# Fluorescence *in situ* hybridization for physical mapping in plant genome

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Gall and Pardue in 1969 described the hybridization of radioactively labeled rRNA to tissue squashes allowing the *in situ* visualization of the complementary sequences, the rDNA, within cells. Since then, *in situ* hybridization has been further developed and widely used for the detection of DNA or RNA sequences. For about two decades, delineation of specific chromosomal sequences was performed using radioactively labeled probes. However, since the development of procedures for non-isotopic labeling of nucleic acids in the early 1980s, fluorescence *in situ* hybridization has become increasingly popular. The reasons accounting for this development, such as increase in speed, sensitivity, signal resolution and long-term storage of labeled probe, has been review multifold. FISH techniques have opened new possibilities for high-resolution genome mapping. Effective utilization of these techniques for the rapid orientation and ordering of adjacent and overlapping probes as well as for the characterization of long-range genomic contigs would facilitate physical mapping and positional cloning efforts. The simultaneous detection of hybridization signals of several probes using fluorescent labels with different colours has made FISH a practical tool at multiple stages of various mapping projects. GISH technique allows a detailed description of the genomic composition of the hybrids. GISH technique is powerful for information on genomic relationships of the parental species involved and the study of morphology and behaviour of alien chromosomes in backcross derivatives at mitotic and meiotic stages. Plasmid-, phage-, cosmid-, YAC- and BAC-clones are frequently used for the analysis of single loci. A high percentage of chimeric clones in a genomic library, such as that observed in many YAC libraries, complicates map construction considerably. FISH analysis provides a rapid method to determine the chimeric status of a genomic clones of BAC.

Genome and chromosome analyses in plants using FISH and GISH methods are discussed. The results of FISH and GISH obtained from *Brassica campestris* var. *pekinenesis, Gentiana scabra* var. *buergeri, Scilla scilloides* Complex and *Nicotiana* tabacum are demonstrated. These results suggest that FISH will become an important addition to the effort to physically map many crop-species genomes and may help to revolutionize the field of plant cytogenetics.