Mouse Longevity Data Explorer App

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Mice have been used as a model for human longevity and lifespan for decades, due to our shared mammalian ancestry and close genetic similarity. However, these studies have been carried out in vastly different conditions, even when described as 'normal controls', and there is no centralized repository for this data. This is important, as each of these studies represent years of effort and public funding.

We present an ongoing project to gather this wealth of data. A significant limitation has been that many publications do not provide full details on the animals used, the conditions they are kept in, or individual data. This is exacerbated by the fact that several factors that have been demonstrated to affect lifespan (e.g. cagemates, temperature, breeding status) are often not reported.

We have used only isogenic animals (e.g. inbred strains and their F1s) as these genomes are replicable across studies, years and laboratories. We have made an exception for the UM-HET3 – an G2 population from four inbred strains – as there is excellent and well documented data. We did not include animals on mixed backgrounds, which excluded many studies in transgenic animals, as there is uncontrolled segregation of alleles in these populations, which cannot be replicated in future studies.

We describe our collection of mouse lifespan data spanning seven decades, and our GeneNetwork web app to share this data (http://longevity-explorer.genenetwork.org/). Our findings have mostly recapitulated those of previous studies, (including heterosis, strain-by-sex effects, and overrepresentation of C57BL/6 substrains), but with important additions.Current data comes from 56 studies of 158 examined, and 523 further publications remain to be examined.

This centralized repository will facilitate more robust cross-study comparisons, minimize unnecessary duplication of effort, and enhance our understanding of genetic and environmental factors influencing mouse, and potentially human, longevity.