FINAL PROGRAM

ICLGG 2017

8th International Conference on Legume Genetics and Genomics
18-22 September 2017
Siófok, Hungary

Monday, 18 September 2017

	Arrival
12:30	**Registration**
12.00-14:00	***Lunch*** *(for those who spent the night of Sept. 17 at Hotel Azúr)*
15:00	**Opening ceremony** • **Anita Potocska Körösi** Vice-Mayor of Siófok • **Dr. Zsolt Feldman** Deputy State Secretary, Ministry of Agriculture
15:15	**Plenary session – General introduction** *Chair: T.H. Noel Ellis, György B. Kiss*
15:15-16:00	*Thomas R. Sinclair* Physiological limits to legume genetic improvement
16:00-16:45	*Alain Charcosset* Statistical models for genetic improvement: towards genotyping guided global analysis of multiple families
16:45-17:15	***Coffee break***
17:15-18:00	*Douglas R. Cook* Harvesting crop wild relatives to improve chickpea cultivation in food-insecure countries
18:00-18:45	*Stig Uggerhøj Andersen* Exploiting systematic mutagenesis to identify targets for gene editing
19:00	***Reception***

Tuesday, 19 September 2017

9:00	**Plenary session – Genomes** *Chair: Doug Cook, Stig Uggerhøj Andersen*
9:00-9:45	*David Bertioli* Genetic behaviour and genome diversity in *Arachis hypogaea*
9:45-10:30	*Judith Burstin* The pea genome
10:30-11:00	***Coffee break***
11:00-11:45	*Kirstin E. Bett* Lentil genomes: Weird and wonderful wildlings
11:45-12:00	*Timothy Close* A reference genome sequence of cowpea
12:00-12:15	*Lars Kamphuis* Development of genomic resources for narrow-leafed lupin, including a reference genome and pan-genome and identification of candidate genes for domestication traits
12:15-12:30	*Abhimanyu Sarkar* The *Lathyrus sativus* genome project
12:30-14:00	***Lunch***
14:00	**Plenary session – Growth, form and N2 fixation** *Chair: Éva Kondorosi, Judith Burstin*
14:00-14:45	*Claire Domoney* Genetic diversity and strategies for seed quality enhancement in pea
14:45-15:30	*Cristina Ferrándiz* The role of MADS-box genes in the evolution of fruit morphology and seed dispersal strategies
15:30-16:00	***Coffee break***
16:00-16:45	*Attila Kereszt* Nodule-specific plant peptides control intracellular accommodation of symbiotic bacteria
16:45-17:00	*Jim Weller* Comparative genetic analysis of flowering time adaptation in legumes
17:00-17:15	*Mauren Jaudal* *MtSOC1a* promotes flowering and elongation of the primary shoot axis in the reference legume *Medicago truncatula*

17:15-17:30 *Colleen Friel*
Complex interactions in the rhizosphere: interplay between rhizobia, mycorrhizae, and the microbiome across *Medicago* genotypes

17:30-17:45 *Georgina Hernandez*
Common bean microRNAs: unraveling novel players for the control of rhizobia nitrogen fixing symbiosis

17:45 **Poster session #1 (odd numbers)**
Chairs: Éva Kondorosi, Judith Burstin

17:45-18:20 **5 min. poster flash talks**

- *Candy Taylor*
  A series of fortunate events: unlocking flowering time variation in narrow-leafed lupin through an allelic series of mutation events at a major flowering time gene, *LanFTc1*
- *Karen Frick*
  Sweetening the deal for narrow-leafed lupin (*Lupinus angustifolius L.*): genomic research to manage quinolizidine alkaloid accumulation in the grain
- *Cristina Caballo Linares*
  Identification of a candidate gene for double podding in chickpea
- *Maria Pazos Navarro*
  Legume response to varied light quality and genetic control of flowering induction
- *Jean-Francois Arrighi*
  Genetics and genomics of the Nod factor-independent *Aeschynomene evenia* to shed light on the evolution of the *Rhizobium*-legume symbiosis
- *Petr Smýkal*
  Wild relatives of domesticated pea in the Mediterranean Region and the Fertile Crescent will respond to global climate change

18:20 **Poster viewing (odd numbers)**

Wednesday, 20 September 2017

9:00	**Plenary session – Biotic stress** *Chair: Cristina Ferrándiz, Péter Kaló*
9:00-9:45	*Karam B. Singh* Using *Medicago truncatula* to tackle disease issues in legumes with a focus on soil-borne fungal pathogens and insect pests
9:45-10:30	*Marie-Laure Pilet-Nayel* Quantitative resistance for durable management of *Aphanomyces* root rot of pea
10:30-11:00	***Coffee break***
11:00-11:15	*Kiran Mysore* Insertion mutagenesis of *Medicago truncatula* and its utilization to identify novel sources of resistance against Asian soybean rust
11:15-11:30	*Valérie Geffroy* *Co*-x, a non-canonical disease resistance gene of common bean to the fungus *Colletotrichum lindemuthianum* the agent of anthracnose
11:30-11:45	*Jonathan Kreplak* An RNAseq approach towards deciphering mechanisms involved in bruchid tolerance in faba bean
11:45-12:00	*Juan M. Osorno* Identifying genomic regions associated with disease resistance using GWAS: some real breeding examples in common bean
12:00-12:15	*Akhouri Nishant Bhanu* Assessment of genetic purity of inter-specific F1 hybrids involving *V. radiata* and *V. umbellata*
12:15-12:30	*Pooja Bhatnagar-Mathur* Successful aflatoxin mitigation in peanut using HIGS and transgenic approaches: technology and translation
12:30-12:45	*David McKenzie Bird* Cross-species eQTL mapping: A new genetic approach to reveal causal interactions between symbionts
12:45-14:00	***Lunch***
14:00	***Business meeting (open for each attendee), then free afternoon***

18:00 **Poster session #2 (even numbers)**
Chair: Karine Gallardo, Attila Kereszt

5 min. poster flash talks

18:00-18:10

- *Seyedehmahsa Mousavi-Derazmahalleh*
  Plant and pathogen genomics: towards building resilience into narrow-leafed lupin crops
- *Karl Pauls*
  Genomic approaches to identifying bacterial and plant genes involved in pathogenicity and resistance to common bacterial blight in *Phaseolus vulgaris*

18:10 **Poster viewing (even numbers)**

Thursday, 21 September 2017

9:00	**Plenary session – Abiotic stress** *Chair: Thomas Sinclair, Richard Thompson*
9:00-9:45	*Marion Prudent* Drought response of nodulated roots in pea: from ecophysiological to transcriptomic analyses
9:45-10:30	*Nijat Imin* The yin and yang of nodulation: regulatory peptides that positively and negatively regulate root and nodule development in response to nitrogen availability
10:30-11:00	***Coffee break***
11:00-11:15	*Shahal Abbo* Drought response and genetic diversity in *Pisum fulvum*, a wild relative of domesticated pea
11:15-11:30	*Charlotte Henriet* The interplay between sulfur nutrition and the drought response in pea: a focus on seed development and composition
11:30-11:45	*Jens Berger* Building the base: widening the genetic & adaptive diversity of chickpea
12:00-13:30	***Lunch***
13:30	**Plenary session – Legumes in the real world** *Chair: David Bertioli, Alain Charcosset*
13:30-14:15	*Maria Monteros* Development of the alfalfa breeder's toolbox: a resource for genomic, genetic and germplasm resources for alfalfa improvement
14:15-15:00	*Karine Gallardo* Recent advances in the regulation of seed protein composition in legumes: from genome-wide studies to new seed protein profiles
15:00-15:30	***Coffee break***
15:30-16:00	*Endalkachew Wolde-meskel* Sustainable intensification of grain legumes with smallholders in Africa through nitrogen fixation: highlights from the N2Africa project

16:00-16:30	*Shoba Sivasankar* *(talk presented by Noel Ellis)* The CGIAR research program on grain legumes and the International Year of Pulses
16:30-16:45	*Roberto Papa* Bean adapt: the genomics of adaptation during crop expansion of common bean
16:45-17:00	*Donal O'Sullivan* Gene identification in faba bean – to synteny and beyond
17:00-17:15	*Parwinder Kaur* TrifoliGATE subterranean clover genomic resources: building a comprehensive user-friendly platform for future forage legume breeding
17:15-17:30	*Samuel Hokin* A collection of online resources for legume research
17:30	**Closing of the conference**
18:30	***Banquet***

Friday, 22 September 2017

Departure

List of accepted posters

P-01
Mohamed Lazali
Approaches for enhancement of phosphorus use efficiency of chickpea (*Cicer arietinum* L.) under limiting phosphorus conditions

P-02
Derya Yucel
Developing drought and heat stress tolerant chickpea genotypes

P-03
Márcia Carvalho
Evaluation of drought stress responses in cowpea genotypes

P-04
Judith Burstin
PeaMUST (2012-2019) – Pea Multi-Stress adaptation and biological regulations for yield improvement and stability

P-05
Weronika Czarnocka
Global analysis and comparison of transcriptomic changes in *Medicago truncatula* and *Lotus japonicus* root nodules during drought stress

P-06
Srinivasan Samineni
Marker assisted breed chickpea lines showed superior performance in multilocation testing in India

P-07
Omar Idrissi
Molecular diversity and quantitative trait loci related to drought tolerance in lentil (*Lens culinaris Medik., Fabaceae*)

P-08
Gordana Petrović
Osmotic stress tolerance in the early vegetative stages of field pea at the molecular level

P-09
Min Young Yoon
QTL identification for UV-B resistance traits in soybean using genotype-by-sequencing

P-10
Patricia Castro Lopez
TEMPRANILLO as a good candidate gene for flowering time in chickpea

P-11
Gholam Reza Zamani
The investigation of silicon effects on yield and growth of chickpea, under salinity stress

P-12
Karl Pauls
Genomic approaches to identifying bacterial and plant genes involved in pathogenicity and resistance to common bacterial blight in *Phaseolus vulgaris*

P-13
Katarzyna Hnatuszko-Konka
The effect of the presence of symbiotic *Rhizobium* on the effectivity of the *Agrobacterium tumefaciens*-mediated transformation of *Phaseolus vulgaris*

P-14
Marcin Nadzieja
Expanding genetic resources of Vicia faba – generation of a reference transcript set

P-15
Virginie Bourion
Comparative genome-wide-association mapping identifies common loci controlling root system architecture and resistance to *Aphanomyces euteiches* in pea

P-16
Ana Torres
Identificacion of new faba bean (*Vicia faba L.*) lines tolerant to *Orobanche* in the Southern Spain

P-17
Kedar Adhikari
Identifying pathogen variability and virulence of *Uromyces viciae-fabae* on common cultivated legumes in Australia

P-18
Lars Kamphuis
Mining wild-chickpea (*Cicer reticulatum* and *C. echinospermum*) for adaptive traits to Australian growing conditions

P-19
Aladdin Hamwieh
Multi-environment QTL analyses for ascochyta blight resistance in a RIL population of chickpea (*Cicer arientinum* L.)

P-20
Julie Pasche
New SNP associated with common bacterial blight resistance in dry edible bean breeding lines

P-21
Cristina Caballo Linares
Identification of a gandidate gene for double podding in chickpea

P-22
Maria Pazos Navarro
Legume response to varied light quality and genetic control of flowering induction

P-23
Pyare Lal Johnson
Heterosis in relation to genetic divergence and hybridity in chickpea (*Cicer arietinum* L.) under rice based bropping system

P-24
Jungmin Ha
Identification of QTLs associated with number of branches in soybean

P-25
Yoon Min Young
Investigation on inflorescence architecture of mungbean associated with synchronous maturity in pods

P-26
Sergio Ochatt
Phytosulfokine-alpha, an enhancer of *in vitro* regeneration competence in recalcitrant legumes

P-27
Rafael Lozano
RNA-seq analysis uncovers common bean genes involved in pod maturation and dehiscence

P-28
Marta Santalla
An examination of QTL architecture underlying pod shattering resistance in common bean

P-29
Marcelino Perez de la Vega
Development of an interspecific linkage map and identification of genomic regions controlling agronomic traits in lentil

P-30
Özlem Cetin
DNA barcoding studies on two endemic species of *Astragalus* L. from Turkey using sequences of nrDNA ITS and cpDNA trnLiIntron and the trnL-trnF IGS

P-31
Mustafa Çelik
DNA barcoding study on *Lotononis genistoides* (Fenzl) *Benth*

P-32
Firouzeh Javadi
Ecological and evolutionary genetics of wild *Cicer species*

P-33
Jiangqi Wen
Finalizing the Tnt1 mutant population in *Medicago truncatula*

P-34
Sergio Ochatt
Flow cytometry measurements montribute to *Pisum* taxonomy

P-35
Nadia Benbrahim
Genetic diversity assessement of some Moroccan lentil landraces using electrophoresis (SDS-PAGE) of seed storage proteins

P-36
Márcia Carvalho
Genetic relationship of *Vigna unguiculata* spp. accessions based on cpSSR markers

P-37
Ambuj Jha
Genome wide association study to identify SNPs associated with folate profile in pea

P-38
Jose Die
Genome-wide identification and expression analysis of the auxin response factor gene family in *Cicer arietinum*

P-39
Rachit Saxena
Genomics advances for enhancing genetic gains in pigeonpea

P-40
Magdalena Kroc
Identification of genes involved in the alkaloid biosynthesis pathway in narrow-leafed lupin (*Lupinus angustifolius L.*) on the basis of transcriptome sequencing

P-41
Ping Wan
Identification of QTL and qualitative trait genes for agronomic traits in adzuki bean

P-42
Péter Kaló
Identification of the translocation breakpoint between chromosome 4 and 8 in the genomes of *Medicago truncatula* A17 and A20

P-43
Hyun-Ju Jang
Improvement of the mungbean reference genome assembly and QTL identification for synchronous pod maturity

P-44
Abdulkadir Aydogan
The first step for adaptation: width and distribution of the first flowering and podding dates in wild chickpeas

P-45
Petr Smýkal
Wild relatives of domesticated pea in the Mediterranean region and the Fertile Crescent will respond to global climate change

P-46
Fatema Bakro
Implementation of reverse genetics tools for improvement of pea cultivation in Poland

P-47
Candy Taylor
A series of fortunate events: unlocking flowering time variation in narrow-leafed lupin through an allelic series of mutation events at a major flowering time gene, *LanFTc1*

P-48
Seyedehmahsa Mousavi-Derazmahalleh
Plant and pathogen genomics: towards building resilience into narrow-leafed lupin crops

P-49
Sandra Rychel
Crosstalk between photoperiod and vernalization pathways – insight into genes involved in flowering induction in the narrow-leafed lupin

P-50
Teresa Millán
Development of chickpea near isogenic lines for QTL_{DF1} linked to flowering time

P-51
Barbara Pipan
Development of the common bean core collection referring to the Central and South Eastern European germplasm

P-52
Marina Ceran
Exploring the potential of genomic prediction in NS soybean breeding programs: preliminary results

P-53
Ana Torres
Genomic approaches to identify candidate genes controlling pod dehiscence in chickpea and faba bean

P-54
Rakesh Chahota
Genomics tools for the improvement of horsegram (*Macrotyloma uniflorum*): an orphan legume

P-55
Deepti Angra
Large scale SNP mining and validation in *Vicia faba*

P-56
Christine Lelandais-Briere
Non-coding RNAs: key actors of root developmental plasticity in *Medicago truncatula*

P-57
Venkata Sameer Kumar Chanda
Renaissance of pigeonpea breeding: via hybrid pigeonpea technology

P-58
Natalia Gutierrez Leiva
SNP genotyping of putative candidate genes involved in broomrape and *Ascochyta fabae* resistance in faba bean (*Vicia faba L.*)

P-59
Karen Frick
Sweetening the deal for narrow-leafed lupin (*Lupinus angustifolius L.*): genomic research to manage quinolizidine alkaloid accumulation in the grain

P-60
Petr Smýkal
The genomic and phenotypic evaluation of chromosome segment substitution lines of wild pea (*P. fulvum*) to widen the genetic diversity of pea crop

P-61
Roland Schafleitner
The International Mungbean Improvement Network – mobilizing the mungbean genetic diversity as a source for new traits for crop improvement

P-62
Rebecca Tacke
Towards a localization of the “vc-“gene which is responsible for low vicine and convicine content in seeds of faba bean (*Vicia faba L.*) and towards a low vicine and convicine winter faba bean cultivar

P-63
Mahendar Thudi
Untapping the potential of genome wide variations discovered through resequencing of germplasm lines for chickpea improvement

P-64
Richard Thompson
Characterization of the biosynthesis of saponins during seed development in peas (*Pisum sativum*) and faba beans (*Vicia faba*)

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Oldřich Trněný
Comparative transcriptomic, anatomical and metabolic analysis of wild pea seed coat in relation to dormancy

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Jose Jimenez-Lopez
Gene expression and localization of narrow-leafed lupin seed proteins evidence the functional interplay between conglutin protein families driving seed germination

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Aijun Yang
Variation in seed coat colour and phytochemicals in *Lablab purpureus* in Australia

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Petr Smýkal
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Jean-Francois Arrighi
Genetics and genomics of the Nod factor-independent *Aeschynomene evenia* to shed light on the evolution of the *Rhizobium*-legume symbiosis

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Izabela Sańko-Sawczenko
Expression of PIN genes in root nodules of fabacean model plants

P-72
Hongyan Zhu
Host genetic control of symbiotic specificity in the legume-rhizobial interactions

P-73
Shawna Rowe
Investigating the role of ethylene in the sanctioning response of leguminous hosts to ineffective rhizobial partners

P-74
Alina Feinstein
Pan-genome assembly of population haplotypes provides a comprehensive solution to common obstacles in modern breeding

P-75
Myoyeon Kim
Transcriptomic profiling of genes involved in epicatechin biosynthesis in soybean

P-76
Sungwoo Lee
Dissection of genetic architectures of soybean protein, oil and amino acids

Local Organizing and Scientific Committee (LOSC):

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