicating a lack of allelic diversity in the targeted genomic regions. These outcomes contrast with prior literature, where the same markers were informative, suggesting either genotypic divergence between the populations or limited applicability of these markers outside specific genetic backgrounds. The absence of polymorphism at known marker loci highlights the need for identification of new, population-specific markers for O. cumana resistance. This study marks the beginning of systematic efforts to address broomrape resistance through molecular approaches in local sunflower germplasm and sets the stage for future marker discovery and validation to support marker-assisted selection in breeding programs.

Keywords: *Helianthus annuus, Orobanche cumana*, genetic resistance, phenotyping, marker-assisted selection, genetic variability, multi-environment testing

Acknowledgement

This work is supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, grant number 451-03-136/2025-03/ 200032, by the European Commission through Twinning Western Balkans project CROPINNO, grant number 101059784, and by Center of Excellence for Innovations in Breeding of Climate-Resilient Crops - Climate Crops, Institute of Field and Vegetable Crops, Novi Sad.

COMPARATIVE GENOMIC ANALYSIS OF THE ORDEB2 LOCUS CONFERRING RESISTANCE TO HIGHLY VIRULENT RACES OF OROBANCHE CUMANA

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ABSTRACT

One of the main constraints currently affecting sunflower (Helianthus annuus) crops is the parasitism by the sunflower broomrape (Orobanche cumana), a holoparasitic weed that attaches to the roots of sunflower plants and extracts water and nutrients, thereby causing severe yield losses. This parasitic plant is widespread across many sunflower-producing regions, ranging from South-Eastern Europe to Central Asia, including parts of North Africa and, more recently, expanding into South America. Among the different management strategies employed to combat O. cumana, the development of resistant sunflower varieties through breeding has proven to be one of the most effective, durable, and environmentally friendly approaches. Over the years, several resistance genes conferring resistance to various O. cumana races have been identified and characterized. One such gene is OrDeb2, which was introgressed into the cultivated sunflower line DEB2 from the wild species Helianthus debilis subsp. tardiflorus. This gene provides resistance to race G of sunflower broomrape through a mechanism that involves early post-attachment blockage of parasite development. Previous genetic studies have localized OrDeb2 to a 1.38 Mbp region on chromosome 4 of the H. annuus HanXRQ reference genome assembly. In the present study, we conducted a comparative genomic analysis across several recently sequenced sunflower genomes, including both cultivated lines and wild species. This analysis revealed a conserved cluster of genes across all genomes examined within the region previously associated with OrDeb2. Among these, we identified strong candidate genes that show features consistent with a role in resistance. These findings represent a significant advancement in the identification of the gene underlying OrDeb2-mediated resistance and provide a valuable framework for further functional analyses aimed at elucidating its role in host-parasite interactions and facilitating the development of new resistant sunflower varieties.

Keywords: Sunflower, resistance, sunflower boomrape, comparative genomics, breeding

REGULATION OF SIGNALING THROUGH COLLOIDAL SILVER AT EARLY STAGES ASSIST THE GROWTH OF SUNFLOWERS DURING DROUGHT AND HIGH TEMPERATURE STRESS

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ABSTRACT

High temperature and drought stresses, along with high light intensity, pose significant threats to global crop production. To remove or reduce the stress conditions of crop plants becomes a complex challenge. One of the recent approaches involves generating crop plants that can withstand such stress conditions. However, this requires considerable effort and time. Even if it is managed, the tolerant plant should follow a specific or enriched pathway to combat the stress. The combination of nanotechnological products, colloidal silver (1.5-3 ppm, 25 ml/da) and calcium carbonate (50 g/da) was applied to regulate signaling pathways at early stages (2 to 5-leaf stage) of growth of sunflower plants in field (50 da) conditions. The defense systems were significantly activated and extended until plants face high temperature stress (over 40°C). At this stage (10-leaf stage, head is formed), the second application was made from the same mixture with the same concentrations. No application was made in the control field (50 da). Followed by the harvest, physiological, morphological, and biochemical parameters of plants were evaluated in both fields. The stress metabolites, such as H2O2, O-2, and malondialdehyde (MDA), were lower in the applied field than in the non-applied field. Physiological parameters, such as head diameter, weight, stem length, 100-grain weight, stem diameter, and leaf area, were higher when compared to those of the control field. We evaluated that the nanotechnological compound regulated signaling pathways and antioxidant metabolism throughout the cultivation period. Hormonal homeostasis and the regulation of stress-related genes may have played a significant role in sustaining tolerance under high temperatures. We suggest that the colloidal silver could be a promising compound to evoke tolerance mechanisms when applied at early stages before the occurrence of stress.

Keywords: Nanomaterials, sunflowers, temperature, stress, colloidal silver

A COMPARISON OF SNP GENOTYPING ARRAYS WITH TARGETED GENOTYPING-BY-SEQUENCING (TGBS) IN SUNFLOWER

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ABSTRACT

Array genotyping using many thousands of SNP markers is widely used during sunflower breeding including for Genomic Selection and genetic research. But for certain applications in breeding there is no need for that many markers. Such analyses include marker-assisted backcrossing, marker-assisted selection for candidate genes, low density analysis of samples for purity and quality analysis. With the advent of low-cost, high-throughput DNA sequencing technologies, targeted Genotyping-By-Sequencing (tGBS) offers the potential to reduce costs in routine sunflower genotyping. To directly compare the quality of genotyping data between tGBS and microarrays, we have analyzed a large set of sunflower samples with both methods. tGBS technologies delivered a high marker conversion rate (>95%) of SNP markers present on genotyping arrays. However, over all marker/sample combinations a considerable percentage (10-15%) did not produce genotype calls. While in homozygous lines, both tGBS and array genotyping produce a comparable data quality for the called marker/sample combinations, the accuracy of the tGBS calls dropped significantly in heterozygous material. After curation including the use of parent/offspring triplets, less than two thirds of the tGBS markers could be reliably scored. We conclude that tGBS employing hundreds of SNP markers can be used cost-efficiently in routine sunflower genotyping if one selects only the best markers from a tGBS marker multiplex and simultaneously obtains a sufficiently high number of reads for each marker/sample combination. Both constraints in combination with a generally lower marker number in the tGBS analysis reduce or eliminate the cost advantage over genotyping arrays in Genomic Selection but mostly retain the advantages of tGBS in breeding approaches such as marker-assisted backcrossing.

Keywords: SNP genotyping, targeted Genotyping-By-Sequencing, array genotyping

DECIPHERING DROUGHT RESPONSE STRATEGIES IN SUNFLOWER

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ABSTRACT

Drought stress is a major constraint in sunflower production, especially during critical developmental stages such as flowering. In this study, we investigated the physiological and molecular responses of two genetically distinct sunflower lines exposed to drought conditions, aiming to understand the underlying mechanisms shaping their adaptation strategies. Physiological measurements, including growth, gas exchange, and chlorophyll fluorescence parameters, revealed clear genotype-dependent differences in response to water limitation. The genotypes differed in their ability to maintain biomass and stomatal conductance, with the more resilient genotype showing stronger physiological stability under drought conditions. Transcriptomic analysis supported these observations by uncovering distinct patterns of gene expression between the two lines. Enriched pathways included those related to cuticle reinforcement, antioxidative defense, and metabolic adjustments. Flavonoid biosynthesis and fatty acid metabolism were prominent in both genotypes, indicating shared mechanisms for mitigating stress. However, broader enrichment of stress-related pathways—including those linked to membrane stability and protective surface compounds—was observed in the more responsive line. This integrative analysis highlights contrasting drought response strategies in sunflower and underscores the value of combining physiological screening with transcriptomic profiling. This work contributes to ongoing efforts in developing climate-resilient sunflower and demonstrates the value of combining functional genomics with physiological screening in sunflower breeding.

Keywords: Helianthus annuus, transcriptomics, gene mining, drought tolerance, climate change

Acknowledgements:
This work is supported by the Horizon Europe HelEx project N°101081974 as well as the by Twinning Western Balkans project CROPINNO, grant number 101059784 funded by the European Commission, Moreover it is a part of Ministry of Science, Technological Development and Innovation of the Republic of Serbia, grant number 451-03-136/2025-03/ 200032 and Center of Excellence for Innovations in Breeding of Climate-Resilient Crops - Climate Crops, Institute of Field and Vegetable Crops, Novi Sad, Serbia.

ROOTS – AN UNEXPLOITED WAY TO DROUGHT TOLERANCE IN SUNFLOWER

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ABSTRACT

As longer and increasing drought periods even challenge sunflower, a moderately drought tolerant crop, research on drought tolerance becomes increasingly important. The root is a major player in drought tolerance as it channels the water uptake to handle increased evaporation under water limiting conditions. In vitro or hydroponic experiments inducing osmotic stress by applying polyethylene glycol are ideal for fast screening for drought tolerance at a seedlings stage. Comparing a drought-tolerant sunflower genotype DF-AB-2 with a drought-sensitive genotype AB-OR-8 significant differences in root length, root volume and fresh weight were observed. As changes in the root architecture to adapt to drought stress conditions require modifications in the cell wall composition, different markers for cellulose, hemicellulose and pectin were analysed. Significant differences in pectin abundance were observed that were accompanied by significant differences in the expression of enzymes for pectin modification and degradation. Quantitative RT-PCR analyses were performed for selected genes to verify the RNAseq data as well as to develop PCR markers for screening. These drought responsive genes in roots offer new starting points for breeding for drought tolerance in sunflower.

Keywords: root architecture, drought tolerance, polyethylene glycol, cell wall

Acknowledgements: This work is supported by Twinning Western Balkans project CROPINNO, grant number 101059784 funded by the European Commission. We like to thank Monja Sundt at the University of Rostock for the excellent technical support. DM and AR were also supported by by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, grant number 451-03-136/2025-03/ 200032, and bythe Center of Excellence for Innovations in Breeding of Climate-Resilient Crops - Climate Crops, Institute of Field and Vegetable Crops, Novi Sad, Serbia

PAVING THE PATH TO SUNFLOWER DROUGHT RESILIENCE: MARKER ASSISTED BACKCROSSING USING KASP TECHNOLOGY

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ABSTRACT

The development of sunflower genotypes with improved resistance to drought is of profound importance to current breeding programs, especially under the light of climate change. The Marker Assisted Back-crossing (MABC) significantly accelerates the introgression of one or a few desirable genes from a donor parent into elite lines (recurrent parent), compared to traditional breeding, especially for quantitative traits. The aim of the study is to implement MABC in the sunflower breeding program at the Institute of Field and Vegetable Crops (IFVCNS) in Serbia in order to improve drought tolerance of two selected recipient IFVCNS sunflower lines. Three sunflower lines developed by INRAE (National Research Institute for Agriculture, Food and the Environment, France) were used as donor lines for 3 identified QTLs (HAMYB111, CWINV2 and DYP12_QTL-Drought-LG12) related to different mechanisms of tolerance to water scarcity, including improved attraction to pollinators in drought conditions. The set of KASP (SNP) markers was developed for these QTLs and tested in the backcross generations to identify the presence of associated traits. For each of the analysed QTLs, KASP marker that showed polymorphism between parental lines was detected and can be further used in MABC. This study gives emphasis to the potential of modern biotechnological approaches in developing climate smart sunflower hybrids through discovery (or identification) of traits related to drought resilience and their efficient introgression into breeding lines using molecular markers specifically by successfully developing polymorphic KASPs.

Keywords: Helianthus annuus, CWINV2, HAMYB111, DYP12_QTL-Drought-LG12, drought tolerance, pollinator attractiveness

Acknowledgements: This work was supported by the Horizon Europe project HelEx, grant number 101081974. KI; SG; DT, SJ, AR and DM were also supported by Ministry of Science, Technological Development and Innovation of the Republic of Serbia, grant number 451-03-136/2025-03/ 200032 and Centre of Excellence for Innovations in Breeding of Climate-Resilient Crops - Climate Crops, Institute of Field and Vegetable Crops, Novi Sad, Serbia.

THE YABBY GENE NETWORK IN SUNFLOWER: EVOLUTIONARY DYNAMICS AND DROUGHT-RESPONSIVE EXPRESSION PROFILING

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ABSTRACT

The YABBY gene family, known for its plant-specific transcription factors, plays pivotal roles in regulating leaf polarity, floral organ development, and responses to environmental stimuli. Despite its functional importance in various plant species, a comprehensive understanding of this gene family in sunflower (Helianthus annuus L.) has remained elusive. In this study, we conducted a genome-wide in silico identification and characterization of YABBY genes in H. annuus, revealing 14 HaYABBY members distributed across 10 chromosomes. Phylogenetic analysis clustered these genes into five conserved subfamilies (FIL/YAB3, YAB2, YAB5, INO, and CRC), while gene structure and motif analyses highlighted both conserved domain architecture and subfamily-specific divergence. Promoter analysis revealed the presence of multiple stress- and hormone-responsive cis-elements, and miRNA target prediction identified HaYABBY05 and HaYABBY09 as potential post-transcriptional targets of four distinct miRNAs. Synteny and duplication analyses suggested that segmental duplication events under purifying selection contributed to the expansion and conservation of HaYABBY genes. Tissue-specific expression profiling via RNA-seq demonstrated diverse expression patterns, with HaYABBY05 exhibiting broad expression and HaYABBY12 showing strong floral organ specificity. Under drought stress, RNA-seq and RT-qPCR analyses revealed significant cultivar- and tissue-specific expression differences between the drought-tolerant (SUN 2235) and drought-sensitive (Turay) sunflower cultivars. Notably, HaYABBY genes showed strong induction in the roots of SUN 2235 but were suppressed in Turay, implicating a potential role in drought adaptation. Together, these findings provide the first comprehensive insight into the structure, evolution, and stress-responsive expression of YABBY genes in sunflower. This study offers valuable candidate genes and regulatory clues for improving drought resilience in sunflower breeding and sets a foundation for further functional exploration of YABBY transcription factors in crops.

Keywords: YABBY gene family; Helianthus annuus; Genome-wide analysis; Drought stress; Gene duplication; miRNA regulation; Expression profiling

ORGANISATION OF THE FERTILITY RESTORER LOCUS RF1 IN SUNFLOWER

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ABSTRACT

Sunflower hybrid breeding founded on the PET1 cytoplasm requires fertility restoration by the dominant restorer gene Rf1 for efficient seed production. Association studies identified three candidate genes for Rf1 on linkage group 13, which are members of the PPR gene family, but little is known about their individual functions. In phylogenetic studies, two of these genes HanXRQr2_Chr13g0609921 (PPR841) and HanXRQr2_Chr13g0609901 (PPR861) formed a group with the restorer gene from Petunia. However, the third gene HanXRQr2_Chr13g0608631 (PPR621) arranges with the restorer-of-fertility gene Rfm1 in Hordeum vulgare. Both genes represent RNA editing factors characterized by the E-domain (HxExnCxxC) and DYW domain at the C-terminal end of the encoded proteins. RNA-editing of the PET1-specific CMS protein ORFH522 may play a role for the pollen fertility. The annotation of the three genes based on the HanXRQ genome assembly, which is a maintainer line, was verified on cDNA level for HA342, RHA325 and Jerusalem Dwarf Yellow. In addition, genome editing constructs have been designed to knock out these genes in sunflower. Based on SNPs specific for the three potential fertility restorer genes, four KASP markers were developed. Applying these KASP markers in an association panel of 577 sunflower accessions, lines with fertility restoration abilities for the PET1 cytoplasm but without the Rf1 were identified. These restorer lines must carry other restorer gene(s), which might be useful in hybrid production to avoid linkage drag based frequently on the use of Rf1. **Funding:** Sunflower accessions were analysed within the project OptiArch by Bundesministerium für Ernährung und Landwirtschaft (BMEL) and Gemeinschaft zur Förderung von Pflanzeninnovation (GFPi) under the guidance of the Fachagentur für Nachwachsende Rohstoffe (Agency for Renewable Resources) (Grant no. 22025215). Personal exchange was funded by the DAAD as a German-Serbian bilateral cooperation project (No. 451-03-01732/2017-09/3 and project code 57393592). AR and DM were also supported by Center of Excellence for Innovations in Breeding of Climate-Resilient Crops - Climate Crops, Institute of Field and Vegetable Crops, Serbia.

Keywords: fertility restoration; PET1 cytoplasm; PPR gene family; Rf1; sunflower, hybrid breeding; KASP marker; RNA editing, genome editing

GENE CLONING IN SUNFLOWER: CURRENT ADVANCES AND FUTURE DIRECTIONS

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ABSTRACT

Gene cloning and functional characterization have become essential tools for advancing molecular breeding and understanding complex traits in sunflower (*Helianthus annuus* L.). Before the advent of large-scale genomic resources, early candidate gene studies focused on key enzymes from well-characterized biosynthetic pathways, such as those involved in fatty acid and tocopherol metabolism, leading to the isolation of genes such as *FAD2* and members of the tocopherol biosynthetic pathway. These pioneering efforts provided the first molecular insights into qualitative traits associated with oil composition and nutritional quality. Over the past decade, the availability of a high-quality reference genome and extensive transcriptomic datasets has greatly expanded the identification of candidate genes associated with oil biosynthesis, abiotic stress tolerance, and disease resistance. However, the functional validation of these genes remains challenging due to the recalcitrance of sunflower to stable transformation and the limited efficiency of transient expression systems. Recent advances in heterologous systems, virus-induced gene silencing (VIGS), and CRISPR/Cas-based genome editing are beginning to overcome these constraints, offering new opportunities to dissect gene function and accelerate trait improvement. Past and current progress in sunflower gene discovery and cloning is discussed. Despite significant progress, the integration of multi-omics data with efficient transformation pipelines remains a key priority to fully exploit sunflower's genetic potential for sustainable crop improvement.

Keywords: Sunflower, Gene cloning, gene silencing (VIGS), CRISPR/Cas, genome editing

ANTHOCYANIN PIGMENTATION AS A MARKER IN SUNFLOWER BREEDING AND SEED PRODUCTION

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ABSTRACT

Preliminary analysis of possibility to use anthocyanin pigmentation as a marker trait in sunflower breeding and seed production was conducted; efficiency and reliability of the marker utilization was shown. The color of sunflower hypocotyls allowed us to differentiate our samples from any impurities. By the appearance of the first true leaves, the hybrids and lines also were easily identified by veins colored with anthocyanin. The ease and reliability of identifying hybrids by the color of the hypocotyl at the seedling stage and further stages of development is shown, which makes this trait attractive for use in sunflower breeding and seed production. Reliable donors of the trait are identified and included in the breeding program

Keywords: Sunflower, Breeding, Seed Production, Marker

ASSOCIATION MAPPING OF SEED MORPHOLOGY TRAITS IN SUNFLOWER

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ABSTRACT

Seed-related traits—specifically seed size (kernel size), husk size (hull size), and seed-to-husk ratio—are critical phenotypes in sunflower breeding and industry. These traits are particularly valuable for developing large-seeded confectionary sunflowers (Lukomets et al., 2021). A common technique for estimating seed size is measuring thousand-seed weight, widely applied in oilseed crops (Khan et al., 2019; Souza et al., 2016), including sunflower (Radic et al., 2013), as husk dimensions strongly correlate with this metric (Gjorgjieva et al., 2015). However, this approach cannot assess the seed-to-husk area ratio—a key parameter for evaluating efficient photoassimilate utilization in yield optimization. X-ray radiography with image analysis offers a non-invasive alternative for quantifying seed size, husk size, and their ratio (Arkhipov et al., 2019). Historically, X-ray methods primarily evaluated seed morphology (Rocha et al., 2014), quality (e.g., viability, emptiness, pathogen damage; Dumont et al., 2015), and germination potential (Al-Turki & Baskin, 2017). In this work, we performed genetic mapping of seed traits using X-ray data provided by collaborators from St. Petersburg Electrotechnical University "LETI". Analyzed traits included husk area, seed area, and seed-to-husk ratio across a genetically and phenotypically diverse collection of 601 sunflower accessions from VIR, VNIIMK, and Agroplasma. Genetic diversity analysis for these 601 lines was published in BMC Genomics (Chernova et al., 2021)

Keywords: seed morphology, genetics, association mapping

ADVANCING SUNFLOWER RESILIENCE TO CLIMATE CHANGE THROUGH INNOVATIVE BREEDING STRATEGIES

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ABSTRACT

Maintaining sunflower productivity under changing climates requires breeding programs to enhance tolerance to multiple abiotic stresses, such as a deeper understanding of genetic diversity, physiological responses, and the molecular mechanisms underlying stress resilience. The integration of advanced technologies, including genomics, transcriptomics, phenomics, and epigenomics, facilitates the identification of adaptive traits and accelerates the development of climate-resilient genotypes. High-throughput, non-invasive phenotyping platforms, particularly those targeting root architecture, stress physiology, and growth dynamics, provide valuable insights into sunflower responses under variable and extreme conditions. The Center of Excellence for Innovations in Breeding of Climate-Resilient Crops – Climate Crops is actively addressing these challenges by combining genetic resources, cutting-edge technologies, and targeted selection strategies. Through this integrated approach, the Center aims to develop sunflower cultivars capable of sustaining yield and quality despite intensifying climate pressures, thereby contributing to the resilience and sustainability of global agricultural systems.

Keywords: Sunflower, Drought, Omics-, Yield, Root traits.

Acknowledgements: This work is supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, grant number 451-03-136/2025-03/ 200032, by Center of Excellence for Innovations in Breeding of Climate-Resilient Crops - Climate Crops, by BREEDTECH -Building Capacity in Plant Breeding and Biotechnology Education and Research through partnership program in Africa, Middle East and Europe for Agricultural transformation, Funded by Erasmus+ Programme, Capacity Building in the field of Higher Education Grant number: 101128862, by bilateral cooperation project between the Republic of Serbia and Turkey 2024-2026, grant number 0260207, financed by The Ministry of Science, Technological Development and Innovations of the Republic of Serbia (NITRA) and The Scientific and Technological Research Council of Turkey (Tübitak), and based upon work from COST Action RECROP (CA22157).

BROOMRAPE (OROBANCHE CUMANA) RESISTANCE GENES IN WILD SUNFLOWER SPECIES

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ABSTRACT

Sunflower broomrape (*Orobanche cumana* Wallr.) is a holoparasitic plant that lacks chlorophyll and depends entirely on a host plant to complete its life cycle. Unlike related species, it shows high host specificity both in nature and under cultivation, parasitizing only sunflower in the latter case. This parasitic weed is currently the major threat to sunflower production in most areas of Asia and Europe, including Spain, due to the continuous emergence of increasingly virulent races. At present, the most effective and sustainable strategy for broomrape control is the development of sunflower genotypes resistant to this parasite. Our research group has developed novel sources of broomrape resistance derived from genes identified in wild sunflower species, such as the OrDeb2 gene, already widely used in commercial hybrids, and more recently the OrAnom1 gene, identified in the wild sunflower species Helianthus anomalus. This new source of resistance is also being transferred to major sunflower breeding companies for the development of commercial hybrids with genetic resistance to broomrape. We are currently working on additional resistance sources derived from wild sunflower species, which will help strengthen the genetic defence arsenal of sunflower against this harmful parasitic weed, offering a sustainable alternative to the massive use of herbicides.

Keywords: Broomrape; Genetic resistance; Resistance genes; Sunflower; Wild species

DEVELOPMENT OF HERBICIDE RESISTANT ORNAMENTAL SUNFLOWER LINES

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ABSTRACT

Besides its industrial use, Sunflower (*Helianthus annuus* L.) is also important as cut flower, potted and landscape design plant. Currently, the commercial hybrid ornamental sunflowers are either fertile or male sterile for which demand is on the rise. The objectives of the breeding program were to develop cytoplasmic male sterile lines - CMS (A) and maintainer (B) lines to use as parental lines for male sterile hybrids. The imidazolinone (IMI) or Sulfunilurea (SU) herbicide resistance were transferred from oil-type restorer line by backcrossing and selecting individual plants. Plant materials also included a public maintainer line (Peredovik), 16 sterile and 15 fertile commercial ornamental sunflower hybrids. During consecutive backcrossing to develop ornamental-type maintainer lines, the presence or absence of restorer of fertility (Rf) alleles were identified using Rf-specific molecular markers. Herbicide resistant plants were selected by spraying related herbicide on the segregating populations. Male sterile hybrids representing different flower colors and plant types with IMI/SU herbicide resistance were developed. Vase life and plant characteristics of SU resistant advanced A / B lines showed that commercially competitive ornamental hybrids can be developed using these lines. The A and B lines representing different plant types, flower colors, and genetic resistance can be used to create potential hybrids. Herbicide resistant hybrids may offer a quick and cheaper weed control especially for open field cut-sunflower production.

Keywords: CMS, IMI, SU, ALS, herbicide resistance, Hybrid seeds, Ornamental plant

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