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This is the author's manuscript

Original Citation:

Availability:

This version is available <http://hdl.handle.net/2318/1712742> since 2019-10-02T11:50:37Z

Publisher:

Università Roma Tre, Dipartimento di Scienze

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80° CONGRESSO NAZIONALE



UNIONE ZOOLOGICA ITALIANA
IN COLLABORAZIONE CON
COMITATO SCIENTIFICO PER LA FAUNA D'ITALIA

RIASSUNTI DELLE COMUNICAZIONI E DEI POSTER

a cura di

Elvira De Matthaeis, Andrea Di Giulio, Marzio Zapparoli

ISBN – 9788883442445

UNIVERSITÀ ROMA TRE, DIPARTIMENTO DI SCIENZE
Viale G. Marconi 446 00146 Roma, Italia

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CHRONIC STRESS INDUCE GENOMIC DAMAGE IN SHELTER DOGS

In mice and rats, exposure to chronic stress was found to induce alterations in gene expression, whereas, in humans, stress and anxiety conditions are associated to modifications in DNA methylation patterns and to increased levels of genomic damage and telomeres erosion. No data are present in literature about the possible correlation between stress and genomic damage in dog. For this reason, we decided to evaluate the level of genomic damage in shelter dogs ($n = 30$), by buccal micronucleus assay. As control group, we sampled family dogs ($n = 30$) matched for age and sex but without any experience of shelters. The tested hypothesis was that stress conditions, like those potentially present in shelter houses, could affect the levels of genomic damage. Moreover, for the first time in literature, the baseline frequencies of buccal micronuclei (MNi) and nuclear buds (NBUDs) were provided for non-human mammals. MNi represent chromosome fragments or whole chromosomes that fail to segregate properly during mitosis, appearing in interphase as small additional nuclei. NBUDs represent elimination processes from cells of amplified DNA and/or excess chromosomes. For both groups, at least 30.000 cells were analyzed. MNi and NBUDs frequencies ($\% \pm SD$) in shelter dogs were 0.300 ± 0.233 and 0.280 ± 0.220 , respectively, whereas in family dogs were 0.083 ± 0.095 and 0.130 ± 0.154 , respectively. Significant differences were found between shelter and family dogs in terms of MNi and NBUDs frequencies ($P < 0.001$ and $P = 0.001$, respectively, ANOVA and Mann-Whitney tests), whereas sex and age did not influence the level of genomic damage in both groups. As general result, we provided evidences of a possible association between stress conditions and highest levels of genomic damage in shelter dogs. Results of this work, also considering the relatively low costs of laboratory procedures, could represent a stimulus for the introduction of genomic techniques in the evaluation processes of stress conditions of animals living in communities. These genomic techniques, associated with more traditional ones, such as cortisol level analysis and behavioral testing, could provide a more complete picture of the health status of animal communities of human interest.

