Sexual Selection: The Weevils of Inbreeding

A recent study has used inbreeding depression to gain insight into the maintenance of additive genetic variation in populations, with intriguing implications for good genes models of sexual selection.

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How can genes that lower fitness remain in circulation when selection favours the fittest [1]? This problem plagues studies of female choice in species where the only plausible benefit is to elevate offspring fitness above that achieved by mating randomly. Such benefits can occur if attractiveness is heritable [2], or if sexual traits indicate genes that improve fitness components under natural selection. For example, if sexual trait expression depends on physical condition, then this might signal the ability to acquire and assimilate resources and, by extension, fitness [3]. The problem is that female preferences for certain males — for example, larger or more ornamented males — reduce the very genetic variation that makes costly choice worthwhile.

To explain the importance of a new study by Tomkins *et al.* [4] we must briefly foray into quantitative genetics. For offspring fitness to be elevated through additive genetic benefits requires variation in male breeding values for sexual traits/fitness (additive genetic variation) so that females can choose males with 'good genes' [5]. By definition, these high quality males have high breeding values (a male's breeding value for a trait is twice the difference between the mean value of his offspring and the average offspring value given random mating in a population; twice because half an offspring's genes are paternal). Breeding values are calculated based on the additive effects of genes across all possible male–female pairings. They predict whether a male's genes 'add to' or 'subtract from' the offspring trait value for the average female compared to when she mates at random [6].

Additive genetic variation is hard to maintain in traits closely associated with fitness, unless another mechanism continually replenishes genetic diversity. Several mechanisms have been proposed, including gene flow between locally adapted populations and frequency-dependent selection favouring rarer genes [7]. The most fundamental process is mutation–selection balance, where the loss of genes through selection is balanced by input of new mutations. Mutations are usually deleterious, and are likely to persist for longer when fully or partly recessive.

Because it has proved difficult to show that preferred male traits confer additive genetic benefits, or that additive genetic variation persists as a result of mutation–selection balance, attention has recently turned towards *non-additive genetic benefits*: choice for males that elevate offspring fitness for individual females, rather than for males with an 'additive' effect for the average female [8]. For example, females should often [9] avoid mating with close kin because of the poorer performance of inbred offspring (inbreeding depression). A major source of non-additive genetic variation is dominance — interactions between genes at the same locus. Under complete dominance, recessive genes are only expressed in homozygotes. Dominance underlies inbreeding depression: inbreeding increases genome-wide homozygosity, exposing the phenotypic effects of previously hidden, or partly hidden, deleterious recessives [10]. It is easy to see how non-additive genetic benefits can persist, but choice driven by these benefits does not readily lead to directional preferences for more ornamented males [11].

Tomkins *et al.*'s [4] insight was to study inbreeding not for its non-additive benefits, but for its ability to expose variation in breeding values (additive benefits). This not only helps to evaluate the importance of 'good genes' but also hints at the processes sustaining the 'bad genes' needed to make choice beneficial. The often large effects of inbreeding are more easily measured than the seemingly small gains derived from 'good genes' preferences. Using cow-pea weevils (*Callosobruchus maculatus*), Tomkins *et al.* [4] posed a deceptively simple question: does the mean breeding value of related parents correlate with the severity of inbreeding depression in their offspring? The link should arise as inbreeding depression reflects the load of partially recessive deleterious mutations carried by parents, while the additive effects of these mutations should lower parental breeding values for fitness-related traits. The correlation is not expected to be perfect (hence the need for quantification), because deleterious mutations in the absence of dominance effects [12] do not affect inbreeding depression, and epistasis (interactions between genes across loci) and environmental factors also affect phenotypes.

Tomkins *et al.* [4] faced an empirical challenge in estimating inbreeding depression at the family level. They needed to compare traits between inbred and outbred offspring, but as well as reducing homozygosity, outbreeding introduces new genes whose additive effects contribute to trait expression. This generates a systematic bias [13]. For families with high breeding values, outbred offspring will have a lower phenotypic value (because of genes from a lower-value parent) than if siblings were 'magically' able to mate with each other without increasing offspring homozygosity. The reverse is true for families with low breeding values. Inbreeding depression due to greater expression of deleterious recessives is thus respectively under- and over-estimated.

Tomkins *et al.*'s [4] solution deployed an under-used technique [13]. They created a multiple-generation pedigree to estimate parental breeding values. The estimated breeding values were used to generate *expected* trait values for 'outbred' offspring from a given brother–sister mating, and these were compared to *observed* inbred offspring trait values from the actual brother–sister mating. The study examined 17 life-history and morphological traits across both sexes. Of greatest interest were body size, as females prefer larger males, and the efficiency with which males convert food into body mass. Condition is notoriously difficult to measure [14] and 'efficiency' in these weevils is arguably the best estimate we have for any species. Each weevil

develops inside a bean so food intake is precisely measured, and assimilation can be directly measured as body size because males lack other sexual ornaments, removing the need to estimate inherent condition (the condition prior to redirecting assimilated resources towards sexual traits).

For most traits, families with greater inbreeding depression had lower breeding values. This means that much of the variation in breeding values is due to deleterious recessive mutations, exactly as predicted by mutation–selection balance models. By some estimates, up to 77% of additive genetic variation in traits might be due to partially recessive deleterious mutations. The correlation was stronger for morphological than for life-history traits and, crucially, the two strongest correlations were for male size and efficiency. If condition is a major contributor to total fitness, then the correlation for efficiency suggests that condition-dependent traits, such as sexually selected body size in these weevils, are good indicators of mutation loads for fitness. One reading of these findings is that, if females can identify males with high breeding values for fitness-related traits, they will reduce the mutation load in their offspring ('good genes' benefits). This is an exciting result. Its generality is readily tested, as the method is applicable in any taxa where controlled matings can be conducted. Although breeding values are best calculated from an extended pedigree, they can also be more crudely estimated from trait heritability and an individual's phenotype.

What are the future challenges? One area of uncertainty is how best to explain variation in the correlation between inbreeding depression and breeding values. Do correlations vary among traits due to differences in the number of loci with recessive mutants, the effect of such mutants when fully expressed, the level of dominance, epistasis, and/or the gene frequencies of recessives? Correlations differ from regressions as they describe goodness-of-fit and not the magnitude of the effect of a change in one variable on a second. Two relationships with different regression slopes can have identical correlations, but simultaneously, measurement error makes detecting a correlation more difficult if the slope is shallow or if the explanatory variable shows little variation. Does a weak correlation for a focal trait imply that the effects of inbreeding are small, or that breeding values are hard to estimate precisely or, perhaps most importantly, that there is genuinely little variation in breeding values? These are questions for the future, but they highlight how this elegant empirical study could reinvigorate interest in good genes processes of sexual selection. The new study [4] also promotes a method to test the importance of mutation–selection balance that can be more widely taxonomically applied than other current approaches, which rely on mutation accumulation in clones/inbred lines, or long-term artificial selection experiments [12].

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DOI: 10.1016/j.cub.2010.06.055

Neuronal Morphogenesis: Worms Get an EFF in Dendritic Arborization

The development of neuronal dendritic trees involves positive and negative control of growth and branching, as well as modulation of the spacing and orientation of branches. A new study reveals the importance of a membrane fusogen in the dendrite arborization of a pair of highly-branched worm sensory neurons.

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A fascinating property of neurons is the striking diversity in the morphology of their dendrites. Dendritic arbors can differ in size, shape, branch complexity, and geometrical features, such as branch angle, with important implications for how sensory or synaptic inputs are sampled and processed by neurons. The emergence of dendritic patterns during development is a dynamic process involving both protrusion and retraction of branchlets over time and long-term stabilization of a subset of branches [1,2]. Our understanding of the molecular mechanisms of dendrite pruning and regression and the importance of these processes during normal dendrite development is still incomplete. Pruning is important during the sculpting of neural circuits in diverse systems, and knowledge about the mechanisms involved has emerged