Phylogeny of Selected Medicago Species Based on rDNA Internal and External Transcribed Spacer Regions and 26S. (C07-campbell113208-Poster)

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Abstract:

Medicago edgeworthii Sirjaev and M. ruthenica (L.) Ledebour, indigenous to China, could contribute genes for stress tolerance to cultivated alfalfa. A phylogenic analysis of these species, eight other Asian Medicago species (lanigera, medicaginoides, monantha, monspeliaca, platycarpa, polyceratia, popovii,and radiata), and M. sativa, was performed based on combined ITS1-5.8S-ITS2, partial-SeqXL, and partial-26S sequences. M. platycarpa, M. ruthenica, M. lanigera, and M. sativa were placed in one major cluster, but M. sativa was distantly related to the other species; M. ruthenica was most closely related to M. platycarpa. In the second major cluster, M. edgeworthii was most closely related to M. radiata. M. popovii was less closely aligned with M. ruthenica than predicted from classical taxonomy. It appears that M. sativa could be more readily crossed with M. ruthenica than with M. edgeworthii.

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