THE C-VALUE ENIGMA

A Thesis

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ABSTRACT

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This thesis is an investigation of the evolution of genome size in animals. The haploid nuclear DNA contents (genome sizes, or "C-values") of eukaryotes vary more than 200,000-fold, and bear no relationship to organismal complexity or the presumed number of coding genes. The basis for this enormous variation in genome size has remained an unsolved puzzle in evolutionary biology for more than 50 years. The initial "C-value paradox" was solved with the discovery of non-coding DNA, but a new and multi-faceted "C-value enigma" has emerged. The thesis begins with a brief review of the history and central concepts of the puzzle, followed by a thorough discussion of the relationship between DNA content and cell size and the presentation of a mechanistic model which may account for it. Patterns of genome size variation in mammals, birds, amphibians, and insects are discussed, and the implications of non-coding DNA for developmental, physiological, and ecological characteristics are explored in these key groups. A novel method of DNA quantification (Feulgen image analysis densitometry) is also presented and used to provide several hundred new invertebrate genome size estimates. Finally, the implications of the C-value enigma for evolutionary theory are considered in the context of the hierarchical theory of macroevolution developed by palaeontologists. A set of appendices comprising a compilation of roughly 3,000 animal genome sizes is also provided in an effort to facilitate the ongoing study of the C-value enigma.

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