



Use of molecular cytogenetic methods in Oilseed Rape (*Brassica napus*) breeding

Rod SNOWDON, Wolfgang KÖHLER, Wolfgang FRIEDT - Institute of Crop Science and Plant Breeding, Justus-Liebig-University

Until the last decade the major tool for cytogenetic analyses in Brassica was light microscopy to investigate meiotic chromosome pairing, and in fact in many cases this still remains the most powerful tool available to investigate chromosome and genome homologies and interactions. Investigations of Brassica mitotic chromosomes are limited by their small size and scarcity of useful cytogenetic landmarks, and because of this it is difficult or impossible to identify Brassica chromosomes using traditional cytological techniques. Today, fluorescence in situ hybridisation (FISH) techniques offer the potential not only for more reliable chromosome identification in Brassica, but also in terms of the information they might be able to offer regarding the integration of genetic and physical maps, for ordering molecular markers and measuring physical distances, and for structural and functional chromosome analysis. We have had particular success in the use of genomic in situ hybridisation (GISH) for the characterisation of introgressions of novel germplasm from wild crucifers into oilseed rape chromosomes. Interspecific hybrids between *B. napus* and *Raphanus sativus*, *Sinapis arvensis*, *Crambe abyssinica*, *B. juncea* and *B. nigra*, respectively, have been used to develop chromosome addition and introgression lines exhibiting traits of agronomical interest including novel pest and disease resistances and improved seed erucic acid content. GISH on mitotic and meiotic chromosome preparations can add to the efficiency of backcrossing programs and detect intergenomic recombinations that potentially lead to translocation of desired genes from the wild species into the crop genome.