

POLLEN FLOW OF *BRASSICA NAPUS* CULTIVAR AND POSSIBLE BREEDING WITH *SINAPIS ARVENSIS*

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Gene flow between crops and wild relatives species has been occurring for thousands of years, but scientific attention on gene flow from crops to wild relatives and other crop populations is more recent, stimulated by concerns about the movement of transgenes. As Genetically Modified Plants (GMPs) might be cultivated and therefore could spread pollen and hybridize with their wild relatives, there is much interest in the extent of sexual compatibility between *Brassica napus* (oilseed rape) and wild *Brassica* species, as it forms spontaneous hybrids with both of its wild progenitor species, *B. rapa* (wild turnip) and *B. oleracea* (wild cabbage).

The objectives of this work were the study of the potential hybridization and gene flow between *Sinapis arvensis* (wild mustard) and cultivated oilseed rape populations in Mediterranean environment. In the selected test areas *Brassica napus* L. var. *oleifera* D.C. (oilseed rape) were cropped and *Sinapis arvensis* was naturally present along the border of the field.

The main wind direction during the time of pollen dispersal was taken into account to install the Sigma-2 pollen samplers (VDI 2007), settled from the border of the oilseed rape cultivated area at increasing distance; the strips "Silkostrip" (Lanzoni srl) for the pollen collection were resting on the bottom of the pollen traps. Pollen species were differentiated on the basis of their morphological and structural characteristics using a light microscopy. Pollen granules were detected up to a distance of 30 m (8 pollen granules/cm²). The highest decreasing rate of the number of pollen granules occurred between 0 m and 5 m remaining nearly constant up to 15 m, and after the value is halved to 8 pollen granules/cm².

Twenty five plants of wild mustard were randomly chosen as mothers and georeferenced. 442 potential fathers of oilseed rape were sampled and their position relative to mothers were registered. About 100 seeds per mother were collected by "Arasystem" (Betatech bvba) traps, and posed in Petri dishes to germinate. To verify possible hybridization between *B. napus* and *S. arvensis* 41 nuclear microsatellite markers, known in literature, were tested. Only 10 primer pairs showed amplification in both species' samples. 2 primer pairs distinguished different alleles between the two species, thus detecting seedlings product of hybridization. Two oilseed rape cultivars were identified. In both cultivars (cv1 and cv2) the first locus had two allelic variants in homozygosis and in heterozygosis. The second locus was monomorphic in cv1, while in cv2 presented two allelic variants in heterozygosis. The same analysis revealed that *S. arvensis* was homozygote at the first

locus for one allelic variant and at the second locus for two allelic variants. Parentage analysis, carried out on three offspring, revealed the presence of breeding, self-breeding and hybridization. Both M3 and M10 (*S. arvensis*) hybridized with cv2, as the offspring showed heterozygosity at the second locus with an allelic variant of oilseed rape.

If GM oilseed rape is to be grown, the possibility of its modified trait being transferred to *S. arvensis* needs serious consideration as the species are widespread.