

Development of molecular tools for targeted improvement of sainfoin

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There is an increasing interest to extend the range of species used for agricultural cultivation. Sainfoin (*Onobrychis viciifolia*) is, besides being a valuable source of tannins and other beneficial compounds, an attractive option due to its low input requirements and its pluriannual character. However, only few varieties are available. Sainfoin suffers from low yield potential and limited competitive ability when compared to other legumes such as alfalfa. Understanding the genetic control and developing molecular markers linked to traits such as yield, stress tolerance or tannin content will allow for targeted improvement of this promising species.

Aims of the PhD Thesis

- ✓ to develop the first linkage map of *Onobrychis viciifolia*
- ✓ to develop a set of molecular markers linked to agronomic traits
- ✓ to investigate the genetic control of tannin content based on candidate gene and comparative genetic approaches.

Development of segregating mapping populations

Seed from four reciprocal pairwise crosses of single plants from *O. viciifolia* varieties was obtained and germinated in the greenhouse at ART. The resulting F1 populations will be planted in the field and will serve for phenotyping after an adaption period.



Fig.1 a) Maternal plants b) Young seedlings of the F1 mapping families c) Field site at Delley seeds and plants Ltd

First Steps

Genotyping:

Plants will be genotyped using SSR markers and next generation sequencing.

Analysis of marker-trait associations (linkage and QTL analysis)



Phenotyping:

Plants will be phenotyped for traits such as flowering time, growth characteristics and tannin content.

Further Steps

- ✓ Validation of markers
- ✓ Association mapping in collaboration with ESR 6
- ✓ Expression of candidate genes for tannin content

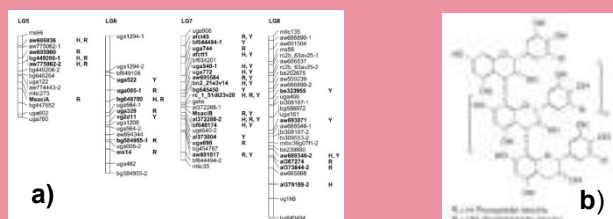


Fig.2 a) Example of a genetic linkage map of *Medicago sativa* L. (Robins 2007)

b) *Onobrychis viciifolia* tannins (Carbonero 2011)