Polymorphism and EST-SSR cross-amplification study on a germplasm collection of *Onobrychis viciifolia*

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1. Abstract

*Onobrychis viciifolia* is an emerging leguminous forage crop, traditionally grown across Europe and North America, where it is used primarily for livestock feed. *O. viciifolia* is also considered an important forage legume due to multiple beneficial properties; however, the knowledge surrounding this species is under developed. We have embarked on an in-depth genetic characterisation of *O. viciifolia* by developing molecular markers and using RNA-seq.

Due to a lack of characterised molecular markers in *O. viciifolia*, we decided to screen a set of EST-SSR derived from Medicago truncatula tested in *O. viciifolia* [1]. From a set of six markers we identified five which were polymorphic across the range of Sanblt et al. ecotypes studied.

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2. Introduction

The decline in the area of *O. viciifolia* and other temperate legumes across Europe since 1950 [2] is particularly reflected in the relative low productivity. However, the interest in this legume has re-emerged due to its notable beneficial properties, including its high-quality nutritional profile, antipollutant compounds, and the low methane emissions. These attributes have been attributed to presence in the foliage of high concentrations of condensed tannins (CT) [3-5].

In order to inform the required agronomic improvement, we developed a genetic characterisation testing the polymorphism and EST-SSR cross-amplification of different markers from *M. truncatula.*

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3. Material & Methods

Seven different accessions of *Sanblt* were evaluated in this study. The lines selected were 3000, 3001, 3002, 3007, 3046, 5075, and 5204 from the *O. viciifolia* germplasm collection at NIAB.

Young healthy tissues were collected with liquid nitrogen and the DNA was extracted using Prep-it kit from GE Healthcare.

We tested six different primers from *M. truncatula* [2]. Using pooled DNA from selected parents per accession, amplified using fluorescent PCR.

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4. Results & Conclusions

From a set of six EST-SSR from *M. truncatula* previously tested in *O. viciifolia*, we found that five of them amplified across the nine pre-existing accessions that were tested. All of primer sets were polymorphic, with the majority showed to be monomorphic/vars. Only polymorphisms, however, the polymorphisms were also identified. Patterns of polymorphism suggest that some ecotypes are more genetically different than others and this will be investigated further.

Continuous efforts will include the screening of cross EST-SSR from different leguminous species, the study of new lines from the extensive NIAB germplasm collection and the development of a cluster distribution of this germplasm collection in order to informs ring breeding programs.

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5. Literature


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