

Comparative genetic analysis of flowering time adaptation in legumes

J.L. Weller¹, R. Ortega¹, J.K. Vander Schoor¹, V. Rajandran¹, O. Williams¹, V. Hecht¹, E.C. Perez-Wright¹, S. Ridge¹, A.J.S. Rubenach¹, R. Lee², D.M. Bond², R.C. Macknight², R.V. Penmetsa³, D.R. Cook³, K.E. Bett⁴, T. Millàn⁵, A. Gonzalez⁶, M. Santalla⁶

¹ School of Biological Sciences, University of Tasmania, Hobart, Tasmania, Australia

² Department of Biochemistry, University of Otago, Dunedin, New Zealand

³ Department of Plant Pathology, University of California, Davis, USA

⁴ Department of Plant Sciences, University of Saskatchewan, Saskatoon, Canada

⁵ Department of Genetics, University of Cordoba, Cordoba, Spain

⁶ Misión Biológica de Galicia-CSIC, Pontevedra, Spain

A better understanding of flowering genes in legume crops will be valuable in understanding their prehistoric expansion from regions of initial domestication, in breeding for new environments and in accessing wider genetic diversity present in wild crop relatives. We are using a comparative approach to explore the genetic network controlling flowering time adaptation in a number of legume species. In addition to the use of induced mutants in pea (*Pisum sativum*) and barrel medic (*Medicago truncatula*), recent work has focused on characterization of natural variation in crop species including pea, lentil (*Lens culinaris*) and chickpea (*Cicer arietinum*). We have performed comparative phylogenetic analyses of many of the major flowering gene families in legumes, and examined the expression patterns of key genes, including members of the *FT* family of florigen genes. A positional candidate gene approach has enabled the identification of putative causal genes for major flowering loci and shown a striking conservation in certain genomic regions conferring flowering time adaptation across several species. Evidence on the molecular and physiological basis for adaptive changes at these loci will be presented and possible reasons for their prominence will be discussed.

How to refer your abstract:

J.L.Weller, R. Ortega, J.K. Vander Schoor, V. Rajandran, O. Williams, V. Hecht, E.C. Perez-Wright, S. Ridge, A.J.S. Rubenach, R. Lee, D.M. Bond, R.C. Macknight, R.V. Penmetsa, D.R. Cook, K.E. Bett, T. Millàn, A. Gonzalez, M. Santalla (2017) Comparative genetic analysis of flowering time adaptation in legumes; ICLGG 2017 - Book of abstracts, ICLGG2017/OL/49