

F1. “A genomic toolkit for improvement of faba bean”

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ABSTRACT: My group has led the collaborative development of a set of over 950 SNP markers for *Vicia faba*; of these approximately 650 have been mapped so far. Our current consensus linkage map of faba bean consists of just 6 linkage groups (=six physical chromosomes), each covered with a reasonable density of SNP markers. The *Vicia faba* genetic map shows a high level of synteny and relatively few chromosomal rearrangements with respect to the model sequenced legume, *Medicago truncatula*. All the SNP markers developed are available as easy-to-use KASP marker assays, and subsets of the full SNP panel polymorphic in different segregating populations have been used to locate and obtain linked markers for traits (so far) such as vicine-convicine and tannin content of seeds, hilum colour, and height. In one study, we have been able to exploit local conservation of synteny to identify and validate a candidate gene underlying the zero tannin trait. My group has recently initiated a large EMS mutagenesis programme based the highly inbred Hedin/2. It is our intention to screen the resulting mutant population for resistance to herbicides to which *Orobanche* is sensitive.

BIOGRAPHY: Donal O’Sullivan is a crop geneticist. He is since April 2013 Professor of Crop Science at the University of Reading, UK and previously spent 10 years as a research leader in the National Institute of Agricultural Botany in Cambridge, UK. He leads work on faba bean in the UK Pulse Crop Genetic Improvement Network to develop a panel of inbred lines and a molecular marker toolkit (www.viciatoolbox.org) for faba bean and while at NIAB was PI on projects mapping resistance to stem nematode and pod set stability. In his new post, he aims to further develop cutting edge resources permitting efficient genetic dissection of multiple traits of interest for faba bean.