B-genome detection and influence in interspecific crosses of *Brassica napus* and *B. juncea*

Chris Schelfhout*[1], Wallace A. Cowling[1,2], Janet Wroth[1]

[1]School of Plant Biology, The University of Western Australia, 35 Stirling Highway, Crawley, Western Australia 6009, Australia, [2]Canola Breeders Western Australia Pty Ltd (same contact details)

We have developed a PCR-based screen from a published cloned *Brassica* B-genome specific sequence. This technique detects B-genome DNA in *B. juncea*, *B. napus*, *B. carinata* and interspecific progeny of *B. napus* carrying B-genome introgressions or chromosomes. There is no reaction with *B. napus*, *B. rapa* or *B. oleracea*, which do not contain the B genome. Interspecific progeny of the cross between canola quality *B. napus* and near canola quality *B. juncea* have been selected for agronomic, quality and disease traits. F_2 and BC_1 progeny were screened using the B genome specific marker. Most of the progeny were canola quality, but over 67% of F2 and 27% of BC1 progeny reacted positively to the B genome marker, and some of these had *B. juncea*-type attributes when tested in the field as F_4 and BC_1S_2 progeny. These *B. juncea*-type traits included yellow seed coats, non-shattering siliqua and blackleg disease resistance. Several F_4 progeny with “normal” *B. napus* morphology also tested positive for the B genome marker. PCR marker amplified products were cloned, sequenced and confirmed to be homologous to the original published sequence. The cloned product can now be used as a hybridisation probe on slot blot membranes to confirm those progeny with putative B-genome introgressions or addition lines. Confirmation of introgressions will be complemented using fluorescence *in situ* hybridisation studies.