# Recent pea genomic resources will enhance complementary improvement strategies in this crop

Judith Burstin, Susete Alves Carvalho, Nadim N. Tayeh, Christelle Aluome, Virginie Bourion, Anthony Klein, Sebastien Carrere, Anne-Lise Brochot, P. Salloignon, Mathieu Siol, et al.

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# PROGRAM & ABSTRACT BOOK

TCU Place
Saskatoon, Saskatchewan, Canada
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University of Saskatchewan

## *Keynote Speaker:* Fundamental and Applied Genetics and Genomics (IFLRC)

**Dr. Judith BURSTIN** is Director of research at INRA UMR1347 Agroecology Dijon-F. With an initial background in agronomy, quantitative genetics and breeding, she has acquired competencies in genomics and post-genomics. Her research focuses on pea and aims at deciphering the control of seed yield and quality in the context of climate change. A major scope of her research is the molecular understanding of plant adaptation. She leads a group working on the genetics and genomics of protein crops (mainly pea and fababean). She has been coordinating large multi-disciplinary projects in the field of pea quantitative molecular genetics, translational genomics and proteomics, and of development of molecular tools and plant material. She co-authored more than 30 papers in peer-reviewed international journals and 5 book chapters. She is expert for the French variety registration office and has been vice-president of the former European association of grain legumes.

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Pea has lagged behind many other crops in terms of dedicated genomic tools for several reasons including its large genome size (ca. 4.5 Gb). The recent development of high-throughput sequencing and genotyping technologies has permitted pea genomics to catch up and enter into the genomic era. We will present the development of functional and structural genomic resources in pea and their application in pea breeding. We developed a pea Unigene expression atlas that allows visualization of expression profiles for any gene of interest in various tissues subjected to different conditions. This was the basis for generating a high density microarray for functional genomics and a high-throughput genotyping BeadChip array for genotyping. These tools will be extremely useful in three breeding strategies followed by the team: (i) ideotype breeding, which pursue an ideal plant model that is expected to meet the desired yield and quality requirements of producers and users; (ii) targeted breeding, which chase the good combinations of genetic factors controlling traits of interest; and (iii) genome-wide breeding, which models phenotypes from high density marker genotypes.