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found are related to the aflatoxin contamination identified in milk and forages. The assessment of the aflatoxin effects on the genetic material integrity of investigated cows emphasizes the role of animals as biological indicators of the environmental pollution.

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Chromosomal instability in Italian Friesian cows exposed to dioxins and raised in proximity of an industrial area producing steel in Taranto city (Southern-Italy)

A. Perucatti¹, V. Genualdo¹, A. Iannuzzi¹, M.A. Colonna², F. Giannico², D. Incarnato¹, G. Lubrano-Lavadera³, L. Vonghia⁴, A. Caputi-Jambrenghi², L. Iannuzzi¹ (angela.perucatti@ispaam.cnr.it)

¹National Research Council (CNR), Institute for Animal Production Systems in Mediterranean Environment (ISPAAM), Naples; ²Department of Animal Production, Agricultural Faculty of Sciences, University of Bari; ³CNR, Institute for Service Industry Research (IRAT), Naples, Italy; ⁴Department of Basic Medical Sciences, Neuroscience and Sensory Organs, University of Bari, Policlinico, Bari, Italy

Dioxins are a large family of congeners which can be fitted in three main groups: polychloro-dibenzo-dioxins (PCDDs), polychloro-dibenzo-furans (PCDFs) and dioxin-like polychlorobiphenyls (DL-PCBs). These chemicals are considered highly toxic, especially the tetrachloro-dibenzo-*p*-dioxin (TCDD). Most PCDDs, PCDFs are produced by both industrial processes and illegal waste burning, while DL-PCBs are produced only during some industrial process like those producing steel. Dioxins are also high persistent in the environment, especially when entering the human or animal body due to their ability to be absorbed by fat tissue where they can remain for long time being their half-life in the body for years. Fifty-six randomly selected Italian Friesian cows from two farms located in vicinity and far (control) from a metallurgic factory of Taranto city (Southern-Italy) underwent cytogenetic investigations to ascertain possible differences in their chromosome fragility. The farm located close to the industrial area

was under legal sequestration due to the presence in the milk mass of higher mean values of dioxins (mainly DL-PCBs) than those permitted. As control, samples of cows of same breed reared far (65 Km) from the industrial area, were employed. The two cytogenetic test we used (chromatid and chromosome breaks, SCE) revealed a significantly ($P < 0.01$) higher chromosome fragility in cells of exposed cows compared to those of control, thus suggesting a new politic of animal breeding to prevent contamination of the food chain and human diseases in urban areas, especially close to metallurgic factories.

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Cytogenetic investigations in two endangered pig breeds raised in Southern-Italy

A. Perucatti¹, V. Genualdo¹, A. Iannuzzi¹, L. Pucciarelli¹, D. Incarnato¹, A. Pauciullo¹, D. Marletta², G. Scopino^{1,3}, B. Castiglioni⁴, V. Peretti³, L. Iannuzzi¹ (angela.perucatti@ispaam.cnr.it)

¹National Research Council (CNR) of Italy, ISPAAM, Laboratory of Animal Cytogenetics and Gene Mapping, Naples, Italy; ²DISPA, University of Catania, Catania, Italy; ³Dept. Veterinary Medicine and Animal Production, University of Naples Federico II, Naples, Italy; ⁴CNR-IBBA, Milan, Italy.

Pig from Casertana and Siciliana breeds are two endangered breeds raised in the southern-Italy (Campania and Sicily regions, respectively) and characterized to have a black skin. Special projects are trying to save and characterize both of them by using several approaches. In this study we report the preliminary results we obtained after a cytogenetic investigation we performed by using both C- and R-banding techniques and the sister chromatid exchange (SCE) test to verify their chromosome stability under the environmental conditions. Fifty-two pigs from Casertana breed and 19 pigs from Siciliana breed were investigated. All animals from both breeds showed a normal karyotype, with the exception of two male pig from Siciliana breed which were found heterozygous carrier of rob(15;17) ($2n=37$, XY), probably being hybrids with the wild pig ($2n=36$) present in the

Nebrodi mountains where this breed is raised in Sicily. SCE-test applied on 42 pigs from Casertana breed (22 males and 20 females) and 19 pigs from Siciliana breed (8 males and 11 females) revealed no statistical differences between the SCE-mean number in Casertana pig (7.13 ± 3.20) than that (6.87 ± 3.12) achieved in Siciliana pig. Statistical differences were found between males (7.26 ± 3.38) and females (6.59 ± 2.90) of Siciliana pig breed, as well as between females of Casertana (7.24 ± 3.26) and Siciliana (6.59 ± 2.90) breeds, while no statistical differences were found between males of the breeds, as well as between males and females of Casertana breed.

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Cytogenetic analyses in rabbits feed in presence of Verbascoside: SCE-test

V. Genualdo¹, A. Perucatti¹, A. Iannuzzi¹, A. Pauciullo¹, L. Pucciarelli¹, C. Iorio¹, D. Incarnato¹, M. Palazzo², D. Casamassima², L. Iannuzzi¹ (viviana.genualdo@ispaam.cnr.it)

¹National Research Council (CNR), ISPAAM, Laboratory of Animal Cytogenetics and Gene Mapping, Naples, Italy; ²Department of Agriculture, Environment and Food (AAA), University of Molise, Campobasso, Italy.

Phenylpropanoid glycosides (PPG), like other phenolic compounds, are powerful antioxidants. Beside phenolic compounds, verbascoside, shows the highest scavenger activity in the PPG and has high antioxidant power in comparison with other phenolic compounds. Previous studies by using in vitro exposure of human blood lymphocytes to verbascoside reported a significant increasing of chromosome fragility compared to control. In the present study four homogeneous groups of rabbits (six animals per group) were used to test in vivo the verbascoside by feeding the animals without Verbascoside and Licopene (*control – group A*), with lycopene (*5 mg/Kg of feeding, group B*), with verbascoside (*5 mg/Kg of feeding, group C*) with verbascoside and lycopene (*5 mg/Kg of feeding each, group D*). Peripheral blood cultures were performed in

three different times: at 0, 40 and 80 days of the experiment. Two types of cell cultures were performed: without (normal cultures) for the AC-test (chromosome and chromatid breaks) and with BrdU (10 µg/ml), the latter added 26 h before harvesting, for the SCE-test. In the present study only data from SCE-test are presented. Mean number of SCEs were generally lower at both 40 and 80 days in groups B, C and D, compared with the same groups at zero day. In particular, they were statistically ($P < 0.01$) lower at 40 and 80 days when using lycopene. In conclusion, on the basis of SCE-test applied on cells of rabbits treated in vivo with verbascoside or/and with lycopene, no chromosome fragility increasing were observed in cells of rabbit feed with verbascoside. However, a final conclusion will be done when data from AC-test will be available.

Evolutionary and Comparative Cytogenetics

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Avian cytogenetics goes functional

D. K Griffin¹, M. Farre², P. Lithgow¹, R. O'Connor¹, K. Fowler¹, M. Romanov¹, D. Larkin² (d.k.griffin@kent.ac.uk)

¹School of Biosciences, University of Kent, Canterbury, UK; ²Department of Comparative Biomedical Sciences, Royal Veterinary College, University of London, NW1 0TU, London, UK.

Whole chromosomes (and sub-chromosomal homologous synteny blocks (HSBs)) have great significance in molecular studies of genome evolution. In birds, our ability to define chromosomes and HSBs precisely has however been impeded by a near intractable karyotype and so has focused primarily on comparative molecular cytogenetics (zoo-FISH) of the largest chromosomes (1–10+Z). Availability of multiple avian genome sequence assemblies has however allowed us, for the first time, to identify chromosomal syntenies across species. In recent work we have made use of comparative maps for 20+ avian genome assemblies (plus out-groups) and presented them on “Evolution Highway” an open-access, interactive freely available comparative chromosome browser designed to store and visualise comparative chromosome maps.