**PREVIOUS TRACK RECORD**

Tsiantis has made key contributions in understanding the mechanisms of plant development and how these were modified during evolution. He showed that leaf development requires restriction of KNOTTED1 homeobox (KNOX) gene expression to the Shoot Apical Meristem (SAM) and that this restriction is implemented by the ROUGH SHEATH2 MYB protein in maize, thus identifying the first KNOX repressor (Tsiantis et al, 1999 Science). Subsequently, he pioneered comparative development studies using *Cardamine hirsuta* and developed this Arabidopsis relative as a powerful experimental system. *C. hirsuta* leaves are compound compared with the simple leaves of *Arabidopsis thaliana*, allowing him to use genetics and reciprocal interspecies gene transfers to understand the genetic basis of these strikingly different leaf forms. This novel approach resulted in breakthroughs in the field by demonstrating that cis regulatory divergence at KNOX loci was responsible for differences in KNOX expression that produced the species-specific growth patterns underlying these different leaf shapes (Hay & Tsiantis, 2006; Barkoulas et al, 2008 Nat Genet). In addition, he showed that KNOX proteins control SAM function via combinatorial regulation of activity of the hormones gibberellin and cytokinin (Hay et al, 2002, Jasinski et al, 2005 Curr Biol). Finally, he made key contributions to understanding plant axial patterning by showing that a single mechanism, based on miRNA repression of HD-ZIP III homeobox gene expression, underpins elaboration of both apical-basal and radial polarity in the embryo and lateral organ polarity in the shoot (Grigg et al, 2005 Nature; 2009 Curr Biol). The significance and impact of his group’s work has been acknowledged by awards of the President’s Medal by the SEB (2004), election to the Balfour Lectureship by the Genetics Society (2006) admission to the EMBO YIP programme (2006) and election to EMBO membership in 2010. *C. hirsuta* research has contributed to high visibility for UK science as it was presented in invited talks in key international meetings over the past five years.

The post-doctoral work of Hay was instrumental in developing *C. hirsuta* as a model system for comparative development studies. She has been awarded an Oxford University Glasstone Research Fellowship, a Junior Research Fellowship at Balliol College, and a Royal Society University Research Fellowship to conduct independent research on this system. Her lab exploits the extensive experimental tools developed in *C. hirsuta* to ask how variation in the organisation of gene networks drives the evolution of fruit and floral structures. She collaborates with Tsiantis and more recently Mott to develop genomics resources for *C. hirsuta*.

**Research Environment**

The Plant Sciences Department where MT and AH are located achieved a very high rating in the latest RAE (25% 4\*, 30% 3\*). RM and JH to add dept and interdisciplinary environment. With the funds requested here we propose to take advantage of the internationally competitive and interdisciplinary environment in Oxford to build a novel community resource with a focus on understanding plant genetic diversity.

**Contribution to UK economic competitiveness or quality of life**

The groups of MT and AH have attracted a large number of high quality researchers from abroad (including six postdoctoral researchers with fellowships from EMBO, FEBS, and Glasstone), thus contributing to the competitiveness of UK science. Brassicas are remarkable for containing more important crop species than any other plant genus and play a significant role in the UK agricultural economy. Brassica crops are grown for the production of animal feed, vegetables and vegetable oil for human consumption, and biofuels - and are more closely related to *C. hirsuta* than *A. thaliana*, therefore, key findings in *C. hirsuta* can directly inform efforts for crop improvement. Parallel genetic studies in related species can also inform more broadly about the developmental logic underlying the diversity of form. Understanding which nodes in developmental networks were modified during evolution to produce morphological diversity, versus which nodes cannot tolerate change, is not only a major goal for biology but will inform plant breeding efforts to ensure food, fibre, feedstock and fuel security in the 21st century.