

Fig. 1. Comparison of sizes of dry seeds (above) and pods (below) between camelina varieties ‘Suneson’ and ‘Pryzeth’.

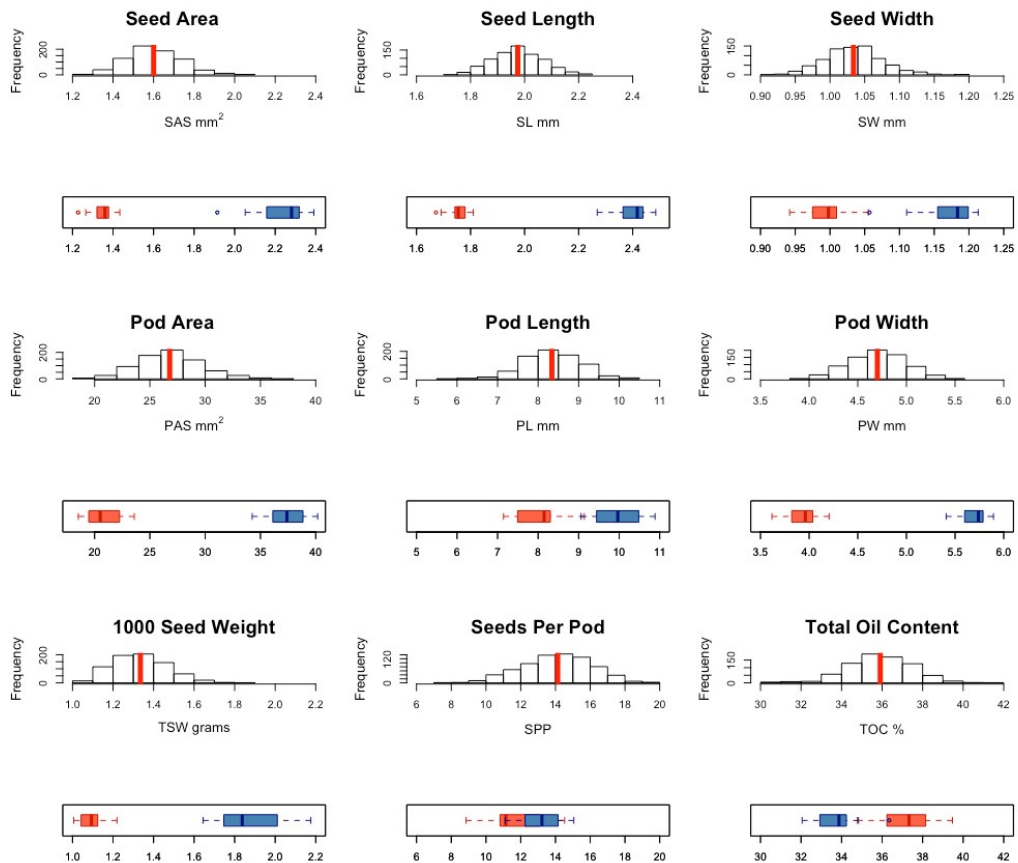


Fig. 2. Phenotypic variations of seed traits in the RIL population. Histograms represent the trait frequency data of the 189 RILs over both years and treatments (n=760). The red line represents the mean of that trait in the population. The two box-plots under the histograms represent the combined data for the two parents over both years and treatments (n=30). Bold lines in the boxes represent mean values and dotted lines show data distribution range of each trait in two parents. Suneson= Red, Pryzeth= Blue.

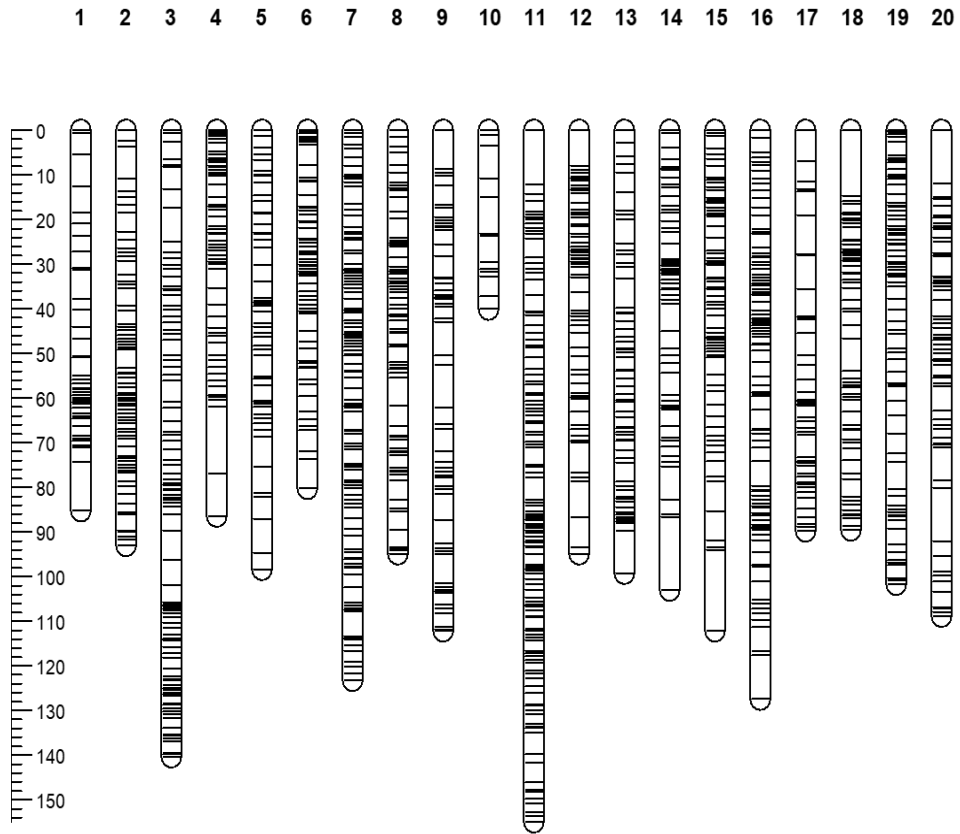


Fig. 3. A genetic linkage map of camelina constructed using the Pryzeth x Suneson population. Each bar represents one group of cosegregating SNP markers showing in bands.

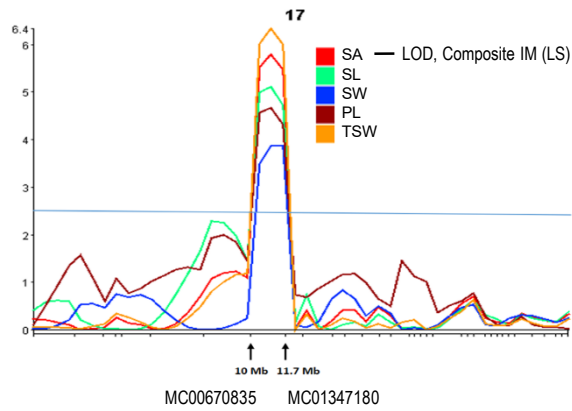


Fig. 4. A major QTL was colocalized for SA, SL, SW, PL and TSW on chromosome 17. The horizontal line indicates the average LOD threshold for significance at the 1% level. Physical locations of flanking SNP markers are indicated by arrows.