

Seed Size in Lentil: iMapping at the U of S

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Introduction

•Seed size is an important quality trait in lentil (*Lens Culinaris* Medic). Seed size decides the type of market class a lentil will belong too. Seed size can also influence cooking and milling qualities.

Objective

•The objective of this study is to evaluate a population segregating for seed size and shape and map the regions of the genome associated with these seed size parameters.

•The outcome of this project could lead development of molecular markers for different seed size parameters which should increase the efficiency of selection for improved seed quality in the breeding program.

Materials and Methods

•A mapping population (LR-18) developed through a cross between a small seeded cultivar (CDC Robin) and a large seeded breeding line (964a-46) was used.

•147 recombinant inbred lines (RILs) were evaluated for seed diameter, thickness, plumpness and flowering time in 2009.

•Grown in a 3-rep test at two locations, SPG and Preston, near Saskatoon in 2009 and 2011.

•Samples from each plot were evaluated for seed diameter, thickness and plumpness. Round hole sieves measured seed diameter and slotted sieves measured seed thickness. Plumpness was determined through thickness/diameter. Flowering time was also evaluated to determine if it has any effect on seed size.

•Join Map 4.0 was used to develop a genetic map consisting of SNPs (LcC and TOG), SSRs and morphological markers. A total of 11 linkage groups were identified.

•MapQTL 5.0 was used for QTL analysis. An LOD threshold above 3.0 was used to declare QTLs.

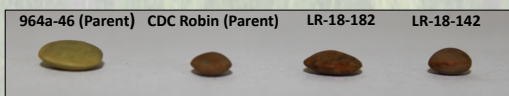


Figure 1. Differences in seed size and shape among parents and RILs

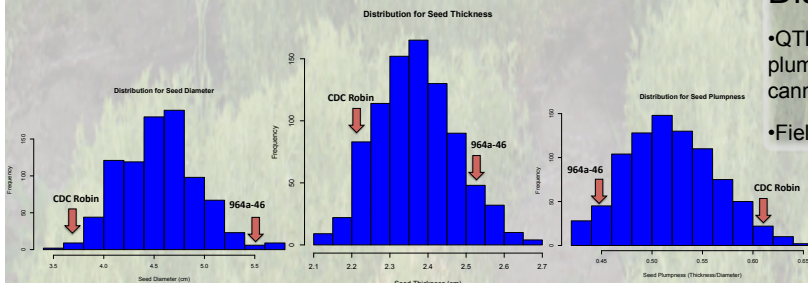


Figure 2. Distributions of three seed size measurements. Parents are labeled with an arrow.

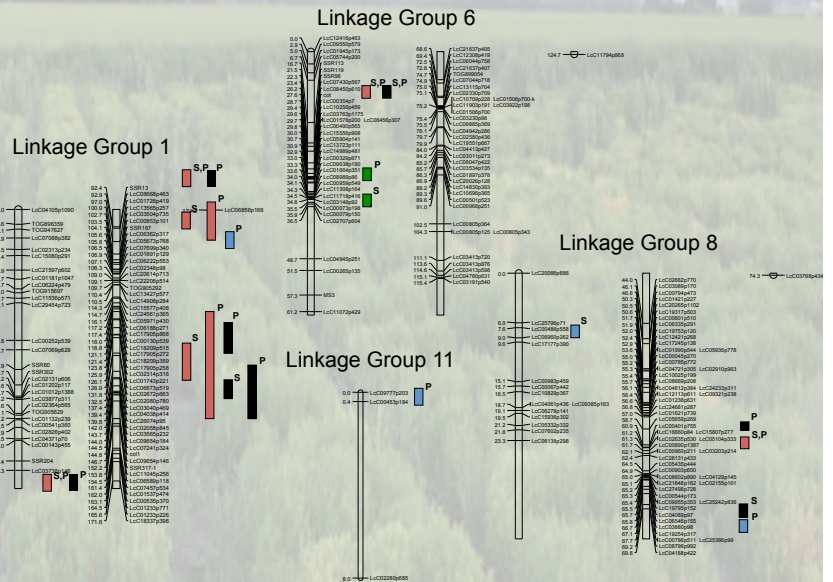


Figure 3. Results of composite interval mapping for 2009. The red bar indicates markers with significant LOD scores for seed diameter. The blue, black and green bars also indicate significant LOD scores for seed thickness, seed plumpness and flowering time, respectively. Above the bars represent which sites the QTL was present for, S for SPG and P for Preston.

Results

•Correlations among traits were measured (Table 1.) All traits showed low correlations, except diameter and plumpness.

•Composite interval mapping revealed QTLs on the linkage groups 1, 6, 8 and 11. For seed diameter and seed plumpness QTLs were located on linkage groups 1, 6 and 8. For seed thickness QTLs were located on linkage groups 1, 8 and 11. Flowering time QTLs were located on linkage group 6.

Table 1. Correlation coefficients for the traits measured at SPG (below diagonal, blue) and Preston (above diagonal, grey)

	Diameter	Thickness	Plumpness	Flowering Time
Diameter				
Thickness	0.36			
Plumpness	-0.91	0.18		
Flowering Time	0.27	-0.12	-0.36	

Discussion

•QTL analysis thus far is showing that traits like seed diameter and seed plumpness are inherited together. This means that either one of those traits cannot be selected independently

•Field trials from two different sites in 2011 are still being phenotyped.

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