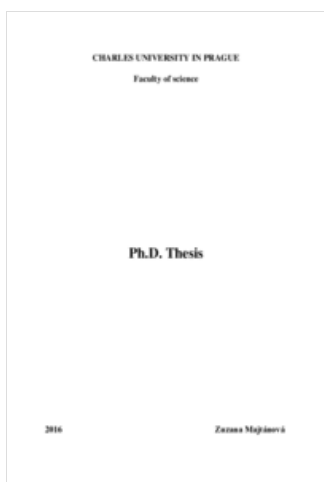


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Molecular cytogenetics of selected actinopterygian fishes: insight from repetitive sequences to whole genome analyses

Molekulární cytogenetika paprskoploutvých ryb: od repetitivních sekvencí po analýzu celého genomu

dizertační práce (OBHÁJENO)



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cytogenetic analysis of genetic materials possible. It is very difficult to follow gene transfer in different genetic lines carrying wheatgrass chromosomes or chromosomal segments in a wheat background because of the lack of molecular and cytogenetic markers. The aim of the present study was to set up detailed FISH karyotypes for three diploid wheatgrass species and. The FISH analysis of *P. spicata* using repetitive DNA revealed highly specific labelling patterns for all the S genome chromosomes. The signal of the 45S rDNA probe on the A. For FISH analysis, epifluorescence microscopes with specific filters and for identifying fluorochromes, a charge-coupled device (CCD) camera that captures the images were needed. A huge range of probes can be used for the identification of the chromosome abnormalities, which includes whole-chromosome painting probes, chromosome-arm painting probes, repetitive centromeric, subtelomeric and locus-specific probes [24]. First, FISH probes obtained chromosome flow sorting [25] or microdissection [26] using universal degenerate oligonucleotide-primed PCR (DOP-PCR) [26]. The m-FISH or the SKY is the best molecular cytogenetics choice to identify these CCRs. 8. Oncogenic amplifications. Amplification refers to the increasing copy number of a gene. Molecular cytogenetics combines two disciplines, molecular biology and cytogenetics, and involves the analysis of chromosome structure to help distinguish normal and cancer-causing cells. Human cytogenetics began in 1956 when it was discovered that normal human cells contain 46 chromosomes. However, the first microscopic observations of chromosomes were reported by Arnold, Flemming, and Hansemann in the late 1800s. Their work was ignored for decades until the actual chromosome number in humans was Whole-genome duplication in teleost fishes and its evolutionary consequences. *Mol Gen Genomics*. 2014;289:1045–60. Molecular cytogenetic study of genome ploidy in the German mirror carp *Cyprinus carpio*. *Fish Sci*. 2014;80:963–8. Tautz D, Renz M. Simple sequences are ubiquitous repetitive components of eukaryotic genomes. *Nucleic acids Res*. 1984;12:4127–38. Nonetheless, more recent robust molecular phylogenetic analyses indicated that Erythrinidae and Hepsetidae are in fact not closely related to Lebiasinidae; instead, the close relationship between Lebiasinidae and Ctenoluciidae was demonstrated (Arcila et al., 2017; Arcila et al., 2018). Preparation of FISH Probes Derived From Repetitive Sequences. In many fish groups with taxa of the small-sized body, the lack of cytogenetic data impairs the knowledge about the chromosomal relationships and it prevents to make any meaningful inferences about the impact of chromosome dynamics on their evolutionary history (Liu et al., 2012).