Genetic differences influence aging rates in the wild

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Long-lived, wild animals harbor genetic differences that influence how quickly they begin to show their age, according to the results of a long-term study reported online on December 13th in *Current Biology*, a Cell Press publication. Evidence for the existence of such genetic variation for aging rates—a central tenet in the evolutionary theory that explains why animals would show physiological declines as they grow older—had largely been lacking in natural populations until now, the researchers said.

“We’ve found that individuals differ in their rates of aging, or senescence, and that these differences are (at least in part) caused by genetic effects so they will be inherited,” said Alastair Wilson of the University of Edinburgh. “While the genetic effects we found are completely consistent with existing theory, scientists hadn’t previously managed to test this theory properly except in controlled laboratory experiments.

“We’ve also done this work on long-lived mammals,” he added. “For someone interested in the evolution of aging and senescence in humans, these are going to be more relevant organisms than Drosophila [fruit flies].”

Scientists normally expect genetic mutations having bad effects to be removed by natural selection, Wilson explained. Conversely, selection will lead to an increase in the frequency of mutations that are beneficial. “On this basis, any genes with bad effects on survival or reproduction

should be removed by selection," he said. "But if that were true then there is no reason for individuals to deteriorate as they get old."

Aging therefore raises a critical question: How has natural selection failed to remove genetic effects responsible for such reduced fitness among older individuals" Current evolutionary theory explains this phenomenon by showing that, as a result of the risk of death from environmental causes that individuals experience over the course of their lives, the force of selection inevitably weakens with age, he continued. This, in turn, means that genetic mutations having detrimental effects that are only felt late in life may persist in a population. Although widely accepted, this theory rests on the assumption that there is genetic variation for aging in natural systems.

To look for such genetic variation in the new study, the researchers examined wild Soay sheep and red deer living on two Scottish islands. Those populations were ideal for the study because they provide unparalleled levels of data, including individual survival and reproductive success, for large numbers of long-lived animals, Wilson said. In both study systems, individually marked animals are followed throughout their lives from birth until death, and their relationships to one another are known.

In both the red deer and sheep populations, they found evidence for age-specific genetic effects on "fitness"—a measure combining the animals' probability of survival and reproduction. "The present study provides, to our knowledge, the first evidence for additive genetic variance in aging rates from a wild, non-model study organism," the researchers concluded. "Furthermore, the age-specific patterns of additive genetic (co)variation evident in the two populations examined here were entirely consistent with the hypothesis that declines in fitness with age are driven by a weakening of natural selection."

Source: Cell Press