



Genotypes: a concept to help integrate molecular phylogenetics and taxonomy

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In order to better integrate molecular phylogenetics and taxonomy, genetic sequences from type materials should be explicitly identified in publications using a consistent nomenclature. Despite relatively frequent sampling of sequences from types (particularly topotypes—samples from the type locality), the practice of explicitly noting that these materials were sampled is uncommon. Because of the lack of an explicit nomenclature tied to taxonomy, the existence of genetic “type sequences” is obscured. Also hindering progress in taxonomy is the increasingly uncommon practice of reporting locality and voucher information (e.g., GPS coordinates, museum catalog numbers) on repositories such as GenBank. To remedy this problem and bring awareness to the situation, I propose the use of the term “genotype” as a label for any sequence data from types (including from holotypes, secondary types, topotypes, etc.).

For nomenclatural purposes, genetic sequences from a holotype should be referred to as a “hologenotype” (from: **holotype** and **genotype**), sequences from a topotype will be a “topogenotype,” and so forth. In addition, the genetic marker(s) used should also be incorporated into the nomenclature (e.g., paragenotype ND2). Having the term “genotype” linked to the traditional taxonomic nomenclature will greatly simplify the process of finding comparative data. If the term “genotypes” is included in the text of a publication, academic search engines such as Google Scholar, Scopus and Web of Science will be capable of finding genetic sequences from types much more rapidly than is currently possible. These genotypes can then be used immediately in comparisons and compiled into databases such as GenBank, GBIF (Global Biodiversity Information Facility), or taxon specific sites such as the *World Spider Catalog* (Platnick 2010), *Amphibian Species of the World* (Frost 2010) or the *Catalog of Fishes* (Eschmeyer 2010). Having a database of genotypes will create a new dimension by which taxa can be compared in decisions related to the taxonomic status of species.

The influence of molecular data on taxonomy is poorly understood as evidenced by the growing rift between molecular biologists and traditional morphologists (Mooi and Gill 2010; Chakrabarty 2010a; Smith in press; Wiley *et al.* in press). However, the divide between these two schools may be repaired by the proposed approach of identifying and utilizing genotypes. Enacting this approach will greatly simplify many aspects of modern taxonomy. By making gene sequences from type materials readily available, researchers will be able to rapidly compare what they suspect to be undescribed species, new populations, or species in synonymy.

Type materials remain essential for taxonomic comparisons, but sequence data have not been fully incorporated into these comparisons, or into the tradition of taxonomy. Access to sequence data from type materials will allow for an objective basis for taxonomic comparisons. Judgments about the amount of sequence divergence that is required to differentiate between taxa remains with the individual researchers and their preferred species concepts.

The genotypes approach is not a call to take tissue samples from newly collected primary types (particularly the holotype, which should be maintained as the morphological ideal). Although primary or secondary types are sometimes sequenced (Sparks and Dunlap 2004; Meyer *et al.* 2008; Chakrabarty 2010b), the lack of an identifying keyword or flag for tracking these sequences makes them exceedingly difficult to discover. Researchers should also consider using specimens that are DNA vouchers as part of a paratype series in the description of a new species. Having a paratype that is also a DNA voucher will ensure that genetic materials are available from the type series. Having paragenotypes will allow comparisons of type materials that are not restricted to morphology. Currently the vast majority of taxonomic decisions (e.g., synonyms, descriptions) rely solely on morphology. Morphological comparisons should always be part of this process; however, adding a molecular component will add a new dimension to taxonomic research.