

#042

Breeding *Brassica napus* canola by use of *B. oleracea*: Mapping flowering time and biomass traits in the C genome of *B. napus* using a population carrying genome content introgressed from *B. oleracea*

Habibur Rahman
Rick A. Bennett, Berisso
Kebede

University of Alberta,
Edmonton, Canada

Earliness of flowering and maturity are important for spring canola – whether grown under a long-day condition in summer in temperate regions, or under a short-day condition in winter in sub-tropical regions where earliness resulting from photoperiod insensitivity is important. Days to flowering (DTF) show a positive correlation with days to maturity; therefore, selection for earliness of flowering reflects the earliness of maturity. To date, the earliness of *B. rapa* has been exploited to improve the earliness in *B. napus*; however, the early flowering spring *B. napus* canola often produces low yield. Therefore, identification of the genes contributing to earliness without negative effect on seed yield is important. We introgressed earliness from *B. oleracea* into *B. napus*, and identified a QTL on C1 affecting DTF without being influenced by photoperiod and a QTL on C9 affecting DTF under a short-day (10 h photoperiod) condition; in both cases, *B. oleracea* alleles reduced the DTF. The C1 and C9 QTL exerted additive × additive epistatic interaction under a short-day condition. Additional QTL from C2, C3, C6 and C8 affecting DTF were identified; however, none could be detected under all photoperiod and trials. No QTL for seed yield could be detected consistently in the field trials; the C1 QTL allele of *B. oleracea* did not show significant negative effect on seed yield in six of the seven trials, while the C9 QTL did not show any association with yield in all trials. Ten QTL on C1, C2, C6, C7 and C9 affecting root biomass and seven QTL on C1, C2, C4 and C8 affecting aboveground biomass were detected; among these, C2 and C6 QTL alleles of *B. oleracea* increased root biomass. However, none of the QTL could be detected consistently in all trials. Two additive × additive interactions were detected for aboveground biomass; epistatic effects were 2–3 folds greater than the main effect of the QTL implying that gene interaction plays an important role for this trait.

ADDRESS

PLENARY TALKS

ORALS

POSTERS

WORKSHOPS