

## **POLLEN MEDIATED TRANSGENE FLOW IN *LACTUCA SATIVA* AND *ZEA MAYS* UNDER FIELD CONDITIONS**

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Transgenes may spread in the environment through seed or pollen. Proper agronomical practices can easily reduce seed dispersal, whereas pollen dissemination is hard to control. The factors influencing the formation of pollen mediated hybrid genotypes (transgenics/non transgenics) are : a) the ability of donor species to make fertile and viable pollen; b) the type of sexual reproduction; c) the efficiency of pollen dispersal (wind, insects); d) the synchronicity of flowering time; e) the competition among pollens of different origins; f) the morphological and genetic sexual compatibility; g) the distance among plants; h) the amount of pollen produced by donor plants and the wideness of receiving populations; i) some environmental factors (temperature, wind, local vegetation, site topography, etc.). Moreover, the evolutionary differences characterising the species concept in plants define three main levels of possible gene flow in crops: 1) within the same species; 2) within strictly related ones; 3) with parental ancestors (where they are present as weeds). All together, these parameters strongly determine the real chance to produce hybrids.

New molecular tools to minimize transgenic pollen dispersal and avoid undesired genetic contaminations among crops have been developed and are under current tests. However, nowadays to perform the coexistence practices, it is necessary to sharply establish isolation distances between transgenic and non transgenic crops through a case by case experimentation. Although these distances were already considered for several crops so as to maintain constant the genetic structure of populations in breeding programs, confirmations with modern molecular tools are still necessary.

We carried out experiments with two crops grown in open field: the lettuce (autogamous) and corn (allogamous). The presence of transgenes was detected by PCR technology in the progeny of the receiving plants placed at increasing distance from donor transgenics.

In lettuce, the gene flow from transgenic donor plants (grouped in a central island) to non transgenic ones was: 0,17% in the progeny of plants sited at the immediate borders, 0,024% and 0,012% in those at a distance of 10 and 20 metres, respectively. In corn, the gene flow from transgenic to non transgenic populations was 2.5% at 10 m, 1% at 40 m, and 0.5 % at 60 m. No transgenic individual was scored in the progeny of plants sited at 80 m from the donor group.

*The results of this work have been published in “Biodiversità e organismi geneticamente modificati” 2004, Claudia Sorlini Editor, “Accordo di programma tra il Ministero dell’Ambiente e della Tutela del Territorio e il Consiglio Nazionale delle Ricerche”. The volume may be requested to Dr Rosanna Godi CNR-DAST, P.le A Moro n.7 00185 Roma.*