



# **PROCEEDINGS OF INTERNATIONAL CONGRESS ON OIL AND PROTEIN CROPS**

**2-4 NOVEMBER, 2023**

**ANTALYA, TURKEY**

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INTERNATIONAL  
CONGRESS ON OIL AND  
PROTEIN CROPS**

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**Organized by  
Trakya University  
European Association for Research on Plant  
Breeding (EUCARPIA)  
International Researchers Association**

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## WELCOME NOTES

International Congress Oil and Protein Crops Section Conference of EUCARPIA which is organized by Trakya University and the International Researchers Association in cooperation with the European Association for Research on Plant Breeding (EUCARPIA). The congress is held in Megasaray Westbeach Hotel, Antalya, Turkey, on November 2-4, 2023 with supporting of several national and international partners.

The Congress topics covers Oil and Protein Crops: Plant Breeding and Genetics, Molecular Genetics and Biotechnology, Biology and Physiology, Genetic Resources, Plant Protection, Agronomy, Economy, Animal feeding, Food Science and Nutrients, Fats, lipids, and Protein studies.

Oil crops are rich sources of oils, proteins, minerals, vitamins, and dietary fibers for both human and animal feeding and provide the raw material for the production of biodiesel. Oil crops are soybean, cottonseed, sunflower, canola, rapeseed, peanut, safflower, flax, sesame, coconut, castor, copra, etc.

Almost 50% of the global food protein supply comes from cereal seeds. Soybean, peanut, common bean, pea, lupine, chickpea, faba bean, lentil, grass pea, cowpea, pigeon pea, etc. are currently the most important legumes for human consumption and animal feed. Because of the protein content of their seeds; grain legumes, cereals, and other minor crops such as amaranth, quinoa, hemp, caraway, etc. are protein crops growing for plant protein for food and feed.

The Congress 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. The Congress languages is in English. Researchers, breeders and others with an interest in the genetics and breeding of oil and protein crops are invited to participate. Among the topics to be discussed are directions of breeding for resistance to abiotic and biotic stresses, improved industrial use, and conventional versus organic production.

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 breeders, seed enterprises, researchers and scientists, in a friendly environment of Antalya, Turkey to share their knowledge and experience and benefit from each other.

There are 38 orals and 63 poster presentation in the congress both joining and presenting normal and online with 141 participants from 20 different countries from the world.

The congress gathered scientists from around the world, and present their recent achievements. The organizers will also invite relevant stakeholders to provide a view on the current situation around the world as well as prospects to overcome the limitation for sustainable crop production to feed the world.

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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## GENETIC STRUCTURE AND VARIABILITY PARAMETERS OF LATHYRUS SATIVUS L. EUROPEAN COLLECTION

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### ABSTRACT

Grass pea (*Lathyrus sativus* L.) is a self-pollinating legume that is well adapted to changing climatic conditions. In our study, the collection of 25 accessions from different parts of Europe (7 from BiH, 2 from Romania, 4 from Portugal, 8 from Serbia, 2 from Bulgaria, 1 from Greece and 1 from Slovenia) was genetically assessed by 15 species-specific nSSR markers (Simple Sequence Repeat). Extraction of gDNA was performed from 3 to 10 individual young plants/genotypes of each accession using an automated magnetic procedure. PCR reaction mixtures and amplification were optimized for each primer pair under two-step touch-down PCR conditions. Fragment analysis was performed on a genetic analyzer (ABI 3130XL) together with the internal standard ROX500. Accurate allele lengths were recorded from the electropherograms in GeneMapper6.0 software. The diversity parameters and genetic structure of the *Lathyrus* collection was observed using various population genetic programmes such as Arleqin, MSToolkit, GenAlEx, Populations, TreeView, and Structure. The selected set of SSR markers (*G* loci) was highly informative with an average polymorphic information content of 0.76. The high level of overall genetic diversity among 15 loci was calculated within the collection ( $H_e=0.79$ ), while deviations from Hardy-Weinberg equilibrium were statistically significant ( $p < 0.01$ ) at loci G18200 and G17922 for all studied accessions. The Bayesian approach divided the collection into three genetically distinct groups with high average genetic distances ( $H_e=0.751$ ;  $F_{st}=0.092$ ). Considering Shannon information index ( $I=1.55$ ) and average number of private alleles (1.33), accession KL2 from Serbia was genetically most diverse. The strongest genetic relatedness was found between accessions from BiH (GB01001, GB00954 and GB01002). Analysis of molecular variability revealed 12% of variability between accessions, 49% between genotypes within accessions and 39% of total variability between genotypes. The obtained results will give us an insight into promising *Lathyrus* germplasm and enable its use for breeding purposes.

**Key words:** grass pea, genotyping, SSR markers, genetic background, breeding