

Community Access to a Barrel Medic (*Medicago truncatula*) Core Germplasm Collection & Its Associated Information

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Barrel medic (*Medicago truncatula* L.) is an autogamous annual legume species native to the Mediterranean. It is a minor crop species but is a model plant for alfalfa, the most important forage legume crop in the world. *M. truncatula* has one of the first fully sequenced genomes and the knowledge gained by researchers, particularly in relation to gene regulation and symbiotic nitrogen fixation, facilitates translational research to improve economically important crop species. In this context, work on genetic diversity is fundamental. In a collaborative effort, a representative nested core collection was developed for *M. truncatula* using genetic data from a large panel of accessions collected in the wild across the species' native range. The full core collection (192 accessions) was also part of a larger sequencing project (HAPMAP) that generated large numbers of publicly available SNP markers. In 2022, the 192 accessions of the core collection were donated to the USDA ARS National Plant Germplasm System (NPGS) for long term conservation, characterization, and distribution. The small initial number of seeds were regenerated to produce enough for distribution. All 192 core accessions plus eight NPGS accessions were field established in 2025. Plants were germinated in greenhouses and later transplanted to the Washington State University Irrigated Agriculture Research and Extension Center research farm in Prosser, WA with two 10-plant replicates in insect proof cages. Since the full core collection was being grown, it was an ideal time to collect phenological, phenotypic and agronomic traits in these diverse accessions. More than 20 traits were measured over the growing season, including time for flower initiation and fruit maturity, plant growth habit and presence and position of leaf markings, as well as fruit characteristics, and both fruit and seed yields. In addition, many high-resolution scanned images of branches, leaves, flowers, pods, and seeds were generated, digitally capturing much of the phenotypic diversity in traits. Phenotypic information is being summarized and analyzed and, along with the high-resolution digital images and the SNP data, is being used in genome-wide association studies. The germplasm is currently available and associated phenotypic trait data will be publicly accessible via the NPGS GRIN-Global database. Ensuring long term availability of this *M. truncatula* core collection and its associated genotypic and phenotypic data will support basic plant science and the legume research community into the future. Any marker trait associations identified could translate into potential breeding advancement in the alfalfa crop. Additionally, the phenotypic data associated with germplasm collections enhances their utility by allowing stakeholders to refine their requests and incorporate the data into their own research.