F111 A Split hand and split foot(*SHFM3*) gene is closely linked to D10S577 in a Korean family.

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Split-hand and split-foot(SHSF) is a human limb malformation characterized by absent central digital rays, deep median cleft, and syndactyly of remaining digits. The disorder is genetically heterogeneous. Three disease loci have recently been mapped to chromosomes 7q21(*SHFM1*), Xq26(*SHFM2*), and 10q25(*SHFM3*), but the causative genes are still unknown. In the present study, we report the mapping of the second autosomal SHSF locus to 10q24-25. A Korean SHSF family was tested for 4 marker loci mapped to the 10q24-25 region. It was found that the causative gene for Korean SHSF was closely linked to D10S577 resulting in the maximum lod score of 1.15 at a recombination fraction of zero. These results strongly suggest that the polymorphic marker D10S577 allows the prenatal diagnosis of SHSF and is a useful marker to identify the causative gene(s) for SHSF.

F201 **Partial cloning of cytokinin-induced genes from Maize cotyledons**

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Cytokinins are important growth hormones that control the proliferation and differentiation of plant. In the maize cotyledons that was treated with 10^{-4}M benzyladenin(BA), a synthetic cytokinin, we found eleven different cytokinin-induced DNA fragments by differential display RT-PCR and these DNA fragments were inserted into *Xho*I/*Xba*I site of pBluescript SKII(+). Two of them are named CI1 and CI2, and each size was about 300 bp. From the result of Northern hybridization, each mRNA of CI1 and CI2 was respectively about 3.1 Kb and 3.0 Kb. Compared with negative control, cotyledon that was treated by water, the amount of each CI1 and CI2 mRNA was approximately increased in BA-treated maize cotyledons. The mRNA level of CI1 was increased within 4hr after BA-treatment but CI2 mRNA was increased within 1hr. Now we are screening the full cDNA of CI1 and CI2 and studying expression pattern of CI1 and CI2 gene in different tissues.