The science of symmetry in biology

Symmetry has long been an important concept in mathematics and physics, but in biology its study was largely limited to isolated cases. It was not until 1953 when Mather revealed the value of studying variation in the degree of bilateral symmetry in zoological specimens that the study of symmetry in biology became a more formalized field. The study of symmetry in biology is now known to be of great importance in the understanding of the evolution of biological systems and the development of new technologies.

The symmetry of a biological system can be described in several ways. One way is to consider the degree of bilateral symmetry, which refers to the extent to which a system is mirror-symmetric. Another way is to consider the degree of rotational symmetry, which refers to the extent to which a system is invariant under rotation.

The symmetry of a biological system can also be described in terms of the number of axes of symmetry. For example, a system with one axis of symmetry is said to be uniaxial, while a system with two axes of symmetry is said to be biaxial.

The study of symmetry in biology has important implications for the understanding of biological systems and the development of new technologies. For example, the study of symmetry in the development of biological systems can help to understand how genes are expressed and how cells differentiate.

In addition, the study of symmetry in biology has important implications for the development of new technologies. For example, the study of symmetry in the development of biological systems can help to design new types of biological devices, such as artificial organs or artificial muscles.

Symmetry is a fundamental concept in the study of biological systems and has important implications for the understanding of biological systems and the development of new technologies.
sex allocation is also desirable. Spatial sex ratio theory has clearly given new impetus to the study of coevolution and the evolution of sex ratios and social evolution in insects.

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References

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Symmetry has long been an important concept in mathematics and physics, but in biology its study was largely limited to relatively few questions concerning the evolution of bilateral symmetry. This is possibly partly due to the different world view of biologists. In the sciences of mathematics and physics, it is assumed that the laws of nature are invariant under a particular group of transformations. This means that if a physical system is transformed in a certain way, the laws governing it remain unchanged. This idea is the basis of many mathematical and physical theories, and it is also a key concept in the study of symmetry in biology.

The concept of symmetry is also important in other areas of biology, such as genetics and biochemistry. In genetics, symmetry is often used to describe the arrangement of genes on chromosomes. In biochemistry, symmetry is used to describe the arrangement of atoms in molecules.

In general, the study of symmetry in biology is a rapidly growing field, and it is expected that it will continue to grow in importance in the future. It is likely that the study of symmetry in biology will lead to a better understanding of the fundamental principles that govern the structure and function of biological systems.
Thermal habit, metabolic rate, and the evolution of mitochondrial DNA

David M. Rand

The hallmark of animal mitochondrial DNA (mtDNA) is a rapid rate of sequence evolution, a small genome carrying the same set of homologous genes, maternal inheritance and lack of recombination. Over the past few years, a variety of different observations have led to these accepted notions of mitochondrial biology. Notable examples include evidence for variable rates of mtDNA sequence evolution among taxa, evidence for large and variable mitochondrial genome sizes in certain taxa, and a growing number of cases in meta-analyses of "pupal leakage" in the inheritance of mtDNA. Several recent studies have uncovered different lines of evidence suggesting that an organism's thermal habit, or metabolic rate, can influence the evolution of mtDNA. David Rand is at the Dept of Ecology and Evolutionary Biology, Box 120, Brown University, Providence, RI 02912, USA.

The one could design a custom-  

ized genetically engineered marker for use in population genetics and evolutionary  

biology. It is quite likely that one would reinvent mtDNA. This is essentially the conclusion reached by Avise and colleagues in drawing up a wish list of the attributes of a molecular marker for phylogenetic analysis. It is not coincidental that the unique genetic characteristics of animal mtDNA (rapid rate of sequence evolution; compact genome carrying a uniform set of homologous maternal inheritance; and lack of recombination, to name a few) are the very characteristics that provide evolutionary biologists with a unique perspective of population differentiation and species relationships.\(^5\)

But if our customized marker was (1) shown to evolve slowly, (2) was observed to be variable in genome size due to sequence duplications, and (3) was capable of being trans-  

mitted by both parents? Some evolutionists might react by casting off the evidence as rare exceptions to the rules that will not continue to use the marker; others might abandon the marker for fear of spurious results; while others might focus in on the exceptions as being important markers that shed light on the processes of molecular evolution. One general message of this review is that each of the three reactions offered above (naked-eye observation, abandoning the marker, and researching the cause) can be appropriate responses to the continued use of mtDNA in light of such exceptions. However, the latter response (clarifying the mechanistic bases of these exceptions that promises to break new ground in our understanding of the natural history of mtDNA and indeed, the organisms that carry it. Here I call attention to some recent work that suggests a relationship between metabolic rates and the tempo and mode of mtDNA evolution.

Mitochondrial DNA and the molecular clock

One of the distinguishing characteristics of mtDNA, and one of the principal justifications for its use in evolutionary  

studies, is its rapid rate of sequence evolution. Mitochondrial DNA has first been estimated to evolve at a rate of 1-2 x 10^-9 substitutions per site per year, or about 2% sequence divergence per species per million years (Reis 4 and 5). This suggested a rate of 5-10 times faster than the evolution of nuclear DNA. Although these initial rate calculations were based on comparisons between mtDNA of sheep and goats and among primate species, mitochondrial or nuclear DNA) within a lineage could be due to different functional constraints\(^5\). Differences in the likelihood that a nucleotide will be mutated or corrected\(^5\), or some combination of these factors. The obvious rami-  

fication of this finding is that the associated error of any molecular clock needs to be calibrated for the specific gene and taxonomic group in question before sequence divergence is used to estimate times of divergence or other evolutionary events. Where calibrations of absolute rates were possible, variation in the timing and extent of divergence among taxa was small. This suggests that mtDNA evolution is constrained to be slower than expected variation among taxa in the relative rates of nuclear and mtDNA evolution\(^4,5\). These studies provided little or no evidence to suggest that the mitochondrial molecular clock was variable\(^7\). Thermal habit and the rate of mitochondrial DNA evolution: what is the evidence? In the past several years, calibrations within and among insects\(^8,9\) and vertebrates\(^10,11\) have provided evidence for variation in the absolute rate of mtDNA evolution. While it seems unlikely that this rate variation can be accounted for by a single mechanism (i.e., differences in the number of four protein-coding genes (ATPase subunit 6, cytochrome oxidase subunit 3, NADH dehydrogenase subunit 3 and

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