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Early Assessments on the Feasibility of Selection for Reduced Secondary Dormancy Potential in Annual *Brassica napus*

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PLENARY TALKS

Secondary dormancy, or induced dormancy, is the mechanism underlying the persistence of volunteer canola seed in weed seedbanks. It is also postulated that the high secondary dormancy potential (SDP) could be one of several contributing factors to poor emergence of canola crops across the Canadian prairies. Persistence of volunteer canola is not only a consideration for rotational crops, but is also a threat to subsequent canola crops as volunteers could lead to unintentional stacking of different herbicide-resistance mechanisms, skewing profiles of specialized seed quality traits and maintenance of pathogen populations throughout the rotation. It has previously been shown that SDP is highly heritable in biennial *B. napus*, thus it may be possible to select against SDP in canola varieties. An untested concern associated with this prospect is the impact reduction of SDP may have on seed vigour traits as well as linkage or pleiotropy with desirable seed quality traits. Given this, we initiated a study to: i) assess the range of SDP across a diversity collection of annual *B. napus*, the parental panel for a Nested Association Mapping population, from seed produced under four contrasting environments; ii) examine the relationship of SDP of the seedlots relative to seed vigour and seed quality traits; and iii) perform preliminary genetic analyses for heritability and for major genes controlling SDP by testing for genomic associations. Results have supported our hypothesis of high heritability for SDP in annual *B. napus* with greatest contribution to variability being due to genotypic differences with moderate contribution due to genotype by environment interaction. Fortunately, no relationship was detected between SDP and various assessments of seed vigour including speed of germination. When various seed quality traits were assessed, positive relationships with seed protein and negative with oil content were detected. A much wider range in SDP across the diverse genotypes was found compared to the range previously found amongst spring Canadian cultivars. Pursuing the identification of genes causing extreme high SDP is paramount to provide canola breeders with the tools to select against inadvertent introduction of higher SDP when accessing novel alleles in this diversity collection.

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