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A Review of Interspecific Hybridization in the Order Testudines

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R13. A Review of Interspecific Hybridization in the Order Testudines

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Turtles (Order Testudines) have been the subject of more baraminological research than any other single group (see Wood, 2005 for review). Nevertheless, a thorough review of interspecific hybridization, with baraminological interpretations, has yet to be reported. We found evidence of interspecific hybridization in eight of the thirteen extant turtle families. Four of the remaining families are represented by a single species each (Ernst et al., 2000). These include crosses between 74 unique species pairs, approximately 1/3 of which are intergeneric. Eighteen small monobaramins (2-4 species) were identified within the families Pelomedusidae, Chelidae, Kinosternidae, Trionychidae, Emydidae, Geoemydidae [=Bataguridae], and Testudinidae. We also reviewed several recent reports of hybridization in the family Cheloniidae (some with molecular verification) published since the release of Robinson's (1997) paper on turtle baraminology (Barber et al., 2003; Seminoff et al., 2003; Witzell and Schmid, 2003). The family Cheloniidae forms a single monobaramin, as suggested by Robinson (1997), with five of the six species connected by hybridization (hybridization between seven unique species pairs). In addition, a large monobaramin (hybridization between 17 unique species pairs, implicating at least 13 species in this monobaramin) was discovered within the family Emydidae that includes several members of the genera *Pseudemys*, *Trachemys*, *Chrysemys*, and *Graptemys*. There are eight instances of intergeneric hybridization within this monobaramin, connecting the following genera: *Emys* x *Glyptemys*, *Graptemys* x *Trachemys*, *Pseudemys* x *Chrysemys*, and *Pseudemys* x *Trachemys*. Finally, a large monobaramin (hybridization between 19 unique species pairs, implicating at least 14 species in this monobaramin) was discovered within the family Geoemydidae that includes members of the genera *Mauremys*, *Cuora*, *Sacalia*, *Cyclemys*, *Geoemyda*, *Chinemys*, and *Heosemys*. There are 12 instances of intergeneric

hybridization within this monobaramin, connecting the following genera: *Mauremys* x *Chinemys*, *Mauremys* x *Cuora*, *Mauremys* x *Cyclemys*, *Mauremys* x *Heosemys*, *Mauremys* x *Sacalia*, *Cuora* x *Geoemyda*, and *Cuora* x *Sacalia*. Hybridization was not found to connect any of the turtle families or Wood's (2005) proposed holobaramins, so we are unable to reject his hypothesis of five turtle holobaramins. Future attempts will be made to increase the membership of the aforementioned monobaramins through the examination of similarity indices (i.e. non-hybridizing turtles will be included in a monobaramin if they fall within the range of variation of hybridizing turtles).

Barber, R.C., C.T. Fontaine, J.P. Flanagan, and E.E. Louis, Jr. 2003. Natural hybridization between a Kemp's ridley (*Lepidochelys kempii*) and loggerhead sea turtle (*Caretta caretta*) confirmed by molecular analysis. *Chelonian Conservation and Biology* 4:701-704.

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Seminoff, J.A., S.A. Karl, T. Schwartz, and A. Resendiz. 2003. Hybridization of the green turtle (*Chelonia mydas*) and hawksbill turtle (*Eretmochelys imbricata*) in the Pacific Ocean: Indication of an absence of gender bias in the directionality of crosses. *Bulletin of Marine Science* 73:643-652.

Witzell, W.N., and J.R. Schmid. 2003. Multiple recaptures of a hybrid hawksbill-loggerhead turtle in Ten Thousand Islands, southwest Florida. *Herpetological Review* 34:323-325.

Wood, T.C. 2005. A creationist review and preliminary analysis of the history, geology, climate, and biology of the Galápagos Islands. *CORE Issues in Creation* 1:1-241.

R14. Metaprogramming and Genomics

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V(D)J (Variable, Diversity, and Joining segments) recombination allows the genome to encode billions of useful, complex immunoglobulin proteins in a small number of germ-line DNA sequences. Immune cells can rearrange a small number of DNA segments into millions or billions of sequences, which are then used as templates for proteins. As opposed to alternative splicing, the DNA physically rearranges itself during cell maturation (Market and Papvasiliou 2003). This is similar to the behavior of metaprograms in computer science which perform source code rearrangements before compilation. The proteins which cut and rearrange the template DNA is a metaprogramming system, and the DNA sequence that is rearranged is a metaprogram.

Metaprogramming is a computer programming technique where a new programming language is defined which is translated into an existing language. The new language only contains constructs that apply to specific sets of tasks. This allows the programmer to operate more directly on specifications, while the complexities of integrating those specifications together into a workable system are in the metaprogramming system itself. The metaprogramming system is tasked with keeping the metaprogramming rearrangements meaningful and consistent (Bartlett 2005).

Similarly, genetic codes for V(D)J segments do not have to