Genotyping Strategies Targeting Crop Improvement in White Clover (*Trifoilum repens* L.)

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White clover (*Trifolum repens* L.) is an allotetraploid cool-season perennial forage legume species grown in temperate region pastures. Previous studies resulted in the identification of genomic regions or quantitative trait loci (QTL) relevant to morphological and agronomic traits of practical value in white clover that were consistent across multiple field locations and years. Target traits for improvement in white clover include stolon production, increased persistence, leaf size and biomass yield. The objectives of this research were to enhance genotyping capabilities (microsatellites and SNP) in white clover to advance mapping efforts and integrate molecular breeding approaches in the white clover breeding program. We utilized the high resolution melting (HRM) analysis platform for genotyping both SSR and SNP markers in white clover. This approach enables detection of sequence differences in PCR fragments by melting the PCR product and measuring the change in fluorescence as the product melts. The HRM-based genotyping results are consistent with previous SSR genotyping efforts in white clover and are more efficient with sample throughput in terms of allele scoring. Efforts are underway to validate SNP markers targeting transcription factors and candidate genes for key traits in white clover. The genomic resources developed and the enhanced genotyping methodologies will be used to increase the marker density in QTL regions associated with stolon productivity and leaf size, jointly with a phenotype-based divergent selection scheme to enhance persistence and yield in the white clover breeding program.