First *de-novo* transcriptome assembly for gene identification, analysis and annotation, transcriptional level study, and molecular marker discovery in *Onobrychis viciifolia*

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**Key words:** de-novo assembly, RNA-seq, *Onobrychis viciifolia*, CLC, AlbySS, Trinity, Velvet/Oases, tannins, molecular markers and annotation.

**Introduction**

*Onobrychis viciifolia* (sainfoin) is an emerging tanniferous leguminous forage crop, traditionally grown as a long term perennial ley across Eurasia and North America, where it is used primarily for livestock feed [1].

Sainfoin has beneficial biopharmaceutical, nutritional and environmental attributes, mainly attributed to the presence of condensed tannins [2].

**Sainfoin benefits**

• Agronomic and environmental: *O. viciifolia* is highly drought tolerant, resistant to most common pests and diseases, and has nitrogen fixing activity in the root nodules [3-5].

• Biopharmaceutical and nutritional: sainfoin has an excellent nutritional profile and anti-parasitic properties attributed to presence of high molecular weight condensed tannins, can reduce methane emissions and improve protein uptake due to ‘rumen-escape’ protein metabolism [6].

*O. viciifolia* could be an alternative to *Medicago sativa* (alfalfa) however its agronomic shortcomings (with 20% lower yields than in alfalfa) allied to little systematic breeding of improved varieties have contributed to low popularity with farmers [7,8]. This project therefore sets out to develop tools to initiate a molecular breeding initiative.

**Objectives:** to i) obtain and annotate the first de novo transcriptome assembly of *Onobrychis viciifolia*, ii) explore principal pathways and their transcriptional levels and iii) produce a large collection of SNPs and SSRs for further mapping analysis.

**Results & Conclusions:** To our knowledge, this is the first comprehensive transcriptome study conducted in *O. viciifolia*. The results headings are:

• Reference assembly/assemblies of 5 accessions (5 methods compared).

• 5 M SNPs + 3,500 SSR – Marker mining.

• Over 98,000 GOs – Annotation and Ontology study.

• RPKM for over 90,000 contigs – Transcriptional level study. Such markers have the potential to be utilized as tools for future molecular breeding approaches in order to improve sainfoin genetic resources.

**Material & Methods:** Fig 5, General Pipeline

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**Fig 1, Sainfoin harvesting**

**Fig 2, SSRs design**

**Fig 3, Expression level study - Metabolism Overview**

**Fig 4, Annotation of the first de novo transcriptome assembly of sainfoin**

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**Bibliography**


