UNIVERSITY OF GOTHENBURG

Faculty of Science

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Next-generation Molecular Systematics and Evolution

insights into *Medicago*

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Abstract

Evolutionary relationships among species have in recent years been inferred using DNA sequences from specific genes and represented by tree diagrams (phylogenies). However, the signal contained in different genes can produce conflicting sets of relationships – i.e., gene tree incongruence. Incongruence among gene trees in *Medicago* L. (Leguminosae) has been observed in several studies but not yet resolved. This thesis aims to re-examine the existing gene phylogenies, generate new data and apply new methods of analysis in order to achieve a deeper understanding of the causes of incongruence among species of *Medicago*.

A comparison and reanalysis of six previously published gene phylogenies for *Medicago* indicates that different biological processes, such as incomplete lineage sorting, paralogy and hybridisation, intervene simultaneously to produce highly incongruent phylogenetic patterns in this plant genus. In order to discern between these different processes, more genomic data is required, and therefore a new approach, using recently developed sequence-capture techniques, is adopted, resulting in the largest, most widely sampled and comparable set of gene phylogenies generated to date for this genus. Identifying causes of incongruence also requires the development a theoretical framework that would allow for the sorting of these data according to different patterns. A model that takes genomic location into account and uses coalescent simulation to compare gene tree topologies is presented. This model is formulated as a flow of tests that culminate in the sorting of data for the inference of species trees, referred to as principal trees when hybridisation is present.

The data produced and the methods developed are used to investigate the phylogeny of two sub-clades within *Medicago*, the *Medicago murex* clade and section Spirocarpos subsection Intertextae. Additionally, coalescent-based species delimitation methods are used to clarify species relationships. A species phylogeny is produced for the *Medicago murex* clade, confirming the separation between *M. murex* and *M. lesinsii*, two species with different karyotype. The inferred species relationships suggest a double event of chromosome speciation in this clade. Two hybridisation events are shown in subsect. Intertextae, both affecting lineages of *Medicago ciliaris*. The principal trees that represent these events are recovered through species tree inference analysis from data sorted by coalescent-based tests. A case of cryptic allopolyploid speciation is discovered in *Medicago prostrata*, a species with known diploid and polyploid karyotypes. Finally, a chloroplast phylogeny of *Medicago* is presented.

This thesis shows that hybridisation has played an important role in the evolutionary history of *Medicago*, both at diploid and polyploid levels. It provides new insights into the evolutionary history of *Medicago* and shows the importance of hybridisation in the evolution of plant species.

Keywords: phylogeny, incomplete lineage sorting, paralogy, hybridisation, *Medicago*