Demonstration of Cost Effective Marker Assisted Selection for Biomass Yield in Red Clover (*Trifolium pratense* L.) – Part 2: Nested Within-Family Linkage Based Selection

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Many linkage and linkage-disequilibrium based marker assisted selection (MAS) methodologies have been proposed. To achieve success, most require mapping populations and/or very high marker genome coverage. Presented is a MAS scheme that requires no mapping populations or known linkage group configuration. This method can be used at very low marker genome coverage. This MAS requires: 1) individually phenotyped plants, 2) co-dominant markers, and 3) known progeny maternal or paternal parentage at a halfsib level. Knowledge of both maternal and paternal parentage increases potential gains. In diploid systems, each progeny in a halfsib family can receive either one (uninformative) or two (informative) possible alleles from its halfsib parent. In informative cases within each halfsib family, the 'good' and 'bad' allele is determined based on individual breeding nursery progeny plant phenotypes. Individually, markers may appear to provide no linkage information; however, if a collective average rating for each progeny across all markers scored is determined (e.g. 'good' = 3; uninformative = 2; 'bad = 1), useful information can be derived. Since the approach is linkage based, markers even distally located from a QTL on the same linkage group can provide information. Efficacy of the system is demonstrated using population C584-Y-07 presented in poster presentation 'Part 1' (Riday, 2010) along with known progeny maternity and molecular marker inferred paternity, individual progeny phenotypes, and 11 SSR markers. A simple 200 permutation validation approach was used to demonstrate selection gains, with 80% of progeny used in estimation or marker ranking sets, which in turn were used to select within the 20% validation sets (Riday, 2010). Selection gains were observed within maternal but not paternal halfsib families (Fig. 1). This is likely due to larger maternal family sizes (~23) compared to paternal family sizes (~5). Individually, none of the 11 SSR showed significant linkage. Maternal halfsib family selection gains were estimated equivalent to a ~20% r^2 QTL. The one drawback of this system is that for each parent only ¼ of the additive σ^2 is selected on.
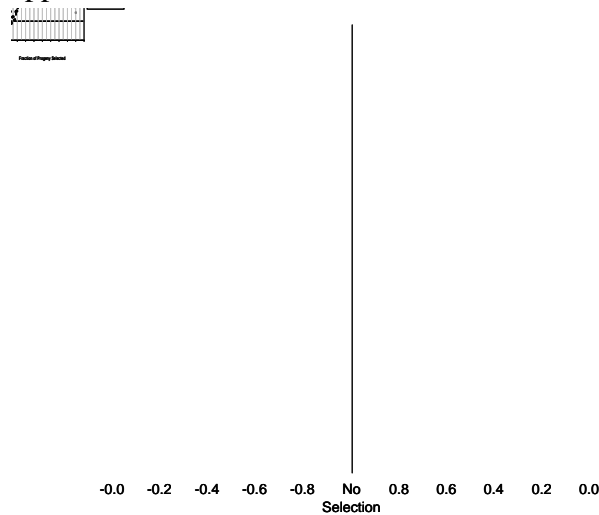

Fig. 1 Maternal and paternal halfsib family nested within-family linkage based selection gains for vigor in red clover (*Trifolium pratense* L.) population C584-Y-07.

Riday, H. 2010. Demonstration of cost effective marker assisted selection for biomass yield in red clover (*Trifolium pratense* L.) – part 1: paternity testing. 42nd NAAIC/ 21st Trifolium Conference, Boise, ID, July 27-30.