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Abstract Book

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on agarose gel, where PCR amplification of the CHD gene produces a double (ZW) and single (ZZ) bands in females and males, respectively. In our laboratory we have implemented method of capillary electrophoresis for identifications the bands. 69 individuals were tested from genera Columba and 45 individuals from genera Aprosmictus, Cacatua, Myiopsitta, Platycercus, Polytelis and Psittacula. Genomic DNAs were extracted from feathers and buccal swabs. Sex-specific products of CHD gene was amplified using the QIAGEN Multiplex PCR and specific pair primer. One of pair primers were labelled with fluorescent dye 6-FAM, the amplified products were separated on 3100xl Genetic Analyzer and genotyped using GeneMapper software (Applied Biosystems). Variation in the intronic sizes of CHD-W and CHD-Z gene was detected by capillary electrophoresis. Two different picks of PCR products was produced from CHD-W and CHD-Z genes in females and one pick of PCR products from CHD-Z gene in males. The tested material had a high genetic diversity, were identified 5 gene variants in the range of 268–320 bp.

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Development of a porcine chromosomal translocation screening device reveals errors in the pig genome assembly

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Balanced chromosomal aberrations have been shown to affect fertility in most species studied leading to hypoprolificacy (e.g. reduced litter size) in agricultural animals such as pigs. With an increasing emphasis in modern food production on the use of a small population of high quality males for artificial insemination, the potential economic and environmental costs of hypoprolific boars, bulls rams etc. are considerable. There is therefore a correspondingly increased need for novel tools to facilitate rapid, cost effective chromosome translocation screening. This has previously been achieved by standard karyotype analysis, however this approach relies on a significant level of expertise and is limited in its ability to identify subtle, cryptic translocations. To address this problem we developed a novel device and protocol for translocation screening using subtelomeric probes and multi-target fluorescence in situ hybridisation. Probes were designed using BACs from the subtelomeric region of the p-arm and q-arm of each porcine chromosome. They were directly labelled with FITC or Texas Red (p and q-arm, respectively) prior to application to a "Multiprobe" device, thereby enabling simultaneous detection of each porcine chromosome on a single slide. Initial experiments designed to isolate BACs in subtelomeric regions led to the discovery of a series of incorrectly mapped regions in the porcine genome assembly which will be rectified in future genome builds, therefore highlighting the importance of accurate physical mapping of newly sequenced genomes. A cryptic translocation that previously challenged detection by standard karyotyping alone was also identified using this approach. The system developed in this study therefore allows for robust and comprehensive analysis of the porcine karyotype as an adjunct to classical cytogenetics. Proof of principle established in this study has led to the development of a similar device for the identification of translocations in cattle with work currently underway to optimise this as a tool for routine screening of bulls.

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Origin and reproduction of interspecific hybrids of Pelophylax esculentus complex in population systems of European Russia

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Animal interspecific hybrids are often unviable and sterile. However, changes in gametogenesis such as genome elimination and endoreplication allow hybrids to reproduce together with parental species. The Pelophylax esculentus complex (European water frogs) is convenient model of natural interspecific

hybridization. The complex consists of two parental species (P. lessonae and P. ridibundus) and their natural hybrid (P. esculentus). Here we aimed to study a role of hybrids in the maintenance of the population systems in the European part of Russia (the Mari El Republic). We obtained tadpoles after laboratory crosses of parental species with each other and crosses of P. lessonae females with hybrid males. In all crosses, all tadpoles were identified as diploid hybrids by FISH karyotyping with (TTAGGG)n probe. Thus, hybrid males formed gametes carrying only P. lessonae genome. In gonads of 30 tadpoles, germ cells were either absent or presented in small quantities. In gonads of 14 tadpoles, micronuclei were observed in the cytoplasm of germ cells indicating genome elimination. For most hybrid females we observed disruptions of genome elimination and endoreplication during gametogenesis. Only one female produced oocytes with 13 bivalents of P. ridibundus, while three others produced oocytes with 26 univalents corresponding to the chromosomes of both parental species. We can conclude that crosses of parental species with each other and crosses of P. lessonae females and hybrid males give viable hybrids. However, a small quantity of germ cells in the gonads of tadpoles and univalents in oocytes of adult hybrid females reveal disrupted genome elimination in gametogenesis of hybrids.

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Chromosomal location and relationships between the two ribosomal gene families in three lobsters (Crustacea, Decapoda)

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The European lobster Homarus gammarus L., the American lobster H. americanus H. Milne Edwards and the norway lobster Nephrops norvegicus L. are the most commercially important and studied species of Nephropidae. H. gammarus and N. norvegicus are widely distributed in the estern side of the North Atlantic ocean and in the Mediterranean sea while H. americanus is commonly found in the western Atlantic. Nephrops and Homarus are considered closely related genera furthermore, differences between the two Homarus species are very slight. Although their economic value, the cytogenetics of lobsters remains poorly understood, due to technical constraints in obtaining good chromosomal preparations as well as the features of the chromosome complement. In fact the karyotype of the three lobsters is made up of a high number of little size chromosomes, more than 100 in all species; furthermore, in N. norvegicus and H. americanus supernumerary chromosomes have been detected. Till now physical mapping studies in crustacean decapods are scarce. In this study we localized on the chromosomes of the three species the major (45S rDNA) and the minor (5S rDNA) ribosomal gene families by the use of double FISH which allowed to deepen the relationships between the two ribosomal families. 45SrDNA FISH localized the major ribosomal gene family in 6 chromosome pairs both in H. americanus and in H. gammarus, and in 8 pairs in N. norvegicus. In all the three specie 5S rDNA FISH localized the minor ribosomal gene family in a single chromosome pair, different from the NOR-carrying chromosome pairs in the two Homarus species. In N. norvegicus both the ribosomal families are located in the same medium-sized acrocentric pair. Moreover we hybridized the pentameric telomeric repeat (TTAGG)n that appears to be the most widespread telomere repeat in Arthropods; the FISH produced bright fluorescent signals at the end of all chromosomes and, additionally, some large telomeric signals were present in the Homarus species.

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Genome size estimation and chromosome number variation in Cimex bed bugs (Insecta: Heteroptera)

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