

D-D2-03

Experimental Design of cDNA Microarray

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Balanced factorial designs are introduced for cDNA microarray experiments. Single replicate designs obtained using the classical method of confounding are shown to be particularly useful for deriving suitable balanced designs for cDNA microarray. Classical factorial designs obtained using methods other than the method of confounding are also shown to be useful. Two color cDNA microarrays are now extensively used to study relative expression levels of thousands of genes simultaneously across biological samples.

Although experimental designs were developed by Shah(1960) and Kshirsagar(1966) mainly in the context of agricultural experiments, factorial designs have been found to be useful in other settings as well. The purpose of this paper is to provide designs for cDNA microarray experiments. Since two experimental conditions are hybridized on each microarray slide, the arrays form blocks of size two. However, loop designs become inefficient for larger number of treatment combinations.

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Development of SNP DNA Markers Based on Soybean Mutants from a Gamma Mutagenesis

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Cultivated soybeans have been reported to have one SNP per 250-300bp and their total number of SNPs is estimated to be a maximum of 5 million in a soybean genome. Advantages of an SNP marker include its redundancy in a whole genome and relatively low mutation rate (10^{-8}) when compared to 10^{-3} in an SSR (simple sequence polymorphism) marker, which allows for a more reliable SNP application. The objective is to develop locus-specific SNP markers from a mutant pool of soybean to detect soybean mutants at a molecular level. A total of thirteen soybean parents were irradiated with a gamma ray from 200 to 250 Gy, from which 180 mutants were selected for a sequence comparison. A core set of 23 SNPs which were unigene-based and evenly spaced over the soybean genome was used to amplify the SNP-containing genomic fragments. The average size of the amplified regions was 750bp. A total of 30 SNP markers were detected, and these SNPs were located on 18 linkage groups. Types of SNPs were classified into 7 groups, encompassing A/-, A/G, A/T, C/G, C/T, G/T, and T/-. Results indicated that the identified SNPs were genotype-specific. These newly identified SNP markers based on the soybean mutants derived from a gamma radiation can be applied to a parent identification as well as an examination of a mutation type and its frequency.

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