# BAC-Based Genetic, Cytogenetic and Physical Map of *Medicago truncatula*

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*Medicago truncatula* is gaining wide acceptance as a model for multiple aspects of legume biology and as a platform for comparative genomics in legumes. Recent genetic analysis from our laboratory, and others, indicates highly conserved gene order among the temperate legume species and significant synteny between temperate and tropical legume species. With the recent initiation of a whole genome sequencing project on Medicago truncatula, the information available for comparative genomics among legumes will increase substantially. Here we report on plans and progress in the development of comprehensive physical map for *Medicago truncatula*. The physical mapping activity aims to integrate the genetic and cytogenetic maps of this species, and to provide a rational road map for the ongoing whole genome sequencing effort. Our goal is to fingerprint ~90,000 BAC clones comprising 20X genome coverage. The emerging physical map is anchored to the genetic map at ~300 gene-based PCR markers, where each marker has been converted to BAC clones by means of a PCR multiplex. As a complement to the BAC fingerprint data, we are using PCR-based screening of the BAC library to identify and confirm BAC contigs by means of a sequence-tagged-site approach. Following this strategy, 3,000 ESTs will placed onto the physical map. In addition to facilitating map construction, we anticipate that this information will move us closer to the goal of developing a unified "genetic" map for legumes. Such an approach should also delimit the gene-rich regions of Medicago genome and thereby focus the BAC-based sequencing project ongoing in the laboratory of Bruce Roe at the University of Oklahoma. The overall structure and the progress of the BAC-based genetic, cytogenetic and physical mapping program will be presented. This research was funded by NSF (DBI-0110206) and Korean 21C Frontier Research Program (CG1536).