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Acetamiprid, a neonicotinoid insecticide, is widely used to control sucking insects on crops. Owing to common usage in agriculture, it is important to investigate their effects on living organism. The objective of this study was to evaluate the genotoxic effects of acetamiprid in bone marrow cells of mice using micronucleus assay.

In the present study, acetamiprid was used as the test material. Mice were exposed intraperitoneally to different concentrations of acetamiprid (0.625 µg/ml, 1.25 µg/ml and 2.50 µg/ml; 0,01 ml per gram) for 24 h. Mitomycin C and distilled water were also used as positive control and negative control, respectively. The slides were prepared according to the methods of Schmid (1975) and Aaron et al. (1989) with minor modifications and stained with May Grunwald and Giemsa. A total of 2000 erythrocytes were scored for each animal at a magnification of x1000. The numbers of micronucleated polychromatic erythrocytes (MNPCE) and micronucleated normochromatic erythrocyte were counted. Polychromatic erythrocytes/normochromatic erythrocyte ratio was calculated. Statistical analysis of data was done using the nonparametric Kruskal–Wallis and Mann–Whitney *U* test. According to the results obtained, acetamiprid did not increase the frequency of MNPCE at any concentrations for 24 h when compared with negative control. PCE/NCE ratio was significantly decreased at only 1.25 µg/ml concentration for 24 h. In the light of these results, acetamiprid is not genotoxic but it may be cytotoxic for mice bone marrow cells. However its effects should be investigated by other test methods.

9.P3

Copy number variation in Japanese quail genome revealed by microarray analysis

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Being a domesticated bird, Japanese quail (*Coturnix coturnix japonica*) represents a popular resource of meat and eggs in certain parts of the world. Besides, it is widely used as the object of experimental research,

particularly in developmental biology. Along with another representative of Phasianidae - chicken (*Gallus gallus domesticus*), the Japanese quail might be recognized as one of most studied avian species. Japanese quail and chicken have very similar karyotypes ($2n=78$) with a high degree of conservation suggesting the absence of interchromosomal rearrangements. In contrast, numerous intrachromosomal rearrangements have accompanied their karyotype evolution. Accumulation of repetitive sequences has probably led to the increased size of quail genome (1.41 pg in Japanese quail vs. 1.25 pg in chicken).

In this study, we performed comparative genomic hybridization on chicken CGH 385 K whole-genome tiling arrays (Roche NimbleGen) to reveal a global variation in Japanese quail genome. Using this method of molecular cytogenetics we have evaluated unbalanced copy number changes (gains/losses) in quail DNA (the test) relative to Red Jungle Fowl DNA (the reference). In total, 183 copy number variants (CNVs) were detected in two quail individuals. Overlapping CNVs form 87 discrete copy number variable regions (CNVRs), of which 59 are losses and 28 gains. Some CNVRs completely or partially overlap with 289 annotated genes and are enriched with four transcription factor binding sites. On the whole, CNV regions are detectable in most chicken chromosome assemblies (except for 15, 17, 19, 32) and cover 9.41 Mb. It is interesting that Japanese quail and chicken being diverged 35 Ma have much more CNVs if compared to phylogenetically distant turkey, duck and zebra finch.

9.P4

Cytogenetic studies on endangered cattle, sheep, horse and pig breeds reared in Southern Italy

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The conservation of animal biodiversity is one of the main and crucial aspects to keep endangered species and breeds. In domestic animals, in

particular in cattle and pig, the use of cosmopolitan breeds have been largely used to substitute local breeds with consequent loss of genetic variability. In Campania Region (Southern-Italy) some breeds of cattle, sheep, horse, pig and goat are actually endangered and a special project is trying to characterize and valorize them throughout various aspects, including the valorization of their products. The breeds actually interested to this project are the following: “Agerolese” cattle, “Laticauda and Bagnolese” sheep, “Napoletano, Persano and Salernitano” horses, “Casertana” pig and “Cilentana” goat. CBA- and RBA-banding techniques were applied on all studied animals, while some specific case has been investigated using also FISH-mapping techniques. One hundred-ninety-six animals were studied so far and all of them showed normal karyotypes, exception of four females: two Agerolese cattle and two Laticauda sheep. The two Agerolese cattle were found heterozygous carriers of rob(1;29) and used also to better clarify the origin of this famous and widely spread translocation by using detailed comparative FISH-mapping with BAC-clones and CGH-array to quantify the genomic region interested to the transposition (with inversion). The two Laticauda sheep were found carriers of two new reciprocal translocations: rcp(4q;12q) and rcp(18;23) as demonstrated by using both RBA-banding and FISH-mapping techniques. Additional investigations have been performed in 25 random selected pig animals of Casertana breed by using sister chromatid exchange (SCE) test to check its genomic stability under the environmental conditions.

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9.P5

Molecular insights into sex-to-autosome translocations indicate common descent for the clade Antilope, Gazella, Nanger and Eudorcas (Antilopini, Bovidae)

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Chromosomal evolution in Bovidae (cattle, sheep, goat, antelopes, $2n=30-60$) is largely attributable to Robertsonian chromosomal fusions that shape karyotypes of many species. In contrast, a great variety of X chromosomes, including changes in centromere placement, multiple transpositions of common segments, heterochromatic variation and autosomal translocation, have been evolved within Bovidae. For a clade Antilopini that includes Antilope, Gazella, Nanger and Eudorcas, X;BTA5 translocation is a synapomorphy. Moreover, Nanger and Eudorcas carry Y;BTA16 translocation. Similar types of rearrangements in humans often result in sterility. On the other hand, their relatively widespread occurrence among mammals indicates that these rearrangements are meiotically acceptable.

Using a combination of region-specific painting probes prepared from cattle we document here the outcome of molecular cytogenetic dissection of the sex-to-autosome compound chromosomes of all representative species of the clade: Antilope cervicapra, Gazella leptoceros, Nanger dama and Eudorcas thomsonii. During the course of sex chromosome evolution in the studied species, addition/deletion of constitutive heterochromatin comprising repetitive DNA sequences has evolved. Sequence analysis of repetitive DNA suggests that such sequences are rapidly evolving and therefore valuable in phylogenetic studies. Characterization of these repeats enabled us to suggest common descent for the clade.

9.P6

Gorilla genome structural variations: towards the resolution of the conundrum of African Great Ape Subtelomeric Heterochromatin

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