

# Selfish Genes

J. J. Bull, I. J. Molineux, J. H. Werren

Most biologists have come to accept the view that natural selection can favor "selfish" genes—genes successful at propagating themselves while being detrimental to the organisms that carry them. Two early discoveries of selfish genes in animals were the *t*-locus complex of mice and the *segregation-distorter* complex of *Drosophila* (1). In both cases a linked cluster of genes achieves a massive fertilization excess relative to the normal chromosome in heterozygous males. This transmission excess gives the gene complex a selective advantage when rare. However, the complexes in both species also carry recessive lethals or sterility factors, resulting in the death or sterility of individuals homozygous for the complex. The list of known or suspected selfish genes now goes far beyond these two examples, and includes B chromosomes, replicative transposons, the *psr* chromosome of wasps, and mitochondria that cause male sterility in plants, among others (2).

That genes detrimental to the organism can be favored in evolution seems paradoxical, but derives from the simple fact that in sexually reproducing species, different alleles at the same locus are in evolutionary competition with each other. Properties of one allele that enable it to outcompete and replace its homologs are selected, even if the competition involves destroying the homologous alleles and sometimes, in the process, the entire genome containing them.

On page 89 of this issue of *Science*, Beeman *et al.* report a new class of selfish genes, discovered in the common flour beetle—the tiny, unwitting ingredient of many a pancake. The locus is termed *Medea* (*M*), for maternal effect dominant embryonic arrest. The allele is advantageous because it causes the death of zygotes that do not carry

it. Specifically, if a mother carries the *M* allele, then her offspring who fail to carry *M* die before pupation (Fig. 1). Necessarily all offspring of an *MM* mother or *MM* father avoid this fate, but an *M+* mother loses one-half of her offspring when mated to a *++* male, and loses one-quarter when mated to an *M+* male; zygotes that are *++* die. Classical genetic mapping of this trait suggests that it is chromosomal, but details of its genetic structure await further study.

One may wonder how such a gene could evolve: when rare, it would kill half of an *M+* mother's offspring because most sires would be *++*. The important distinction is that the *M* allele kills only those offspring that lack *M*. The *M* allele will increase in frequency under two conditions. First, in populations divided into small groups, a rare *M* allele may become more frequent in the population because it decreases the frequency of *++* progeny. Second, if the progeny of a mother compete with each other for resources, then the death of *++* "siblings" will free additional resources for the *M+* portion of the brood, translating into a fitness gain for *M*.

The arguments for the evolution of *M* factors closely parallel those for the evolution of bacterial colicins and the "poison-antidote" systems found on some low copy number bacterial plasmids: all three cases involve gene complexes that kill potential competitors that lack the complex (3). The prokaryotic systems achieve their selfish ends by a variety of molecular mechanisms that have in common the existence of a gene whose product is lethal. Protection is afforded by a linked gene that either serves to prevent synthesis of the lethal gene product or confers immunity (provides an antidote) to its action (4). It would not be surprising if the molecular mechanisms underlying killing of *++* zygotes by the flour beetle *M* locus are comparable to those used by one or more prokaryotic selfish genes.

The *M* allele is found in only some populations of flour beetles, and there even appear to be different *M*-type genes at other loci that do not complement the original *M* allele. The authors briefly consider the possibility that the differential buildup of *M* factors between populations could lead to

reproductive isolation and speciation. However, although these factors could cause hybrid inviability in backcrosses between populations, the introduction of novel *M* factors into a population might also sweep through the newly exposed population and thereby eliminate the basis of the incompatibility.

The *Medea* gene is unusual among known selfish genes in that it segregates as a typical chromosomal gene that achieves its ends by post-fertilization killing of diploid progeny. Others are non-chromosomal (for instance, mitochondrial male sterility in plants) or achieve their selfish ends prior to fertilization (segregation distortion complexes), although spore killers in yeast may provide a parallel (5).

In making their discovery, Beeman *et al.* have provided an empirical foundation for some controversial extensions of selfish gene theory in sociobiology. In particular, "parent-offspring conflict" is a theoretical concept in which parent-offspring interactions are viewed in a selfish context (6). The foundation of this theory is that natural selection acting on offspring selects greater levels of intra-brood competition than are favored by natural selection acting on parents. These ideas have been studied in various mathematical models during the last two decades, but unambiguous empirical support for extreme levels of sibling competition has been lacking until now.

Although sibling-killing selfish genes are presently a novelty, it will not be surprising if they are eventually found in many other species. Their existence may be expected especially in species with high levels of sibling resource competition, such as many insects, mammals, and plants. One may in fact anticipate that the failure to discover them before now lies with the difficulty in detecting them. Unless such genes have serious deleterious effects when homozygous, they will become fixed within populations and will only be detectable in interracial crosses, as was the case for *Medea*.

## REFERENCES AND NOTES

1. P. Chesley and L. C. Dunn, *Genetics* 21, 525 (1936); L. Sandler, Y. Hiraizumi, I. Sandler, *ibid.* 44, 233 (1959).
2. J. H. Werren, U. Nur, C.-I. Wu, *Trends Ecol. Evol.* 3, 297 (1988); M. W. Shaw and G. M. Hewitt, *Oxf. Surv. Evol. Biol.* 7, 197 (1990).
3. L. Chao and B. R. Levin, *Proc. Natl. Acad. Sci. U.S.A.* 78, 6324 (1981); J. A. Mongold, *Am. Nat.*, in press.
4. K. Gerdes *et al.*, *New Biol.* 2, 1 (1990); S. E. Luria and J. L. Suit, *Escherichia coli and Salmonella typhimurium*, F. C. Neihardt, Ed. (American Society for Microbiology, Washington, DC, 1987), pp. 1615-1624.
5. B. C. Turner and D. D. Perkins, *Am. Nat.* 137, 416 (1991).
6. W. D. Hamilton, *J. Theor. Biol.* 7, 1 (1964); R. L. Trivers, *Am. Zool.* 14, 249 (1974).

J. J. Bull is in the Department of Zoology and I. J. Molineux is in the Department of Microbiology at the University of Texas, Austin, TX 78712. J. H. Werren is in the Department of Biology at the University of Rochester, Rochester, NY 14627.

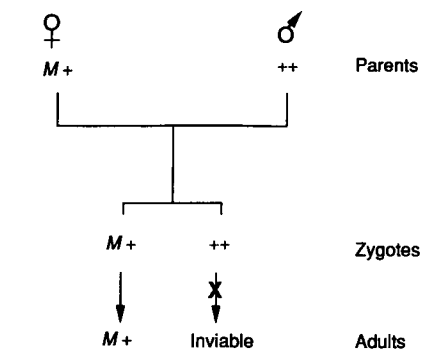


Fig. 1. Pedigree of *Medea* factor killing in flour beetles.