A study of DNA discontinuities in Sacchromyces cerevisiae cells

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Summary

By the colony-forming test, I confirmed that the chromatin fragmentation phenomena observed reflect features of ~ 100 % viable, non-apoptotic cells.

20-200 kb fragmentation of agarose embedded deproteinized *S. cerevisiae* and *S. pombe* chromatin derived from logarithmic or stationery cultures were observed after S1 nuclease digestions and urea/heat- or alkaline denaturation, establishing that there are ss discontinuities marking loop-sized fragments in the genome of both yeast strains.

I have not determined differences in the DNA fragmentation patterns of cells synchronized in G1-, S- or G2 phases.

I have established that the loop-sized fragmentation can be detected in all of chromosomes of *S. cerevisiae* or *S. pombe* after S1 nuclease digestions and urea/heat-denaturations.

Nicks and ARS sites exhibited an overall co-localization on chromosome I of *S. cerevisiae*.

The ~1.5 Mb rDNA cluster containing 100 – 200 units of 9.1 kb showed loop-sized fragmentations similar to total DNA, i.e. nicks occur in every 11. unit on the average.

The nicks in the rDNA units were mapped by Southern blotting using rDNA specific probes. One of the nicks coincides with a region of RFB.

I have developed a new method called “Ab-Southern” to detect discontinuities and RNA/DNA hybrids in DNA molecules.

New gel electrophoretic and flow-cytometric microbead assays have been established as part of my Ph.D. work.

Kulcsszavak: élesztő, kromatin, fragmentáció, rDNS

Key words: yeast, chromatin, fragmentation, rDNA