

there are no data in literature to explain this condition however it has been demonstrated that in Agerolese cattle carrying rob(1;29) there is one fragile site more than in other animals, future studies will evaluate a possible correlation between the increase in SCEs on X chromosome and the presence of this fragile site.

This research was supported by PSR Campania 2007–2013—Misura 214, RARECA project.

P32

Sister chromatid exchange (SCE) test in river buffalo cells treated with Furocoumarins

A. Iannuzzi¹, A. Perucatti¹, V. Genuardo¹, A. Pauciullo¹, L. Pucciarelli¹, D. Incarnato¹, R. Melis², C. Porqueddu², M. Marchetti³, L. Iannuzzi¹ (alessandra.iannuzzi@ispaam.cnr.it)

¹National Research Council (CNR), Institute of Animal Production Systems in Mediterranean Environments (ISPAAM), Laboratory of Animal Cytogenetics and Gene Mapping, Naples, Italy; ²CNR-ISPAAM, UOS-Sassari, Italy; ³CNR-ICB, UOS-Sassari, Italy.

Cytogenetic test can be very useful to detect chromosome (genome) fragility in both animal and human cells. Furocoumarin derivatives constitute a class of compounds widely investigated for the development of photo-chemotherapeutic drugs and effective in treating many diseases. The interest inside this research field originated from the effectiveness of PUVA therapy, realized by oral or topical administration of a linear furocoumarin (psoralen) followed by irradiation with UVA light, for the treatment of psoriasis and cutaneous T-cell lymphoma. Furocoumarins are also present in *Psoralea* plants elected to be also used as alternative feed for animals considering that it's a perennial leguminous and, more important, it's green during the summer time. In the present study we report the preliminary results obtained using the SCE-test in river buffalo cells exposed in vitro to furocoumarin extracts from a Sardinian population of *Posoralea morisana* (L.) Stirton (Punta Giglio). Peripheral blood samples from five young river buffaloes (2 males and 3 females) were incubated at 38 °C for 72 h in presence of different quantities of furocoumarin extracts: 0 (control), 50, 100, 200 and 400 µg/ml. Thirty cells for each cell culture (and furocoumarin dose) were analyzed. Although the cell growth appeared normal in both

treated and untreated (control) cells, a significant ($P<0.01$) higher number of SCEs observed in treated cells, compared to those achieved in the control. On the basis of these results, cells from five river buffalo cows were treated with 0 (control), 100 and 200 µg/ml of furocoumarins for only 3 h after 24 h of incubation, in presence and absence of S9. No statistical differences were found between treated and untreated cells with furocoumarins both in presence and absence of S9.

Acknowledgements. The study has been supported by CISIA-VARIGEAV project, National Research Council (CNR) of Italy.

P33

Chromosomal abnormalities in cattle induced by aflatoxin contamination of forages

I. Nicolae¹, A. Gurita¹, D. Vidmichi¹, M. Voiculescu¹, C. Petrescu¹, N. Isfan²

¹I.C.D.C.B. Baloteşti; ²U.S.A.M.V. Bucuresti (ioana_nicolae2002@yahoo.com)

During the last year, in the south-eastern part of Romania, a high aflatoxin contamination of milk was identified in many cattle farms. The values of aflatoxin concentration of milk was higher than permitted (0.05 ppb), ranging from 0.06 to 0.228 ppb. In this context a cytogenetic investigation was carried out for 45 Romanian Black and Spotted cows from two cattle farms: one with aflatoxin contamination and one free of aflatoxin contamination. Our study revealed that four cows from contaminated farm presented a large number of mono- and bichromatidic breakages on autosomes and heterosomes, loss of chromosome fragments and gaps. Our investigation continued through SCEs-test, which is a specific test for identifying the effects of toxic agents on the genetic material integrity. For animals with many chromosomal breakages the number of sister chromatid exchanges (SCEs) was extremely high (11.7 ± 2.56 SCEs/cell) compared to the normal animals (6.73 ± 2.47 SCEs/cell). Chemical analyses were performed on feed samples (alfalfa hay, corn silage, mixed fodder and bran) used for feeding of the cows raised in the two farms. In the contaminated farm it was identified a level of aflatoxin content more than maximum allowed (<4.0) in 2 of the 4 forages analyzed as follows: alfalfa hay (4.93 ± 0.03) and bran (5.17 ± 0.05). With this results, we can appreciate that the chromosomal abnormalities we