

Genetic mapping of resistance to *Fusarium oxysporum* in tulip

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Fusarium oxysporum is a major problem in the production of tulip bulbs. Agronomic measures such as avoiding wounding, removing diseased bulbs and crop rotation are insufficient to control the disease and therefore the control strategies rely on the frequent use of chemicals. The chemical use causes environmental risks and the prolonged use is likely to lead to fungicide resistance in the pathogen. Breeding for *Fusarium* resistant tulip cultivars is therefore an attractive alternative and a main target for breeding companies. Unfortunately, tulip has a long life cycle (4-5 years) and therefore conventional breeding is a slow process. Marker-assisted breeding has the potential to speed up the breeding process considerably. Obstacles for this approach are the large genome size (1C≈30GB) for which few molecular marker have been published, and the absence of a genetic

map. To remove these obstacles, we constructed the first genetic linkage map for tulip and searched for markers linked to resistance to *Fusarium*. A mapping population segregating for *Fusarium* resistance was genotyped using SNP, AFLP, NBS and SSR markers which were used to generate two parental maps. The mapping population was phenotyped in two consecutive years by soil infection tests, in which the infection degree was scored visually on a 1-5 scale. In addition, we used a GFP (Green Fluorescent Protein) tagged *Fusarium* strain to monitor and quantify the infection on the mapping population using the newly developed PathoScreen platform. We demonstrate that *Fusarium oxysporum* resistance in tulip is a quantitative trait for which five putative QTLs were identified derived from both the resistant and susceptible parent.