



## Conference Paper

# Mapping self-fertility for hybrid breeding in perennial ryegrass (*Lolium perenne* L.)

### Author(s):

Cropano, Claudio; Manzanares, Chloe; Yates, Steven; Do Canto, Javier; Boerboom, Nic; Koch, M.; Wolters, Lukas; Lübberstedt, Thomas; Studer, Bruno

### Publication Date:

2019-06

### Permanent Link:

<https://doi.org/10.3929/ethz-b-000353850> →

### Rights / License:

[In Copyright - Non-Commercial Use Permitted](#) →

This page was generated automatically upon download from the [ETH Zurich Research Collection](#). For more information please consult the [Terms of use](#).

# Mapping self-fertility for hybrid breeding in perennial ryegrass (*Lolium perenne* L.)

Cropano C.<sup>1,2</sup>, Manzanares C.<sup>1</sup>, Yates S.<sup>1</sup>, Do Canto J.<sup>3</sup>, Boerboom N.<sup>2</sup>, Koch M.<sup>2</sup>, Wolters L.<sup>2</sup>, Lübberstedt T.<sup>4</sup> and Studer B.<sup>1</sup>

<sup>1</sup>Molecular Plant Breeding, Institute of Agricultural Sciences, ETH Zurich, Universitaetstrasse 2, 8092 Zurich, Switzerland; <sup>2</sup>Deutsche Saatveredelung AG, Weißenburger Str. 5, 59557 Lippstadt, Germany;

<sup>3</sup>Instituto Nacional de Investigación Agropecuaria (INIA), Ruta 5 km 386, 45000 Tacuarembó,

Uruguay; <sup>4</sup>Department of Agronomy, Iowa State University, 716 Farm House Ln, 50011 Ames, USA

**Introduction:** Self-incompatibility (SI) prevents the creation of homozygous parental lines by self-pollination for hybrid breeding in perennial ryegrass (*Lolium perenne* L.). Although SI is highly effective, its breakdown leading to self-fertility (SF) has been reported. Recent research has fine-mapped one major locus conferring SF in a perennial ryegrass population to a 1.6 cM region on linkage group (LG) 5 (Do Canto *et al.*, 2017). Our goal was to confirm, by marker-trait association using genome-wide markers, this previously described locus as being solely responsible for SF variation.

**Materials and methods:** A genotyping-by-sequencing (GBS) library was prepared using 75 individuals from a SF F<sub>2</sub> population described by Do Canto *et al.* (2017). SNPs were called as described in Begheyn *et al.* (2018) using a genome assembly of *Lolium multiflorum* L. (unpublished). SNPs passing a minor allele frequency threshold of 5% with a minimum of 30 genotypes were used for marker-trait association. Kruskal-Wallis was used to detect significant associations (Bonferroni corrected:  $-\log_{10}(P/n) \geq 4.64$ ) between SNPs and the SF phenotypic traits from Do Canto *et al.* (2017). Synteny to *Hordeum vulgare* L. was used to confirm the position of scaffolds harbouring significant SNPs.

**Results:** After filtering, 2,215 SNPs were used for marker-trait association (Figure 1). A total of 44 SNPs were found to be significantly associated with SF. Of these, 37 SNPs could be allocated to genome positions and peaked in close proximity of the SF locus on LG 5.

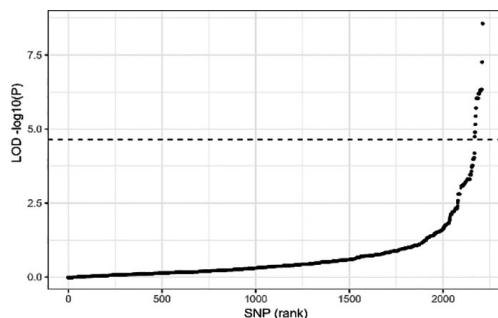


Figure 1. Marker trait association analysis between SF scores and SNPs. x-axis = ranked order of SNPs; y-axis = LOD score; dashed line = significance threshold (Bonferroni corrected: 4.64).

**Conclusions:** The marker-trait association confirmed the presence of one major SF locus on LG 5. Moreover, these data are currently exploited for marker development to further refine the SF locus and identify causal gene candidates.

Begheyn R.F., Yates S.A., Sykes T. and Studer B. (2018) Genetic loci governing androgenic capacity in perennial ryegrass (*Lolium perenne* L.). *G3: Genes, Genomes, Genetics* g3-300550.

Do Canto J., Studer B., Frei U. and Lübberstedt T. (2017) Fine mapping of a self-fertility locus in perennial ryegrass. *Theoretical and Applied Genetics* 131(4), 817-827.