GENERATING A POLLEN FUNCTIONAL MAP USING OAT-MAIZE ADDITION LINES


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Even though pollen is a rather simple two- or three-celled organism, the construction of a functional male gametophyte requires the coordinated activity of a large pool of genes. Although gene sequences and expression data are rapidly being accumulated, constituting a valuable source of information that should be exploited to integrate genetic maps with functional information, only about 2900 maize EST contigs (TC) out of a total of approximately 29400 have been mapped so far onto existing linkage maps. The recent development of oat-maize addition lines has supplied a shortcut to the creation of maize functional maps, avoiding the identification of sequence polymorphisms and the use of large segregating populations. In the present paper we report the use of oat-maize addition lines for mapping 1000 maize pollen EST contigs. The strategy used is based on PCR amplifications performed on DNA derived from oat-maize addition lines corresponding to the 10 maize chromosomes. The analyzed EST contigs, retrieved from the TIGR database, have been selected according to the presence of at least one EST derived from a pollen cDNA library. Map position was unavailable for all ESTs but one. Using the same standardized PCR conditions for all primer pairs, it was possible to assign about 57% of the TCs to specific maize chromosomes. Important information concerning gene duplication and chromosomal distribution were obtained. Those results represent a good starting point in the construction of a pollen functional map and they will certainly be very useful for the identification of candidate genes underlying mutants affecting viability and functions of the male gametophyte. Furthermore, those results could contribute to the assembly of sequence data, produced in the maize sequencing project, by identifying overlapping BAC clones and resolving alignment conflicts and doubts. Finally, it is currently under development the analysis of radiation hybrid lines obtained from the single oat-maize addition lines, to obtain finer chromosomal localization of the EST contigs.