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SHORT COMUNICATION

Quantification of pollen mediated gene flow in maize

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One approach to ensuring coexistence of genetically modified (GM) and conventional maize (Zea mays L.) is the understanding of maize pollen dispersal in the atmosphere in order to quantify the potential contamination of non-GM maize due to pollen-mediated gene flow from GM maize [1, 3, 4, 5].

For this purpose our experiments were conducted in 2008 and 2009 in two different cultivation systems: experimental fields and comercial cultures.

The experimental fields were developed by Monsanto Company as follows: a plot of GM corn (300 x 250 m), surrounded by conventional plants - 36 rows on each geographical direction. The cobs were sampled from each of the sixth rows (6 samples for each geografical direction).

The comercial cultures were located in pedo-climatic conditions favourable for the maize cultivation, in South (Calarasi county), East (Braila county) and West (Timis county) of Romania. In 2008, the cobs were sampled from the rows 3, 9, 12, 18, 24 and 71 (50 m), counting from the contact between the two types of maize, on the dominat wind direction, according to a precise scheme.

In 2009, the cobs were collected only from one farm (Calarasi county), following three sampling schemes, from the refuge rows 43, 46 and 50. It was followed the methodology elaborated by the Co-Extra project, developed in FP6 program.

Material and methods

First the corn seeds were grinded, the flour was homogenized and then the analytical samples were prepared (100 mg for each sample).

The DNA was extracted using CTAB method. The primers ZEIN 3 and ZEIN 4 specific to the maize zein gene was used to confirm the presence and quality of DNA extracted from the corn samples. If an intact and amplifiable extracted DNA was present, a band of 277 bp was visualized.

Then, for GMO screening the 35 S promoter was identified as target sequence. For its specific detection, primers mg1 and mg2 were used. The expected amplicon is a 401 bp fragment where the primers have been positioned in the corresponding region of the CaMV 35S- hsp 70 intro sequence.

Once a sample has been found to be positive for GM events the quantitative reactions were performed. As MON 810 specific target a 92 bp fragment of the single copy DNA integration-border region of the genomic sequence and the inserted sequence element originating from CaMV (35S promoter) is amplified in TaqMan PCR, compared with a reference gene [2].

Results and discussions

According to the European Union Regulation, any product with a GM content higher then 0,9% have to be labeled as genetically modified, therefore this threshold was taken into account when the coexistence results were evaluated.

For the experimental fields the GM content in the conventional maize was different depending on the geographical direction. The average distance, where the GM content was less then 0.9% for all of the fourth directions was 20 m in 2008 and 25 m in 2009.

The samples collected from commercial cultures in 2008, from two different locations – Chiciu (east) and Chirnogi (south) pointed out a lower content of GM in the refuge, the distance necessary to decrease the percent below 0,9% being 8 m.

The experiments performed in 2009, when the cobs were collected following four sampling schemes showed an average content of 0.47%, for the rows 43, 46, 50 (30m – 35m). From 11 samples, only two showed a higher content, probably because a sampling contamination.

The results obtained in all of the experimental systems pointed out a decreasing of the GM contamination if the distance from the GM source is higher. Comparable results were obtained in both experimental and comercial fields, thus a 35 m distance seemed to be enough as a spatial isolation area for comercial cultures.

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