Chromosomal Distribution of Maize Repetitive Sequences. (C07-odland180617-Oral)

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Abstract:

Microarray technology used in conjunction with labeled DNA from oat-maize addition (OMA) lines enable chromosomal analysis of the organization and distribution of maize repetitive elements. Each OMA line contains an individual maize chromosome allowing for an analysis of its composition. The probes in this research were specifically designed to detect unique motifs of repetitive sequences or whole elements. This microarray technology is a fluorescence comparative assay utilizing differently labeled genomic DNA from OMA lines hybridized to immobilized probes. Target sequences are quantified for their relative abundance per chromosome. In addition, fluorescence in situ hybridization (FISH) is used to show the physical distribution of the major elements along a maize chromosome. Microarray and FISH techniques together elucidate specific repetitive elements within a maize chromosome, clarify genomic organization, and can reinforce chromosome duplication models. This work is based upon work supported by the National Science Foundation under Grant No. 0110134.

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Presentation Information:

Presentation Date: Tuesday, November 12, 2002

Presentation Time: 9:15 am

Keywords:
Maize, Repetitive elements, Microarrays, Chromosomal distribution