Transgenerational effects and radiosensitivity in non-human species

C. Adam-Guillermin^a, N. Horemans^b on behalf the related ALLIANCE topical Working Group

^aInstitut de Radioprotection et de Sûreté Nucléaire (IRSN), PSE/SRTE/LECO Cadarache, St Paul Lez Durance cedex, France ; email: christelle.adam-guillermin@irsn.fr; ^bBelgian Nuclear Research Centre (SCK•CEN), Biosphere Impact Studies, Boeretang 200, 2400 Mol, Belgium ; email :

Belgian Nuclear Research Centre (SCK•CEN), Biosphere Impact Studies, Boeretang 200, 2400 Mol, Belgium ; email : nele.horemans@sckcen.be

Abstract-The issue of potential long-term or hereditary effects for both humans and wildlife exposed to low doses of ionising radiation is a major concern. Animal and plant studies suggest that gamma irradiation can lead to observable effects in the F1 generation that are not attributable to inheritance of a rare stable DNA mutation. Several studies provide evidence of an increase of genomic instability detected in germ or somatic cells of F1 from exposed F0 organisms. This can lead to an induced radiosensitivity and phenotypic effects such as reproductive effects and teratogenesis. The ALLIANCE working group on effects of ionising radiation on wildlife brings together European researchers to work on this topic of transgenerational effects and radiosensitivity. The available studies show that differences of radiation sensitivity and mechanisms may be observed across species. In particular, studies are conducted to understand the possible role of epigenetic modifications such as DNA methylation, histone modifications or microRNAs in radiosensitivity as well as in adaptation effects. Understanding the main factors involved in these transgenerational effects across species will help to identify radiosensitive species that may require special attention in monitoring and protection. Finally, further investigation is required into the potential role of defined epigenetic effects in radiation-associated somatic diseases and heritable effects. Research using biological models in which the relative contribution of genetic and epigenetic processes can be elucidated is highly valuable.