**Optimizing cross efficiency and seed multiplication in faba bean via insect pollination and retrospective genotyping**

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As one of the highest-yielding cool-season legumes, faba bean is a promising crop in temperate climates to help meet growing demand for plant protein. However, faba bean suffers from low yield stability due to poor heat and drought adaptation. Since stress adaptation traits generally have complex inheritance, breeding programs must recombine and select genotypes carrying as many as possible beneficial genome-wide quantitative trait loci from different donors. However, achieving effective recombination for complex traits requires large segregating families, which are difficult to generate in faba bean due to poor crossing efficiency and a low seed multiplication rate. To overcome these bottlenecks, we used bumblebees in enclosed greenhouse chambers for mass crossing among genetically diverse F1 plants. Seeding rates were around seven times higher than hand crossing, enabling generation of large populations of offspring. Subsequently, plants were genotyped using an Illumina 10k SNP chip, and the marker data from parents and offspring allowed us to retrospectively identify the pollen donor of each seed from each mother plant. This allows assignment of every genotyped seed to a family of either F2 siblings from a self-pollinated maternal plant, or to a specific four-way cross combination with known grandparents. Subsequently, all families are advanced to recombinant inbred lines (RIL) via speed-breeding. This procedure enables us to rapidly generate a very large and diverse base population of fully genotyped biparental and multi-parental families as a basis for quantitative genetic analyses and breeding to increase genetic gain in faba bean.