

Development of genomic resources for *Fragaria iinumae* – a second diploid ancestor to the octoploid cultivated strawberry

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The cultivated strawberry, *Fragaria x ananassa*, and its immediate ancestors *F. chiloensis* and *F. virginiana*, are octoploids ($2n=8x=56$). The subgenome compositions of these octoploid species have yet to be fully determined. An abundance of evidence indicates that at least one of the octoploids' subgenomes is derived from a diploid ancestor that resembles contemporary diploid *Fragaria vesca*. On this basis, the strawberry genomics community has adopted *F. vesca* as a model species. Transformation systems and linkage maps have been developed for it, and the genomic sequence of *F. vesca* subsp. *vesca* "Hawaii 4" was published in early 2011. In recent years, phylogenetic and other evidence has accumulated implicating another diploid species, *F. iinumae*, as a second subgenome contributor to the octoploid strawberries. Intriguingly, a mitochondrial marker is shared uniquely between *F. iinumae* and all octoploids examined, suggesting that *F. iinumae* may be the source of the octo ploid's mitochondrial genome. We are developing germplasm and genomic resources for *F. iinumae*, including high throughput genomic sequence data, molecular markers, and the first *F. iinumae* linkage mapping population. This map is based on segregation data from an F2 population of 150 seedlings derived from a cross two *F. iinumae* accessions collected in Hokkaido, Japan by Tom Davis and Kim Hummer in 2004. The status of knowledge and resource development in *F. iinumae* will be described.

Identification of self(in)-compatibility genotypes and microsatellite marker based fingerprinting of traditional italian sweet cherry accessions

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Italy is one of the main European sweet cherry producers and it has a rich germplasm, including many minor local varieties that have not been well studied or used in breeding programmes. Sweet cherry is self-incompatible, with few exceptions; its incompatibility is controlled by a multi-allelic S locus, which is gametophytically expressed. The knowledge of S-alleles and cross-incompatibility groups of sweet cherry genotypes and