F217 무릇(*Scilla scilloides* complex) 게놈의 유전적 분석

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무릇에서 A(X=8)와 B(X=9) 게놈 간의 상조성과 게놈 조성에 따른 유전적 차이를 알아보기 위하여 AA(2n=16), BB(2n=18), AABB(2n=34) 게놈 식물을 재료로 단백질, 동위효소 및 PCR을 이용한 RAPD 분석을 수행하였다.

단백질의 전기영동에서는 세 게놈 유형에서 차이를 보이지 않았으나, esterase, catalase, acid phosphatase, peroxidase에서는 게놈 간의 차이를 관찰할 수 있었다. Esterase에서 A게놈의 특징적인 band가 관찰되었으며, catalase는 세 게놈에서 모두 동일한 band pattern이 관찰되었다. Acid phosphatase는 두 개의 band가 세 가지 게놈에서 모두 공통으로 나타났고, AA 게놈에서 특징적인 band가 나타났다. Peroxidase에서는 BB게놈에서 특징적인 band가 관찰되었다. Random primer 이용한 RAPD 분석에서는 10개의 primer 중 #1, #13, #15에서만 특이한 band pattern이 관찰되었다.

F218 Identification and Clonning of Ripening-related Messenger RNAs from Tomato by PCR-based Differential Display

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Fruit ripening represents a model for developmental regulation unique to plants. Identification of the genes whose expression patterns are correlated with fruit ripening represents an important avenue for elucidating the genetic regulation of this developmental process unique to plants. Although a number of ripening related genes have been cloned on the basis of differential expression in ripening versus unripe fruit, none have been isolated using a PCR based strategy targerting both rare and tightlyregulated messenger RNAs. We have applied the PCR-based differential display technique to simultaneously compare messenger RNAs representing different stages of fruit maturity. DNA free total RNA was utilized as template for synthesis of first strand complementary DNA using each of 12 possible 5′-T11XY-3′ anchor primers where X=A, C, or G and Y=A, C, G, or T. PCR products of complementary DNA generated by the combination of a upstream random primer and a downstream anchor primer were displayed on 6% polyacrylamide-urea gels. Several amplification products specific to ripe fruit cDNA were isolated directlyfrom display gels and cloned to test for ripening-related gene expression as hybridization probes in RNA gel-blot analyses. We are screening more primers to develop a largecollection of additional ripening-related genes, and attempting to develop this tool to screen for and isolate rare ripening-specfic mRNAs which may have been missed in previous differential screens