

# Proceedings of the XIV International Lupin Conference

Milan, Italy 21-26 June 2015

**Developing lupin crop into a major  
and sustainable food and feed source**

## Editors

Jessica Capraro

Marcello Duranti

Chiara Magni

Alessio Scarafoni



---

## Main Sponsors

---



---

## Sponsors

---



---

## Partners

---



Department of Food,  
Environmental and  
Nutritional Sciences



With the Patronage of



MILANO 2015  
FEEDING THE PLANET  
ENERGY FOR LIFE



Events Congress IT solutions Services

## **Local Organizing Committee**

Marcello Duranti  
Alessio Scarafoni  
Jessica Capraro  
Chiara Magni  
Simona Corsini

## **Scientific Committee**

Erik von Baer  
Jon Clements  
Marcello Duranti  
George Hill  
Colin Hughes  
David Mc Naughton  
Joao Neves Martins  
Ana Planchuelo  
Brigitte Ruge Wehling  
Edzard van Santen  
Bogdan Wolko

## **Conference Organizer and Secretariat**

H2O srl  
via Dante 2/142  
Palazzo della Borsa - 16121 Genoa - Italy  
ph. + 39 0108936258 - fax + 39 0108936269  
Mrs. Simona Corsini (s.corsini@h2osrl.org)  
[www.h2osrl.org](http://www.h2osrl.org)

# Proceedings Book

## XIV International Lupin Conference

### Content

**Preface, II**

*Lectio Magistralis, 1*

**Oral contributions per session:**

**Session 1:** Lupin genome and beyond, 2

**Session 2:** Lupin genomics and advanced selection tools, 8

**Session 3:** Lupin cultivation and farming worldwide, 18

**Session 4:** Lupin.....omics, 37

**Session 5:** Physiology and pathology of lupin, 44

**Session 6:** Lupin for foods and ingredients, 59

**Session 7:** Lupin: nutrition and human health, 76

**Poster contributions, 96**

**Workshops:**

**W1:** Is lupin a real and valuable source of nutrients and ingredients for the food industry?, 149

**W2:** Lupin genomic workshop, 150

Workshop Scientific contributions, 151

**Analytical index, 157**

**List of Authors, 161**

## Comparative genomics of *Lupinus angustifolius* L. gene-rich regions

**Książkiewicz M<sup>1</sup>, Wyrwa K<sup>1</sup>, Rychel S<sup>1</sup>, Szczepaniak A<sup>1</sup>, Susek K<sup>1</sup>, Zieleziński A<sup>2</sup>, Bielski W<sup>1</sup>, Karłowski W<sup>2</sup>, Naganowska B<sup>1</sup>, Wolko B<sup>1</sup>**

<sup>1</sup>Department of Genomics, Institute of Plant Genetics of the Polish Academy of Sciences, Poznań, Poland; <sup>2</sup>Institute of Molecular Biology and Biotechnology, Adam Mickiewicz University, Poznan, Poland;

Corresponding Author's e-mail: mksi@igr.poznan.pl

**State of the art and aim:** Recently, a significant development of molecular genetic resources for the narrow-leafed lupin (*Lupinus angustifolius* L.) has been observed. These include genetic maps with gene-anchored markers, nuclear DNA libraries, a draft genome sequence aligned to the linkage groups, reference transcriptome assembly and cytogenetic markers tagging specific chromosomes. The aim of this research was to localize and analyze several *L. angustifolius* gene-rich regions (GRRs) using the resources mentioned above, together with those generated for other legume species. Complex approach involved: DNA fingerprinting, sequencing, genetic mapping and molecular cytogenetics, followed by bioinformatic analyses.

**Results and discussion:** The *L. angustifolius* genomic BAC library was screened with several gene-based probes, to track genes involved in symbiotic nitrogen fixation and fatty acid synthesis, as well as with SSR-probes to focus on gene-rich regions in general (Książkiewicz *et al.* 2013, 2015). BAC clones carrying particular sequences were isolated, fingerprinted and assembled into contigs. BAC-end sequence (BES) annotation allowed us to choose clones for sequencing, targeting particular genome regions. *L. angustifolius* reference genetic map (Kamphuis *et al.* 2015) was supplemented with new BES- and BAC-derived markers. Physical and genetic mapping was supported by multi BAC-FISH; new chromosome-specific landmarks were identified. BESs and BACs were aligned to *L. angustifolius* genome draft assembly, where they tagged several hundred sequences. Orientation of more than half of anchored scaffolds was identified by paired BESs. The *in silico* detection of coding regions revealed that the average gene density was higher than 10 genes/100 kb. Using genetic linkage distances and consensus band size data, the ratios of physical to genetic distances were calculated. Values obtained for gene-rich regions were below 150 kb/cM. The physical-to-genetic distance ratios supported the results of functional annotation. Comparative analysis of sequenced *L. angustifolius* GRRs revealed numerous syntenic links to the sequenced legume genomes (*Arachis duranensis*, *A. ipaensis*, *Cajanus cajan*, *Cicer arietinum*, *Glycine max*, *Lotus japonicus*, *Medicago truncatula*, *Phaseolus vulgaris*, and *Vigna radiata*). Some regions of the nuclear genomes retained their quasi-ancestral structures, visualised by identical order and orientation of microsyntenic blocks. The maximum-likelihood and Bayesian phylogenetic inferences provided novel evidences for ancient duplications and triplications in the *L. angustifolius* genome, which putatively have occurred after the divergence of ancestor lineage to *Lupinus*, *Arachis*, and *Glycine*.

### References:

Książkiewicz *et al.* (2013) *BMC Genomics*, 14, 79

Kamphuis *et al.* (2015) *Plant Biotechnol J*, 13(1), 14-25

Książkiewicz *et al.* (2015) *Plant Mol Biol Rep*, 33, 84-101

**Acknowledgements:** Financial support: The National Centre for Research and Development project 244227 SEGENMAS. Ministry of Agriculture and Rural Development Nr 39/2015.

**Tags:** genome; synteny; sequencing; BAC-FISH; molecular marker; narrow-leafed lupin

# Genotyping by sequencing of white and narrow-leafed lupins

**Rychel S<sup>1</sup>, Książkiewicz M<sup>1</sup>, Rudy E<sup>1</sup>, Nelson M<sup>2</sup>, Naganowska B<sup>1</sup>, Wolko B<sup>1</sup>**

<sup>1</sup>Institute of Plant Genetics, Polish Academy of Sciences, Poznań, Poland; <sup>2</sup>School of Plant Biology, The University of Western Australia

Corresponding Author's e-mail: [sryc@igr.poznan.pl](mailto:sryc@igr.poznan.pl)

## **State-of-the-art and aim:**

Over the last years significant progress in generation of publicly available sequence resources has occurred, including three crop lupin species: white (*Lupinus albus*), yellow (*L. luteus*), and the narrow-leafed (*L. angustifolius*) (Książkiewicz et al. 2015). Flagship achievements encompass: transcriptome assemblies and gene indices (all three species), linkage maps (white and narrow-leafed lupin), and a draft genome assembly (narrow-leafed lupin). These resources, together with DNA-based molecular markers, can facilitate the gene-based prediction of phenotype. Marker assisted selection (MAS) has recently become an integral part of plant breeding programs and has accelerated new cultivar development. However, the most of the marker systems provided for lupins are ineffective due to high cost of scoring and low level linkage with particular traits. Advances in sequencing technologies have driven down sequencing costs and launched increasing interest in genotyping by sequencing (GBS), which generates ready to use markers based on sequence polymorphism.

**Results and discussion:** The aim of our ongoing research is to generate a technology of monitoring the narrow-leafed and white lupin lines carrying particular QTLs (quantitative trait loci) conferring agricultural traits. It will enable allele-directed selection in breeding programs. This target will be reached by determination of relationships between variability of white and narrow-leafed lupin phenotype quantitative traits, genetic polymorphisms of markers linked to these traits, genetic information contained in genome regions carrying these loci, and transcriptional activity of genes encoded by these sequences. The narrow-leafed lupin accessions from the world germplasm collection, together with recombinant inbred lines (RILs) from two mapping populations, 112 of narrow-leafed lupin and 193 of white one, are currently being profiled by GBS. Polymorphisms of obtained markers will be correlated with agricultural traits by association mapping. Phenotype observations include plant morphology and physiology, content of alkaloid and other non-nutrient and nutrient components, and resistance to biotic and abiotic stresses. Consensus, high density linkage maps containing both newly developed GBS and existing gene-based PCR and AFLP markers (Phan et al. 2007 and Vipin et al. 2013) will be constructed to support the identification of genomic regions in the marker-trait association study. Obtained linkage maps, composed mainly of sequence-based markers, will be also used for synteny survey in comparative mapping approach to sequence legume genomes (*Arachis duranensis*, *Arachis ipaensis*, *Cajanus cajan*, *Cicer arietinum*, *Glycine max*, *Lotus japonicus*, *Medicago truncatula*, *Phaseolus vulgaris*, and *Vigna radiata*).

## **References:**

Phan et al. (2007) *DNA Research*, 14, 59-70  
Vipin et al. (2013) *Breeding Science*, 63, 292-300  
Książkiewicz et al. (2015) *Plant Mol Biol Rep*, 33, 84-101

**Acknowledgements:** Financial support: The National Centre for Research and Development project 244227 SEGENMAS, Ministry of Agriculture and Rural Development project Nr 39/2015.

**Tags:** GBS, white lupin, narrow-leafed lupin, molecular markers, next-generation sequencing