

Cross-cutting topics

Flash presentations on Monday 29. August, 17.45 – 18.30

Poster session on Monday 29. August, 18.30-19.15

1. Better breeding decision using high throughput de novo assembly and advanced genomic big data analytics

Kobi Baruch

2. Localization of metabolites in plant tissues using high-resolution mass spectrometry imaging

Dhaka Ram Bhandari

3. A new lab guide on genotyping-by-sequencing for plant genetic diversity analysis

Yong-Bi Fu

4. Applying segregation distortion approach in QTL analysis of three non-BSSS doubled haploid populations in maize

Maja Mazur

5. BRIDGE: Biodiversity informatics for harnessing barley genetic diversity hosted at the genebank of IPK Gatersleben

Sara Giulia Milner

6. Development and characterization of a new wheat-rye Robertsonian translocation with resistance to stem rust

Mahbubjon Rahmatov

7. How next-generation sequencing can improve and speed up breeding of new crop varieties

Florian Schröper

8. Improvement of plant growth and stress tolerance using cyanobacterial flavodiiron proteins (FDPs)

Fahimeh Shahinnia

9. RABBIT: reconstructing ancestry blocks bit by bit in experimental populations

Chaozhi Zheng

10. Genetic gains in bi-parental population improved through marker assisted recurrent selection under drought stress

Rekiya Abdulmalik

11. Organic vegetable breeding at Sativa Rheinau

Charlotte Aichholz

12. A R-based integrated pipeline for genomic and application to a wheat breeding programme

Gilles Charmet

13. Optimized and cost-efficient genotyping arrays for plant breeding

Martin Ganal

14. mppR: an R-package for QTL mapping in multi-parent populations

Vincent Garin

15. Multiparameter quantification and metabolomics in plant science and breeding: NMR based test systems

Roland Geyer

16. Application of biotechnology methods in plant breeding in Latvia

Dace Grauda

17. Expression of a variety of recombinant proteins in plants

Mokhtar Jalali-Javaran

18. Single cell genomic sequencing in *Brassica napus* and wheat: Applications in monitoring recombination frequency

Sateesh Kagale

19. Refined scaffold construction using PacBio sequences and LMP libraries of Korean pear (*Pyrus pyrifolia*)

Jung Sun Kim

20. Innovative approaches to optimize genetic diversity for sustainable farming systems of the future (INSUSFAR) – project presentation

Samuel Knapp

21. Plant variety – “frozen” or plastic

Liga Lapse

22. Looking for *TaCKX* genes associated with grain yield

Agnieszka Onyśk

23. Germplasm exchange and use in Italian national research institutions

Maria Antonietta Palombi

24. High-throughput screening tools for identification of traits contributing to salinity tolerance in *Arabidopsis thaliana*

Klára Panzarová

25. Information system GRIN Czech of plant genetic resources in the Czech Republic

Ludmila Papouskova

26. Major quantitative trait loci and putative candidate genes for powdery mildew resistance and fruit-related traits revealed by an intraspecific genetic map for watermelon (*Citrullus lanatus* var. *lanatus*)

Young Hoon Park

27. Hyperspectral image processing using visual programming

Stefan Paulus

28. Harmonization of resistance tests to diseases for DUS testing – Harmores 2

Sophie Perrot

29. Metabolic profiles and viral charge genome wide mapping in *Arabidopsis thaliana* in response to TuMV (*Turnip mosaic virus*) in a natural environment

Bernadette Rubio

30. A comprehensive research in genetic structure of drought tolerance in Iranian RIL population

Hossein Sabouri

31. Phytochemical study of some native ajowan ecotypes from Iran

Seyed Ahmad Sadat Noori

32. A DNA repository platform for germplasm collections

Eva Sehr

33. Increasing the seed yield through better-quality pollination bags

Hannah Senior

34. National Plant Genetic Resources in the Vilnius University Botanical Garden

Gitana Stukeniene

35. Longevity of elite cultivars is a matter of conservation rather than maintenance breeding

Ioannis Tokatlidis

36. The gene machine: exploiting TILLING populations in a forward-genetics fashion

Roberto Tuberosa

37. Association of grain yield, drought tolerance indices and proline accumulation in selection for drought stress tolerance in soybean

Rouxlene Van der Merwe

38. Impedance flow cytometry - an ingenious method for pollen viability determination

Ruthger van Zwieten

39. Comparing the light transmissibility of pollination bag materials

Daljit S. Virk

40. High throughput phenotyping of winter wheat canopy cover and plant height development in response to temperature

Kang Yu

Crop-specific topics

Flash presentations on Tuesday 30. August, 16.00 – 16.45

Poster session on Tuesday 30. August, 16.45 – 17.45

41. Nicotianamine synthase genes as a valuable genetic resource for improving bread wheat growth and nutrition

Julien Bonneau

42. The manifestation and phytohormone response of leaf pubescence genes in bread wheat

Alexey Doroshkov

43. *Lr22a* gene is effective and does not alter other disease resistances, yield or bread making quality

Dario Fossati

44. A large-scale association mapping analysis of wheat resistance to multiple fungal pathogens across three years in multiple locations in NW Europe

Keith Gardner

45. Resistance to *Fusarium* head blight of winter wheat lines derived from crosses between winter type cultivars and resistant spring wheat ‘Sumai 3’

Tomasz Góral

46. Winter wheat and climate change adaptability – finding functional markers in elite wheat germplasm

Suncica Guberac

47. A snapshot on wheat breeding for the Canadian Prairies

Santosh Kumar

48. Variations in the D-genome chromosomes of hexaploid/tetraploid wheat crosses analysed utilising cytology and molecular markers

Sriram Padmanaban

49. Influence of individual bread wheat chromosomes on double haploids (DHs) production

Myroslava Rubtsova

50. Investigation of drought tolerance in bread wheat mapping population of Plainsman V x Mv Magma in field experiments

Krisztina Balla

51. Infection severity and mycotoxin production of *Fusarium culmorum* in wheat grown at elevated CO₂ level

Szilvia Bencze

52. Detection of mutations in carotenoid genes in a durum wheat tilling population by DHPLC technology

Antonio Blanco

53. Selecting for high anthocyanins and high carotenoids to enhance the antioxidant activity of durum wheat

Antonio Blanco

54. Detection of leaf rust resistance genes *Lr24*, *Lr25*, *Lr28*, *Lr34* and *Lr35* in winter wheat cultivars

Pawel Czembor

55. Contribution of stem reserves to grain weight in wheat under terminal drought

Dejan Dodig

56. Agronomic performance of two generations (F_{12} and F_{13}) of thirteen winter wheat composite cross wheat populations with differing cultivation histories in 2014/15

Maria Finckh

57. Yield stability analysis for three winter wheat composite cross populations under organic and conventional management over five years

Maria Finckh

58. A century of Swiss wheat breeding decreased rooting depth under well watered conditions but maintained deep rooting in drying soil

Cordula Friedli

59. The effect of dwarfing genes on coleoptile length of bread wheat under conditions of osmotic stress

Anastasiia Honcharova

60. Rethinking on wheat seed system in Pakistan: fast tracking delivery of new genetic gains to farmers

Krishna Joshi

61. Microsatellite loci associated with heading time in Ukrainian bread wheat varieties

Olga Kolesnyk

62. Effect of *Ppd* alleles on yield performance in wheat

Ankica Kondic-Spika

63. The influence of medium composition on embryogenic callus induction and plant regeneration from mature embryos of wheat cultivars with various resistance to *Parastagonospora nodorum*

Lidia Kowalska

64. Identification of eyespot resistance genes in breeding lines of hexaploid wheat (*Triticum aestivum* L.)

Michał Kwiatek

- 65. Genetic variation of Asian wheat revealed by HMW glutenin and maturity**
Sukyeung Lee
- 66. Integration of wild genetic resources with high-throughput genotyping to breed for drought tolerance in durum wheat**
Stuart Lucas
- 67. QTLs for partial resistance to *Zymoseptoria tritici* in the cultivated durum wheat germplasm investigated by means of a high-density SNP array**
Marco Maccaferri
- 68. *Pch2* eyespot resistance genes in the double haploid lines of winter wheat (*Triticum aestivum* L.)**
Maciej Majka
- 69. Finding new winter wheat ideotype for Southeast Pannonian region**
Sonja Maric
- 70. Early generation differences in concentration of trace elements in winter wheat grain**
Sonja Maric
- 71. Variability of oil and tocopherol content in wheat**
Ana Marjanović-Jeromela
- 72. Identification and validation of reference genes for analysis of wheat (*Triticum aestivum* L.) genes expression under drought stress**
Michał Nowak
- 73. 1BL/1RS translocation effects on efficiency of wheat DH lines production**
Piotr Ogrodowicz
- 74. Microsporogenesis and drought tolerance of wheat**
Waclaw Orczyk
- 75. Breeding for new climate - screening agro morphological traits of wheat genepool**
Sonja Petrovic
- 76. Reaction of European winter wheat cultivars to six isolates of *Puccinia triticina***
Magdalena Radecka-Janusik
- 77. Development of transcript-based markers tagging 1RS wheat-rye translocations**
Yong Weon Seo
- 78. Identification of allelic variation at powdery mildew resistance gene *Pm3* in a collection of tetraploid wheats**
Rosanna Simeone

79. Genome-wide association mapping for phenolic acids concentration and composition in a collection of tetraploid wheats

Rosanna Simeone

80. Development of bread wheat lines with super-soft endosperm texture - the carriers of two genes *Ha* and *Ha-Sp* for grain softness

Alexander Simonov

81. Molecular selection in three winter wheat populations for *Fhb1* resistance gene to fusarium head blight

Piotr Slowacki

82. Genetic structure of NS wheat core collection

Dragana Trkulja

83. Domains of products of *Rht* genes in bread wheat

Andrii Venger

84. Breeding for improved gluten strength in winter durum wheat

Gyula Vida

85. Selection of resistant to leaf rust genotypes on haploid and diploid level

Dorota Weigt

86. Early selection of winter wheat (*Triticum aestivum* L.) recombinants resistant to eyespot using enzymatic and molecular markers for *Pch1* gene in haploid and double haploid (DH) lines

Halina Wiśniewska

87. Landraces and obsolete cultivars of common oat – valuable and unused genetic resources

Maja Boczkowska

88. Dynamic management of winter barley genetic resources

Lorenz Bülow

89. WHEALBI: WHEAt and barley Legacy for Breeding Improvement : An EU project to link Genomics and Agronomy

Gilles Charmet

90. Variation in leaf traits in spring barley (*Hordeum vulgare* L.)

Anna Florence

91. Different cold sensitivities in rice unveiled by anther morphologies and genome-wide expressions

Yuji Kishima

92. Genomic prediction in a Finnish breeding programme of six-row barley

Timo Knürr

93. Analysis of the genetic and environmental factors influencing grain quality in oats

Maria Jose Martinez Martin

94. Genotypic and environmental impact on spring cereals yield and quality

Ievina Sturite

95. Genetics of malting barley ‘processability’

William Thomas

96. Analysis of molecular mechanism of resistance to *Fusarium* head blight in triticale at the proteome level

Adam Augustyniak

97. Identification of pollen fertility restoration markers in rye with CMS Pampa

Piotr Bednarek

98. Virulence of *Puccinia triticina* on triticale in Poland

Grzegorz Czajowski

99. Resistance to powdery mildew in winter barley in Poland

Jerzy Czembor

100. BSMV-VIGS as a post-transcriptional gene silencing strategy to dissect biological function of *ScBx1* in rye

Jolanta Groszyk

101. Genetic evaluation and saturation of linkage map in seedling stage of F8 rice RILs under Drought, Salinity and Cold stresses

Mahnaz Katouzi

102. Association analysis of roots and shoots traits in rice (*Oryza sativa* L.) using AFLP markers under field drought stress

Mahnaz Katouzi

103. Introgression of the *LTP2* gene through marker assisted backcross breeding in barley (*Hordeum vulgare* L.) with *LTP2* gene analysis expression

Anetta Kuczyńska

104. Wild barley (*Hordeum vulgare* ssp. *spontaneum*) as a potential source of drought tolerance genes for barley improvement

Mohammad Mahdi Majidi

105. Phenotyping *Fusarium* head blight resistance of oat by analysis of morphological and biochemical properties of grains

Charlotte Martin

106. Impact of *Fusarium* infections on β - glucans in barley grains

Charlotte Martin

107. Relationship between photoperiodic reaction and susceptibility to Fusarium head blight in spring barley
Krzysztof Mikołajczak

108. The influence of the genotype, developmental phase of the spike and developmental Stage of microspores on the induction of androgenesis in anther cultures of rye (*Secale cereale* L.)
Sylwia Mikołajczyk

109. Novel dwarfing gene in triticale – influence on the straw length and key gibberellin biosynthesis pathway genes expression
Michał Nowak

110. *Avena sterilis* L. genotypes as a potential source of resistance to oat crown rust
Tomasz Ociepa

111. Variability analysis some elements of production to 13 genotypes spring barley two rows in non – competitive system the culture
Ioana Porumb

112. Next generation evolutionary breeding for sustainable agriculture: experiences with barley
Lorenzo Raggi

113. Role of *HvCKX5* and *HvCKX4b* genes in growth and reproductive development of barley
Izabela Rajchel

114. Genetic structure and identification of genetic regions associated with root traits in rice under drought stress using AFLP markers and hydroponic culture
Hossein Sabouri

115. The image-based phenotyping to analyze the genes involved in salt stress tolerance of rice
Hyejin Yoon

116. Metabolite profiling of diverse rice germplasm and identification of conserved metabolic markers of rice roots in response to long term mild salinity stress
In Sun Yoon

117. Separation of endophytic and epiphytic phyllosphere bacterial communities of *Lolium* spp.
Martina Birrer

118. Freezing tolerance of diploid versus tetraploid in perennial ryegrass
Gintaras Brazauskas

119. Breeding maize for resistance to fusarium ear rot: impact of plant morphology for disease development and deoxynivalenol formation
Elzbieta Czembor

121. Automated field phenotyping of early vigour and senescence progress in soybean and maize

Frank Liebisch

122. Sequencing and comparative analysis of mitochondrial genomes of fertile and male-sterile lines in perennial ryegrass (*Lolium perenne* L.)

Istvan Nagy

123. Root system performance under water deficit conditions in *Lolium multiflorum*/*Festuca arundinacea* introgression forms

Dawid Perlikowski

124. Advantages of using haploid technologies in maize breeding

Valeriu Rotarencu

125. Improvement of drought tolerance of forage perennial ryegrass by breeding of root characteristics and deep root production

Dejan Sokolović

126. Genetic mapping of root traits in *Lolium perenne*

Debbie Allen

127. Identification of forage grasses germplasm for water-limited environments and different soil type

Elzbieta Czembor

128. Molecular indicators of resistance to *Microdochium nivale* in *Lolium multiflorum*/*Festuca arundinacea* introgression forms

Katarzyna Masajada

129. Using genome wide allele frequency fingerprints to identify allele frequency changes in seeded perennial ryegrass swards

Aude Perdereau

131. Investigating the genetics of self-fertility in an F2 population of *Lolium perenne* L.

Lucy Slatter

132. Assessment of performance of early-maturing white maize hybrids and testing sites using GGE biplot analysis

Rekiya Abdulmalik

135. Maize landraces as a source for increased content of tocopherol and β -carotene in inbred lines

Violeta Andjelkovic

136. Morphological and molecular identity testing of maize accessions collecting in the same area at different time scale

Violeta Andjelkovic

137. UPOV morphological versus molecular markers for maize inbred lines variability determination

Vojka Babic

138. Characterisation and further evaluation of local maize landraces within prebreeding activities

Vojka Babic

139. Characterisation of maize inbred lines of unknown pedigrees or heterotic groups for pre-breeding

Ankica Kondic-Spika

140. Development of dual use maize cultivars for grain and biogas production

Luisa Pfalsdorf

141. Agronomic characteristics and chemical composition of ZP sweet corn hybrids

Jelena Srdić

142. Variation in water use efficiency among maize inbred lines with different drought tolerance

Jelena Srdić

143. Molecular characterisation of *Fusarium graminearum* chemotypes originated from Serbia

Slavica Stankovic

144. Improving biodiversity in energy crop production by mixed cropping of maize and climbing beans

Mathias Starke

145. Assessment of the degree of relatedness of some inbred lines adapted to the early maize growing regions, created at ARDS Turda

Andrei Varga

146. A fifteen-year tendency of productivity and grain moisture of Bulgarian maize hybrids by FAO groups

Stefan Vulchinkov

147. A breeding value assessment of Bulgarian maize local varieties

Stefan Vulchinkov

148. MicroRNA analysis of flax (*Linum usitatissimum* L.) genotypes in regard to alpha-linolenic acid content

Lucia Hlavačková

149. Antisense oligodeoxynucleotide treatment as a new method of gene expression manipulation in flax (*Linum usitatissimum*)

Anna Kostyn

150. Dissection of year related climatic variables and their effect on winter oilseed rape (*Brassica napus* L.) development and yield

Ana Marjanović-Jeromela

151. Marker assisted breeding of new winter oilseed rape lines (*Brassica napus* L.) with changed seed oil fatty acid composition

Katarzyna Mikolajczyk

152. Global inventory and evaluation of wild perennial cereal, pulse and oilseed species for pre-breeding and domestication

Allison Miller

153. Identification of cinnamyl alcohol dehydrogenase isoforms in flax and preliminary assessment of their specificity in response to the biotic and abiotic stresses

Marta Preisner

156. Flowering time diversity for U.S. groundnut mini-core collection produced under Mediterranean climate type

Engin Yol

157. Evaluation of selected cowpea lines for agronomic performance and use in breeding program in South Africa

Joseph Asiwe

158. Screening of soybean germplasm for *Rsv4*, a gene conferring soybean mosaic virus resistance, using SSR markers

Yu Mi Choi

159. Legumes germplasm collection at the MBG-CSIC, Spain

Antonio De Ron

160. Classification on maturity group and maturity locus by genotyping of Korean soybean cultivars

Kil-Hyun Kim

161. Genome-wide association study for common bean phenolic compounds in Portuguese germplasm

Susana Leitao

162. Evaluation of genetic diversity of broad beans genetic resources in the Baltic Region

Liga Lapse

163. Propagation of honeybush (*Cyclopia subternata*)

Gugu Mabizela

164. Featuring diversity of Portuguese common beans (*Phaseolus vulgaris* L.) through the study of phenolic composition

Elsa Mecha

- 165. Beans with Benefits: Integrating improved mungbean as a catch crop into the dryland systems of South and Central Asia**
Svein O. Solberg
- 166. Genetic, proteomic and physiological background for common bean breeding to abiotic stress**
Jelka Šuštar Vozlič
- 168. Landrace common bean (*Phaseolus vulgaris* L.) genotypes collected from western Mediterranean region of Turkey**
Kamile Ulukapi
- 169. Selection of white lupine genotypes for yield and tolerance to alkaline soils**
Dimitrios Vlachostergios
- 170. Variability of sterols content in oil of white mustard (*Sinapis alba* L.)**
Iwona Bartkowiak-Broda
- 171. Response of glucosinolate (GSL) accumulation to sulphur in low and high GSL lines of *Brassica juncea***
Priyakshee Borpatra Gohain
- 172. The variation of bioactive compounds in black and yellow seeds of winter oilseed rape (*Brassica napus* L.)**
Teresa Cegielska-Taras
- 173. Phenotypic variability of resynthesized oilseed rape (*Brassica napus* L.)**
Teresa Cegielska-Taras
- 174. Characterizing genes isolated from tetralocular ovary of *Brassica rapa* by RNA-seq**
Jung Sun Kim
- 175. Identification and characterization of *NF-YA7* gene in potato**
Doolyi Kim
- 176. *Fusarium oxysporum* infection in flax results in salicylic acid level increase associated with phenylpropanoid pathway activation**
Kamil Kostyn
- 177. Assesment of genetic diversity among oilseed rape (*Brassica napus* L.) cultivars using single locus microsatellite markers**
Katarzyna Mikolajczyk
- 178. New canola (*Brassica napus* L.) mutant lines with similar phenotypes and different fatty acid composition**
Anna Shirokova
- 179. Molecular cytogenetic analysis of three generations of resynthesized rapeseed (*Brassica napus* L.)**
Anna Shirokova

180. Evaluation of resistance to ZYMV among selected orange cultivars *Cucurbita maxima*

Jiri Svoboda

181. Efficient production of doubled haploid plants of oilseed rape by in vitro and in vivo colchicine treatment

Laurencja Szała

183. Crossbreeding of transgenic flax plants producing polyhydroxybutyrate and overexpressing β -1,3-glucanase gene results in the increase in the polyamine content

Wioleta Wojtasik

184. Comparative transcriptomics of *Rosa corymbifera* 'Laxa' roots with regard to replant disease

Carina Hieger

185. Preserving the Swiss pear diversity

Christina Kägi

186. Towards *Silybum marianum*'s domestication: establishment and screening of a mutagenized population

Tommaso Martinelli

187. Towards the development of a sterile chamomile variety (*Matricaria recutita* L.) using breeding, molecular and genomic tools

Lars-Gernot Otto

188. Sensory, chemical and molecular analysis of fresh strawberries (*Fragaria* \times *ananassa* Duch.) over different cultivars in Western Greece, reveals factors affecting eating quality

Vassilis Papisotiropoulos

189. Pyramiding of four QTLs for fire blight resistance in apple

Andrea Patocchi

190. Genotoxic effects of heavy metals on intergeneric *Helianthus* \times *Echinacea* hybrid lines

Galya Petrova

191. Comparing the efficacy of polyester tents and isolation chambers for hybridisation in *Miscanthus*

Daljit S. Virk

193. Comparison between grapevine leaf and inflorescence upon downy mildew infection, based on a new in vitro phenotyping method and on fruiting cutting production

Silvia Vezzulli

194. Cryopreservation of pear germplasm by encapsulation-dehydration

Jung Yoon Yi

195. Seed longevity in tobacco – studies on intraspecific diversity and genetic determination

Andreas Börner

196. Response mechanisms of hop (*Humulus lupulus* L.) plant under drought stress

Andreja Čerenak

197. Genetic resources of cultivated forms of beet (*Beta vulgaris* L.) as potential donors for breeding

Kamilla Kuzdowicz

198. Characterising cannabinoid composition in diverse *Cannabis* germplasm to accelerate the genetic metabolic engineering of chemotype-specific cultivars

Matthew Welling

199. Medicinal plant harbor a high presence of antagonistic rhizobacteria

Dilfuza Egamberdieva

200. Genetic diversity and analysis of antimicrobial properties of selected oregano clones for use in the aquaculture industry

Vassilis Papatziropoulos

201. Histochemical approaches to relation between pollen wall and fertility in natural diploid and triploid *Lilium lancifolium*

Gyung Ran Do

202. In vitro induction of tetraploid hairy roots in purple coneflower (*Echinacea purpurea* (L.) Moench)

Ahmad Moieni

203. Chrysanthemum genome project

So Youn Won

204. Chrysanthemum transcriptome analysis by 3rd generation sequencing

So Youn Won

205. Identification of candidate genes involved in plant defense response against some important potato viruses using microarray meta-analysis

Mohammad S. Sabet

206. Who is sowing our seeds? The role of the UK Vegetable Genebank in supporting plant breeding and research

Charlotte Allender

207. *Lactuca aculeata* and *L. georgica* are wild lettuce species, harboring unique genetic resources for crop improvement

Alex Beharav

208. Whole genome resequencing in *Cynara cardunculus*: detection of intra-specific variability and the identification/annotation of novel polymorphisms

Sergio Lanteri

209. Investigation for suitability of three new interspecific rootstocks for eggplant grafting aiming to breeding purposes

Athanasios Mavromatis

210. Development of a new screening method for resistance towards *Clavibacter michiganensis* subsp. *michiganensis* (Cmm) in tomato

Mas Muniroh Mohd Nadzir

211. Changes in carotenoid metabolism in response to biotic and abiotic stresses in various carrot genotypes

Florent Perrin

212. Identification of quantitative trait loci (QTL) linked to increased lateral root emergence and growth in an intra-specific *Lactuca sativa* cross for the improvement of lettuce transplants

Justin Roberts

213. Deciphering old diversity in the origins of pepper (*Capsicum* spp)

Cristina Silvar

214. Genetic inheritance resistance to yellow virus in melon (*Cucumis melo* L.)

Ridwani Sobir

215. Yield and sugar contents of melon lines and their hybrids influenced by field salinity stress

Mahmoud Akrami

216. The aimed tomato breeding for the special hydroponic technology

Irina Balashova

217. The whole genome microsatellite database of eggplant

Lorenzo Barchi

218. Elites – a possibility to evaluate tomatoes landraces

Gallia Butnaru

219. Assessing the genetic variation in cultivated tomatoes (*Solanum lycopersicum* L.) using genome-wide single nucleotide polymorphisms

Youngwhan Choi

220. Development of molecular markers for sex expression in oriental melon (*Cucumis melo* L.)

Sang Min Chung

221. Study of adaption and yield ability ecotypes of fennel in Bojnourd-Iran

Vahid Jajarmi

222. Anti-VEGFR2 nanobody expression in lettuce using an infectious *Turnip mosaic virus* vector

Mokhtar Jalali-Javaran

223. Development of a high-resolution melting marker for selecting *Fusarium crown root rot*-resistance in the tomato

Jumsoon Kang

224. *In vitro* polyploidy induction in persian endemic *Papaver bracteatum* (Papaveraceae)

Ghasem Karimzadeh

225. Environmental factors affecting *Bemisia tabaci* resistance of tomato

Atiyeh Kashaninia

226. Identification of cytosine-5 DNA methyltransferases and demethylases in eggplant and their expression during fruit ripening

Sergio Lanteri

227. Development of DNA markers associated with monoecious sex expression in melon (*Cucumis melo* L.)

Young-Guen Lee

228. Genome-wide sequence variants and their implication for breeding in watermelon

Youngjae Lee

229. Heritability of artichoke important traits in hybrids developed by a USA-Italy agreement

Mario Pagnotta

230. Exploitation of diversity in cultivated lettuce through genome wide association analysis

Daniela Palma

231. New germplasm resources and genetic variation of *Cucumis melo* var. *flexuosus* (Fagqous)

Rafael Perl-Treves

232. Selection and breeding of Valencian local tomato varieties

Jaime Prohens

233. Understanding hybrid seed failure in wild tomatoes: phenotypic and transcriptomic signatures

Morgane Roth

234. Identification of heterotic groups in summer squash (*Cucurbita pepo* L.) through morphologic and molecular methods and heterosis in agronomic characteristics

Nebahat Sari

235. A preliminary analysis of onion (*Allium cepa* L.) genetic diversity in Europe
Cristina Silvar

236. Diversity of genetic stabilities measures, how to interpret them
Ridwani Sobir

237. Morphological characterization of dihaploid altinbas melon (*Cucumis melo* L. var. *inodorus*) lines developed by haploidization technique
Ilknur Solmaz

238. Single nucleotide polymorphisms linked to *SIMYB12* gene that controls fruit peel color in domesticated tomatoes (*Solanum lycopersicum* L.)
Beung-Gu Son

239. Genetic diversity and population structure assessed by SSR in a large germplasm collection of pepper (*Capsicum* spp.)
Li Hao Wang