Physical map of the soybean genome. (C07-shultz161049-Poster)

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Abstract:

A physical map derived from BACs was built from 86,386 fingerprint images. Clones are from five libraries; 'Forrest' Hind III (30,720, mean insert 125 Kbp), BamHI (20,736, 134 Kbp), EcoRI (30,720, 157 Kbp), Williams 82 Hind III and Fairbault Eco RI libraries (3,384, 145 Kbp). There are 370 SSR anchors for Forrest, 267 SSR and 105 RFLP anchors for Williams 82 and Fairbault. Anchored BACs have been end sequenced. FPC automatic assembly created 5,597 contigs. The contigs were redundandant as they had 396,843 bands and spanned 1,667 Mbp. About 10% of contigs contained false merges due to clone contamination. Manual editing 81 linkage group G contigs resulted in 10 large contigs encompassing 50 Mbp. Therefore, a contig map with more than 95% of the soybean genome in 200-500 contigs will be built by the end of 2002. A minimally overlapping clone tile of 13,110 BACs is available for efficient STS mapping, genome sequencing and marker development. Integrating ESTs identified several gene rich islands. From 512 Kbp of genomic sequence mean predicted gene density was 1 gene per 7.2 kbp, The physical map can be viewed at www.siu.edu/~pbgc.This work was supported by NSF project #9872635.

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