

New life for old data - The European Radiobiological Archives and the e.ERA database

M. Birschwilks^a, C. Adelman^b, M. Gruenberger^c, P. Schofield^c, S. Tapio^d and B. Grosche^a

^aFederal Office for Radiation Protection, Ingolstaedter Landstr. 1, 85764 Oberschleißheim, Germany; ^bFederal Office for Radiation Protection, Willy-Brandt-Str. 5, 38226 Salzgitter, Germany; ^cUniversity of Cambridge, Downing Street, CB2 3DY Cambridge, United Kingdom; ^dHelmholtz Centre Munich, Ingolstaedter Landstr. 1, 85764 Neuherberg, Germany

mbirschwilks@bfs.de

Molecular and genetic research is now providing us with the opportunity to quantify the risks of radiation exposure at the individual level. The retrospective analysis of earlier epidemiological and animal studies will be an important resource for modelling and evaluating such new risk parameters. With great foresight the EU and EULEP have created a database collecting and collating data from almost all of the available animal radiation biology studies carried out in Europe, the US and Japan between 1960 and 1998, plus those of two human cohort studies. This database is called the European Radiobiology Archives (ERA), which is part of the International Radiobiological Archives (IRA). The archives will be accessible on line via internet. The respective data base is named e.ERA. In addition, e.ERA was made compatible to and interoperable with other relevant radiobiological databases, namely PATHBASE and other mouse phenotype projects. To do so, pathology data in ERA were recoded to conform with accepted ontology standards (MPATH) for the mouse. The data included in the database underwent and undergo continuously quality assurance measures to reassure that the available information is as good as possible. e.ERA has become a unique repository of archival data, the project will soon put into effect an easy to use database of invaluable data for further exploitation by the scientific community. Further, there is the possibility of expanding the database to include data from other projects. During the meeting, the current version of e.ERA will be demonstrated. The interface provides a quick and easy to use way of data retrieval. Data can be browsed by organism, pathology observation, treatment, and various disease codings, e.g. MA, MPath, DisRod, DisFam, ICD9. The complete database version will presumably be available to the scientific community by 2009.