

MEDIA RELEASE

NEWS FROM THE UNIVERSITY OF TASMANIA

DATE: TUESDAY 4 DECEMBER 2012

ATTENTION: Chiefs of Staff, News Directors



Researchers discover the key to unlocking crop plant 'jet-lag'

A University of Tasmania-based research project examining how plants respond to seasonal changes has identified a gene that has a major influence on where and when certain crop plants can be grown.

The work will be published this week in the journal *Proceedings of the National Academy of Sciences USA*, and involved collaboration with researchers in France and New Zealand.

The project is being led Dr Jim Weller, a senior lecturer and ARC Future Fellow in the UTAS School of Plant Science. It investigates the factors that control how long a plant takes to flower, and focuses on legumes, an important group of crop plants that includes peas, lentils, beans and chickpeas.

"Flowering time is a very important part of a plant's adaptation to its environment, whether it is a wild plant growing in nature or a crop plant grown for human purposes," Dr Weller said. "The wild ancestors of many of our crops had quite restricted distributions, and major genetic changes were required before they could spread and be successfully grown at different latitudes and in different climatic zones.

"In this case we surveyed a large collection of wild and domesticated pea varieties from around the world in our specialised glasshouse facility that can simulate different day lengths year-round."

This work resulted in the identification of a gene called *High Response to Photoperiod* that has been important for development of early-flowering varieties of peas and lentils. "Plants with variants of the gene have an abnormal internal biological clock – they essentially have permanent jet-lag. As a result, they have difficulty recognising what season they are in," he said.

The gene discovered by Dr Weller's team is important for how these crops perform in different locations. "In both peas and lentils, variants of the *HR* gene shorten the production cycle, improving crop performance in the short summers of northern Europe or in drought-prone conditions of southern India."

The team's results suggest that one particular mutation in this gene may have enabled the original expansion of pea cultivation from southern to northern Europe during prehistoric times. They will also help to improve the efficiency of modern breeding efforts.

Dr Weller said the UTAS contribution included detailed genetic and molecular work by PhD students Lim Chee Liew and Vinodan Rajandran, postdoctoral research associate Dr Valérie Hecht, and research assistants Jackie Vander Schoor and Stephen Ridge.

Information released by:

The Media Office, University of Tasmania

Phone: (03) 6226 8518 or 0429 336 328 (Peter Cochrane)

Email: Media.Office@utas.edu.au