

Characteristics Analysis and Hereditary Variations in Animals over time

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Abstract: Hereditary variation means that biological systems individuals and populations – are different over space. Each gene pool includes various alleles of genes. The variation occurs both within and among populations, supported by individual carriers of the variant genes. Hereditary variation is brought about, fundamentally, by mutation, which is a permanent change in the chemical structure of chromosomes. Hereditary recombination also produces changes within alleles. Cooperative species have long been the focus of much research due to the ‘special difficulty’ cooperation poses to the theory of evolution via natural selection. Despite this long history of scientific interest we actually know relatively little about the evolutionary genetics of cooperative mammalian species, especially in the wild.

Keywords: hereditary variations, animals, analysis, population.

Introduction

The characteristics variation among individuals within a population can be identified at a variety of levels. It is possible to identify characteristics variation from observations of phenotypic variation in either quantitative traits (traits that vary continuously and are coded for by many genes or discrete traits (traits that fall into discrete categories and are coded for by one or a few genes.

Hereditary variation can also be identified by examining variation at the level of enzymes using the process of protein electrophoresis. Polymorphic genes have more than one allele at each locus. Half of the genes that code for enzymes in insects and plants may be polymorphic, whereas polymorphisms are less common in vertebrates.

Ultimately, genetic variation is caused by variation in the order of bases in the nucleotides in genes. New technology now allows scientists to directly sequence DNA which has identified even more genetic variation than was previously detected by protein electrophoresis. Examination of DNA has shown genetic variation in both coding regions and in the non-coding intron region of genes.

Hereditary variation will result in phenotypic variation if variation in the order of nucleotides in the DNA sequence results in a difference in the order of amino acids in proteins coded by that DNA sequence, and if the resultant differences in amino acid sequence influence the shape, and thus the function of the enzyme.

Biological diversity occurs at different levels, including between individuals within a population, and the study of quantitative, or continuous, trait variation between individuals essentially forms the field of quantitative genetics. One of the major aims of quantitative genetics is to quantify the genetic basis of traits as this serves as an essential step in understanding their evolutionary potential. This paper describes an analysis of sources of variation in, and associations, between ranges of key phenotypic traits in a wild population of cooperatively breeding. In this introductory section, the fields of quantitative genetics and hereditary variation in animals and cooperative breeding have been studied. I also give more detailed backgrounds on the principles underlying inbreeding, inbreeding depression and quantitative genetic methods of analysis, and describe the utility of genetically validated pedigrees in addressing questions pertaining to these areas of research.

Evolutionary quantitative genetics of Animals

The study of quantitative genetics in animals is currently a burgeoning field of research. In the past, with some notable studies of the genetic basis of quantitative traits ('quantitative genetics') have typically focused on captive or laboratory populations, the findings from which have greatly advanced our understanding of many aspects of evolutionary biology, including elucidating the mechanisms and effects of inbreeding and the quantitative genetic architecture and response to selection of many traits. Captive or laboratory-based populations do not, however, necessarily accurately reflect the true conditions experienced by animals of organisms. Organisms in the wild tend to experience more temporally and spatially heterogeneous biotic and abiotic environmental conditions and so are likely to be subject to different selective pressures than either captive or laboratory based organisms. Studying the evolutionary quantitative genetics of animals is not, however, without its challenges and the recent growth of research in this field has been facilitated by a number of factors including the availability of long-term, individual-based data from wild populations, molecular advances in pedigree construction, and the application of more sophisticated methods of statistical analysis.

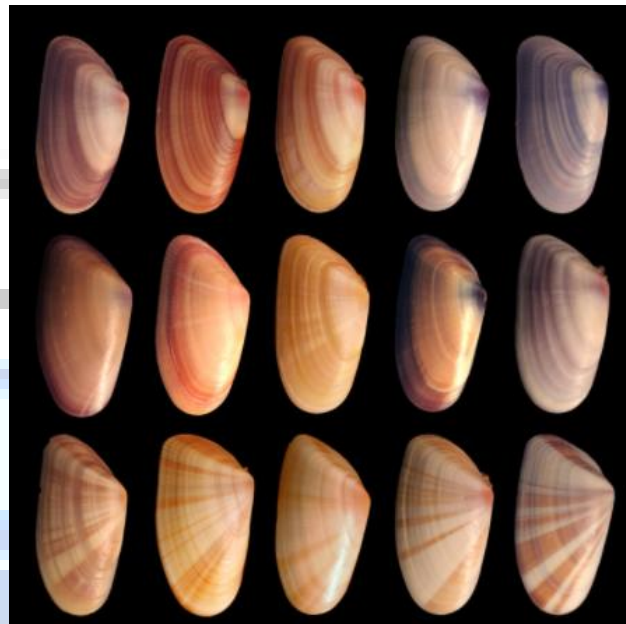


Figure 1: Hereditary variations in the shells over time

Long-term, individual-based studies of animals are an extremely valuable resource. The investments required to establish and maintain long-term, individual based studies of animals should not be underestimated, but they do produce a wealth of data, and it is due to the great foresight and dedication of certain scientists that there are now a handful of, primarily mammalian and avian, long-term field studies that are ongoing. Long-term data from animals are valuable in a number of regards. Amongst other things, long-term data provide greater sample sizes of individuals than point estimates from a population, which reduces the margin of error involved in any subsequent analyses.

Long-term studies also span multiple generations, yielding accurate measures of individuals' life-history traits, such as survival and lifetime reproductive success measures, which are key components of evolution by natural selection. Individuals from long-term studies can also be measured for a trait more than once over their lifetimes, which can reveal the individual variation, and age related and/or environmentally influenced changes, for any given trait. For example, longitudinal studies have been shown to reveal patterns of within-individual age-related declines that are otherwise missed in cross-sectional studies.

Genetic relatedness is an important component of social animal systems. The 'monogamy hypothesis' states that monogamy was the most likely ancestral state of cooperative breeding. In contemporary mammals, cooperative breeding is almost totally restricted to species where a single female virtually monopolizes reproduction and breeds with a single dominant male. Furthermore, recent phylogenetic reconstruction has shown that transitions to cooperative breeding have been restricted to lineages characterized by monogamy. This suggests that relatively high levels of kinship between group members are a necessary condition for the evolution of cooperation. The importance of genetic relatedness in cooperation

also has interesting potential implications for the effect of inbreeding on social organisms. While the consensus is that the negative consequences of inbreeding are thought to have selected for the evolution of inbreeding avoidance mechanisms, there is also an alternative suggestion that the increased kinship within social groups that results from inbreeding may in fact promote or maintain cooperative behaviour in line with kin selection theory.

Evolution and Adaptation to the Environment

Populations of wild cheetahs have very low genetic variation. Because wild cheetahs are threatened, their species has a very low genetic diversity. This low genetic diversity means they are often susceptible to disease and often pass on lethal recessive mutations; only about 5% of cheetahs survive to adulthood.

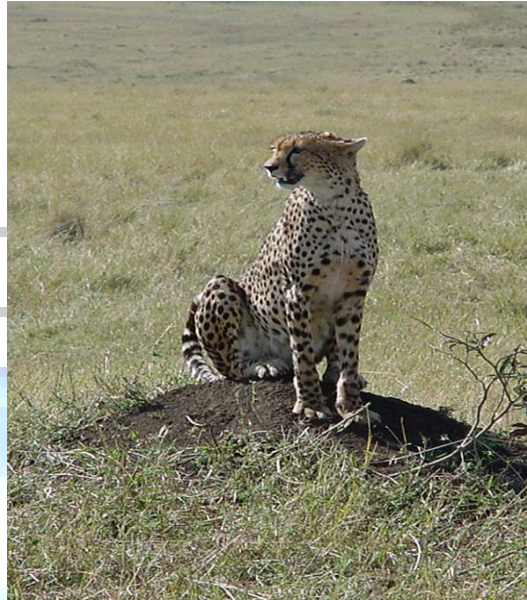


Figure 2: Low genetic diversity in the wild cheetah population

Variation allows some individuals within a population to adapt to the changing environment. Because natural selection acts directly only on phenotypes, therefore, more genetic variation within a population usually enables more phenotypic variation. Some new alleles increase an organism's ability to survive and reproduce, which then ensures the survival of the allele in the population. Other new alleles may be immediately detrimental (such as a malformed oxygen-carrying protein) and organisms carrying these new mutations will die out. Neutral alleles are neither selected for nor against and usually remain in the population. Hereditary variation is advantageous because it enables some individuals and, therefore, a population, to survive despite a changing environment.

Geographic Variation

Some species display geographic variation as well as variation within a population. Geographic variation, or the distinctions in the genetic makeup of different populations, often occurs when populations are geographically separated by environmental barriers or when they are under selection pressures from a different environment. One example of geographic variation are clines: graded changes in a character down a geographic axis.

Sources of Hereditary Variation

Gene duplication, mutation, or other processes can produce new genes and alleles and increase hereditary variation. New genetic variation can be created within generations in a population, so a population with rapid reproduction rates will probably have high genetic variation. However, existing genes can be arranged in new ways from chromosomal crossing over and recombination in sexual reproduction. Overall, the main sources of genetic variation are the formation of new alleles, the altering of gene number or position, rapid reproduction, and sexual reproduction.

DNA Mutation: A mutation is a change in the DNA sequence. These variations in gene sequences can sometimes be advantageous to an organism. Most mutations that result in genetic variation produce traits that confer neither an advantage nor disadvantage.

Gene Flow: Also called gene migration, gene flow introduces new genes into a population as organisms migrate into a new environment. New gene combinations are made possible by the availability of new alleles in the gene pool.

Sexual Reproduction: Sexual reproduction promotes hereditary variation by producing different gene combinations. Meiosis is the process by which sex cells or gametes are created. Hereditary variation occurs as alleles in gametes are separated and randomly united upon fertilization. The genetic recombination of genes also occurs during crossing over or the swapping of gene segments in homologous chromosomes during meiosis.

Independent Assortment

Mendel's law of independent assortment states that genes do not influence each other with regard to the sorting of alleles into gametes: every possible combination of alleles for every gene is equally likely to occur. The independent assortment of genes can be illustrated by the dihybrid cross: a cross between two true-breeding parents that express different traits for two characteristics. Consider the characteristics of seed color and seed texture for two pea plants: one that has green, wrinkled seeds (*yyrr*) and another that has yellow, round seeds (*YYRR*). Because each parent is homozygous, the law of segregation indicates that the gametes for the green/wrinkled plant all are *yr*, while the gametes for the yellow/round plant are all *YR*. Therefore, the F1 generation of offspring all are *YyRr*.

For the F2 generation, the law of segregation requires that each gamete receive either an R allele or an r allele along with either a Y allele or a y allele. The law of independent assortment states that a gamete into which an r allele sorted would be equally likely to contain either a Y allele or a y allele. Thus, there are four equally likely gametes that can be formed when the *YyRr* heterozygote is self-crossed as follows: *YR*, *Yr*, *yR*, and *yr*. Arranging these gametes along the top and left of a 4 × 4 Punnett square gives us 16 equally likely genotypic combinations. From these genotypes, we infer a phenotypic ratio of 9 round/yellow:3 round/green:3 wrinkled/yellow:1 wrinkled/green. These are the offspring ratios we would expect, assuming we performed the crosses with a large enough sample size.

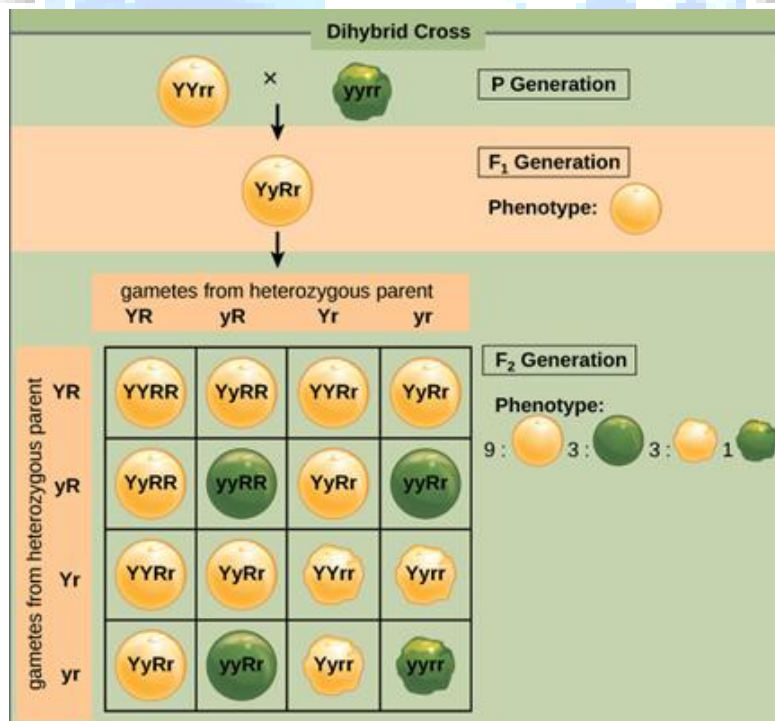


Figure 3: Independent assortment of 2 genes for seed color and texture

CONCLUSION

Hereditary variation is an important force in evolution as it allows natural selection to increase or decrease frequency of alleles already in the population. It can be caused by mutation (which can create entirely new alleles in a population), random mating, random fertilization, and recombination between homologous chromosomes during meiosis (which reshuffles alleles within an organism's offspring). This variation is advantageous to a population because it enables some individuals to adapt to the environment while maintaining the survival of the population. Furthermore, it can be concluded that apportioning trait variance, especially to additive genetic effects, has especial problems in cooperative breeders, highlighting a new 'special difficulty' involved in the study of cooperative societies.

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