



Anatomical nomenclature: homology, standardization and datasets*

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Abstract

Strictly homology-based character names have the benefit of a consistent, evolutionary basis but must overcome practical problems in terms of the function that names serve as tools for communication. Character names should be fixed at the level of primary (rather than secondary) homology in order to maintain nomenclatural stability between competing phylogenies and to allow characters to potentially re-optimize with the addition of data. Inconsistent rules determine the priority of names for anatomical structures, in marked contrast to the stability and clarity provided by Codes for taxonomic nomenclature. Standardized anatomical nomenclature is amenable to a web-based, ontology-driven framework. Imagery and associated metadata linked to phylogenetic datasets facilitate character documentation, nomenclatural stability, and repeatability without requiring a formal process of typification.

Key words: Primary homology, Priority, Secondary homology, Standardized nomenclature, Typification

Introduction

Biologists (indeed, all humans) name anatomical structures for innumerable reasons, all of them ultimately hinging on communicating some idea about identity. My focus herein will be on the way we name anatomical structures for a particular endeavor in comparative biology, the construction of datasets that we use as tools for inferring evolutionary history.