
# *ABSTRACT*

*"Floral heteromorphy in Primula: genetics, genomics and gene identification"*

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Floral heteromorphy is an out-breeding mechanism that is characteristic of, although not limited to, the Primulaceae. The phenomenon was described in detail by Charles Darwin, but first documented over a century earlier. In *Primula* species, individuals develop one of two forms of flower, known as pin and thrum. Pin flowers are characterised by a long style that presents the stigmatic surface at the mouth of the flower, and contain anthers attached half way down the inner wall of the corolla tube. Thrum flowers have a short style. half the height of that found in pin flowers, and anthers attached to the inner corolla wall at the mouth of the flower. This reciprocal positioning of male and female reproductive structures promotes insect-mediated cross pollination. These developmental characteristics, and other features of floral heteromorphy, including differential pollens size, as well as a sporophytic self-incompatibility system, are controlled by a co-adapted linkage group known as the *S* locus. Pin plants are homozygous recessive *s/s*; thrum pants are heterozygous *S/s*.

With the objective of identifying the genes at the *S* locus that control style length, anther height and pollen size, we have taken a multifaceted approach involving classical genetics, molecular

genetics, transcriptomics and genomics. We have identified and characterised a number of genes and polymorphic markers, as well as developmental mutations that are linked to the *S* locus. Using these sequences and *S* locus-linked mutant phenotypes we have developed a classical genetic linkage map in P*rimula vulgaris*, spanning the *Primula S* locus and delineated by flanking markers. Subsequent construction and screening of BAC libraries has enabled us to generate a BAC contig spanning the *S* locus and to identify pin and thrum specific BACs.

Transcriptomic analysis of pin and thrum plants has identified morph specific floral transcripts, and transcriptomic and genomic analyses of linked mutations, including *Oakleaf*, *sepaloid* and *Hose in Hose* has been used to probe the molecular basis of these phenotypes. In addition to these analyses we have undertaken *de novo* genome sequencing of *Primula vulgaris* to generate a reference genome and have used genome sequencing of individual parents and pools of pin and thrum progeny to define polymorphic markers surrounding the S locus. Comparative genomic analyses are underway based on *de novo* sequencing of the four additional UK native species; *P. veris*, *P. elatior*, *P. farinosa* and *P. scotica.* We have, in parallel, undertaken a large scale of plants derived from fast neutron bombarded *P. veris* seed to identify long and short homostyle as well as self compatible mutants.

We will present our most recent work arising from these studies to highlight progress towards identifying the genes that underpin Darwin's descriptions of this breeding system.