

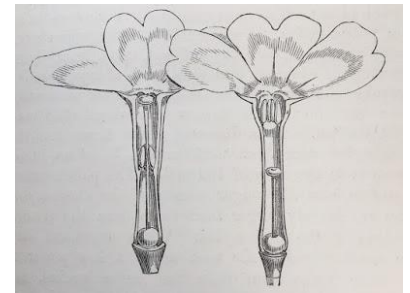
University of Tsukuba
41th PTraD Research Seminar
7th T-PIRC Research Seminar

Date and Time: 2018/5/25 (Fri) 13:30 – 14:30
Place: Gene Research Center, Seminar Room (211)

Primula genomics: new insights on the heterostyly supergene

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Floral heteromorphy (heterostyly) in *Primula* has been studied for over 150 years. *Primula vulgaris* (primrose) plants produce self-incompatible pin- or thrum-form flowers, that present anthers and stigma at reciprocal heights. Darwin concluded that this arrangement promotes insect-mediated cross-pollination; later studies revealed control by a cluster of tightly-linked genes, or supergene, known as the *S* (*Style length*) locus. This phenomenon is thought to have evolved independently in over 28 angiosperm families. Occasionally, plants with self-fertile homostyle flowers occur, displaying anthers and stigma at equal heights; these were predicted to arise through rare recombination events in heterozygous thrum plants. We identified the *Primula vulgaris* *S* locus and showed it is absent from pin plants, and hemizygous in thrum plants (thrum-specific), rather than heterozygous as previously assumed; homostyles result from mutation of *S* locus genes, not recombination as predicted. Our 411 Mb *P. vulgaris* genome assembly covers ~87% of the genome, and is generated from an inbred long homostyle plant with high genome-wide homozygosity. This assembly facilitated our identification of the *S* locus genes and surrounding genomic regions. Using phylogenetic analysis we estimate the origin of the supergene at 51.7 MYA. Further studies indicate conserved hemizygous genetic architecture for the *S* locus in multiple *Primula* species. These findings reveal novel insight into the structure and origin of the *Primula* *S* locus, whilst providing genomic resources for future studies on the evolution and function of heterostyly.

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