

"Gene-Spliced" Fish Experiments

Mark Fischetti's article "A feast of gene-splicing down on the fish farm" (Research News, 2 Aug., p. 512) contains a number of errors. The article states that the fish were genetically engineered by Thomas Chen at the University of Maryland's Center for Marine Biotechnology (including the injection of the cloned growth hormone gene into fish embryos). The article then states that the fish seemed robust in the Maryland laboratory, "so Chen sent them off to Dunham to see how they would thrive under real aquaculture conditions." These and several other statements are incorrect. First, the genetic engineering was a collaborative effort of our three laboratories. The genetic constructs were generated by a postdoctoral fellow, C. M. Lin, working with Powers and Chen while they were in the Department of Biology at Johns Hopkins University (not the University of Maryland). The genetic constructs were sent to Dunham at Auburn University, where his group (Chris Joyce and Mohammad Hayat) injected the DNA into the fish eggs (none of the eggs were injected in Baltimore). After the fish grew to an adequate size, Dunham's group (Anne Ramboux and Pat Duncan) took tissue samples and sent them to Johns Hopkins University, where they were analyzed by Peijung Zhang and Irene Gonzalez-Villasenor, who were working with Powers and Chen to determine what fraction of the injected fish integrated the gene and what fraction expressed the growth hormone. Dunham's group grew the transgenic fish under laboratory conditions until the fish could be bred to produce offspring. Once the offspring of these fish grew to an adequate size, tissue samples were taken and sent to Johns Hopkins, where they were analyzed to determine what fraction of the next generation carried the foreign gene.

Fischetti's article also states that exogenous growth hormone treatments were initiated by Chen's group in the 1980s and that Dunham was involved with those experiments. While the experiments on trout were done by Chen's group (1), Dunham was not involved. Their studies confirmed previous work done by S. Sekine *et al.* (2) on chum salmon.

Although we have very stringent and effective confinement procedures for the ponds at Auburn University where the transgenic fish are being grown, they are not as elaborate as Fischetti describes. For example, we do not have camera surveillance, and we do not have automated poisoning mechanisms for these ponds.

Scientists are often wary of interviews because reporters do not always check back with them about the accuracy of the finished article. In this case, Fischetti did not check with any of us about the final wording. As a result, errors were made. We hope that in the future more science writers will consider the wisdom of checking the accuracy of their work with all sources.

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Age Structure of Populations

Natural populations are usually thought to lack significant numbers of older individuals, because the high dangers in the feral world allow few to achieve venerable ages. Annual mortality rates typically range from 5 to 50% for species that mature at an age of 1 year or later. Nevertheless, many vertebrates exhibit slow maturation, long individual life-spans, and population age structures that extend over several generations. Besides providing evidence for considerable longevity, field studies show that fulmars, gull-like sea birds, continue reproduction for up to at least 35 years without increased mortality or other signs of senescence, as do species of rockfish for up to at least 100 years (1).

Populations of birds and other animals may require balanced proportions of older, experienced individuals to survive. Vital knowledge about the location of dangers as well as food and water is often maintained by older individuals. Moreover, older individuals may have special social roles in some animal species. While most information on the wisdom of elders is anecdotal, it is clear that continued learning is important and that older individuals facilitate this learning.

Studies of natural populations with extended age structures would be valuable for neurobiology, evolution, and gerontology. Species with extended reproductive schedules may have selected genes that allow neural circuits to

acquire new information and retain memories over many decades. Natural selection might minimize genes predisposing an individual to early neurodegeneration. For example, since birds generally have much higher blood glucose than mammals, it would be worthwhile investigating whether there are mechanisms in birds that protect lens and other proteins from glycation (nonenzymatic linkage of glucose to proteins). It would also be of interest to evaluate the effects of parental age on chromosomal and other genetic abnormalities in gametes and embryos. Mitochondrial DNA deletions increase with age in the mammalian brain (2). Similar genetic changes may occur in somatic cells in other species. The evolutionary theory that senescence results from the accumulation of germ-line mutations in a population with the late onset of harmful effects should be examined in old individuals of natural, nonmammalian populations.

Many longitudinal studies of natural populations depend on the inspired persistence of lone researchers, who often support their work from personal funds. Such studies are often endangered by the effects of encroaching age on the investigator, that is, a study ends just when substantial numbers of marked individuals are approaching the end of the species' life-span, when they would be most valuable for our understanding of old-age phenomena. We propose that age structure in populations be considered a crucial aspect of endangered species and biodiversity studies and that it should be made a prominent objective of conservation and population monitoring programs.

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Conservation of Hybrid Plants

There is currently considerable debate about the treatment of natural hybrids in conservation legislation. The "hybrid policy"