

THE IDENTIFICATION OF DIFFERENTIAL cDNA CLONES FROM TWO FLORAL LIBRARIES IN CUCUMBER *CUCUMIS SATIVUS* L.

MAGDALENA EWA KOWALCZYK, EWA URBAŃCZYK-WOCHNIAK
and ZBIGNIEW PRZYBECKI

Department of Plant Genetics, Breeding and Biotechnology, Warsaw
Agricultural University – SGGW, Nowoursynowska 166, 02-787 Warsaw
E-mail: kowalczykm@alpha.sggw.waw.pl

Numerous experiments were performed to isolate the genetic factors of sex determination in flowering plants. Cucumber is a monoecious species in which sex expression was extensively studied. The main genetic factors responsible for sex determination have been described but the mechanism of their action remains unexplained. In this study we attempted to find clones from two floral cDNA libraries which can be connected with sex in cucumber. Two pairs of nearly-isogenic lines, gynoeious GY3 (FFMMGG) versus hermaphrodite HGY3 (FFmmGG), and monoecious B10 (MMffGG) versus gynoeious 2gg driver (MMFFgg), were used to isolate clones from floral cucumber cDNA libraries. To obtain differentially expressed clones, we performed differential screening of two cDNA libraries: GY3 (tester) which was screened using sscDNA HGY3 (driver); and B10 (tester) which was screened using sscDNA 2gg (driver). 454 clones from the floral cDNA GY3 library and 478 clones from the cDNA B10 library were isolated. The clones were subcloned. PCR reactions with plasmid DNA and primers designed on the basis of vector sequence were performed. Amplifiable inserts were used as probes in Southern-blot hybridization. We performed a bulked segregant analysis with DNA from four parental lines – GY3, HGY3, B10, and 2gg – and F₁ and F₂ crosses in order to check the segregation of previously isolated clones. The results of RFLP analysis with 20 representatives of groups showed no clones which cosegregate with sex in cucumber. These 20 clones were sequenced. Two of them show similarity to plant proteins of know function: chaperonin chain precursor and dehydrogenase 2-oxoglutarate. Five did not show any similarity to known protein sequences existing in data bases. The rest of them show similarity to putative plant proteins or to prokaryotic proteins.