ABSTRACT # 32

METABOLIC PROFILING OF A MUTANT MEDICAGO POPULATION OVER-EXPRESSING ARABIDOPSIS TRANSCRIPTION FACTORS

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Medicago truncatula is the model plant for molecular and genetic studies of legumes, which are important agricultural protein crops. Furthermore, legumes synthesize several unique (pharmaceutical interesting) compounds, such as iso-flavonoids, saponins, triterpenes, alkaloids and phytosterols. In order to study regulation of metabolite biosynthesis pathways, and to generate metabolic biodiversity we produced a mutant population of Medicago. This population was generated by introduction of 500 transcription factors (TFs) of Arabidopsis into Medicago hairy root cultures. Metabolic fingerprints of mutants were obtained using high-resolution accurate mass LC-MS (QTOF Ultima with lock spray source).

The dedicated MetAlign software was used to align all chromatographic mass peaks and to find differences in peak areas in mutants. A small group of mutants has been analyzed in detail for changes in the saponins and flavonoid content by LC-MS (IonTrap), followed by principle component analysis. TF lines showing significant changes in the metabolite profile are re-transformed to verify the authenticity of the TF effect.

We show that untargeted metabolic fingerprinting by LC-MS coupled to MetAlign software is a sensitive and reproducible method to detect metabolic mutants in a large population. The specific effect of TF over-expression in Medicago will be analyzed in more detail by targeted metabolomics.