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Mélanie Noguero, Christine Le Signor, Vanessa Vernoud, Isabelle d'Erfurth,  
Jérôme Verdier, Gregoire Aubert, Jerome Gouzy, Jean-Marie Prospero,  
Thierry Huguet, Judith Burstin, et al.

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# IFLRC VI & ICLGG VII

6<sup>th</sup> International Food  
Legume Research  
Conference

7<sup>th</sup> International  
Conference on Legume  
Genetics and Genomics

## ***PROGRAM & ABSTRACT BOOK***



**TCU Place**

**Saskatoon, Saskatchewan, Canada**

*July 7-11, 2014*



## Keynote Speaker: Seeds and Nutrition (ICLGG)

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**Richard D. Thompson.** After a Ph.D. in Molecular Biology U. Edinburgh (1979) and periods at the PBI Cambridge UK, and the MPI for Plant Breeding Research, Köln, currently researcher in the INRA Agroecology Unit, Dijon, (2002-present, Grain Legumes Unit Director 2002-2010), focussing on the genetic control of seed development and composition in legumes, using the *Medicago truncatula* model, and more recently, Pea (*Pisum sativum*). By applying proteomics and transcriptomics approaches, gene expression profiles for isolated tissues of the seed have been obtained and clusters of co-regulated genes acting during discrete stages in seed filling identified. To narrow down candidate genes for the control of seed composition and yield, we have selected genes that co-locate with QTLs for these traits and are analysed the phenotypes of corresponding TILLING and TnT1 insertion mutants. Also coordinating the EU project LEGATO (Legumes for the Agriculture of Tomorrow (2014-2017)), aimed at increasing grain legume cultivation in Europe.

### Use of translational genomics to identify genes important for legume seed development

Noguero, M.<sup>1</sup>, Le Signor, C.<sup>1</sup>, Vernoud, V.<sup>1</sup>, D'Erfurth, I.<sup>2</sup>, Verdier, J.<sup>3</sup>, Aubert, G.<sup>4</sup>, Gouzy, J.<sup>5</sup>, Prosperi, J-M.<sup>6</sup>, Huguët, T.<sup>7</sup>, Burstin, J.<sup>8</sup>, Gallardo, K.<sup>8</sup>, and Thompson, R.D.<sup>8</sup>. <sup>1</sup>INRA, UMR Agroécologie, DIJON, FRANCE; <sup>2</sup>INRA, UMR1347 Agroécologie, DIJON FRANCE; <sup>3</sup>Shanghai Center for Plant Stress Biology, Shanghai Institutes of Biological Sciences, Chinese Academy of Sciences, Shanghai, PR China; <sup>4</sup>INRA, UMR1347 Agroécologie DIJON, FRANCE; <sup>5</sup>INRA, Lab. Interactions Plantes - Microorganismes, TOULOUSE; <sup>6</sup>UMR Diversité et adaptation des plantes cultivées, MONTPELLIER; <sup>7</sup>ENSAT, TOULOUSE; <sup>8</sup>INRA, UMR1347 Agroécologie, DIJON, FRANCE. \*(thompson@dijon.inra.fr)

We have been using genomics approaches with *Medicago truncatula* as a tool to identify key genes determining seed yield and composition in *Medicago* and in closely related legumes. Analyses of the proteome and transcriptome of the component tissues of the developing seed revealed extensive compartmentalization of gene expression and metabolic activities (Gallardo et al, 2007). Using a TF (Transcription Factor) qRT-PCR platform (Verdier et al., 2008) the Affymetrix Gene Chip (Benedito et al, 2008), and more recently, Nimblegen arrays (Buitink et al. submitted), putative regulatory genes specific for each seed tissue were identified, along with putative target genes of transcription factors (TFs). These genes have been located on the *M. truncatula* genetic map and correlations between map positions of TF loci and QTLs for protein quantities and other seed phenotypes were detected. These correlations were confirmed in certain cases by the existence of similar QTLs at syntenic positions in pea. This approach has enabled us to attribute roles to two genes, both specifically expressed in the developing endosperm of *M. truncatula* and present in pea. One encodes a DOF class transcription factor, whose mutant phenotype severely affects endosperm development. The second gene encodes an endosperm-specific subtilase (*SBT1.1*), which affects final seed weight in both species (D'Erfurth et al, 2012). The importance of the endosperm in determining legume seed size and composition will be discussed.

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