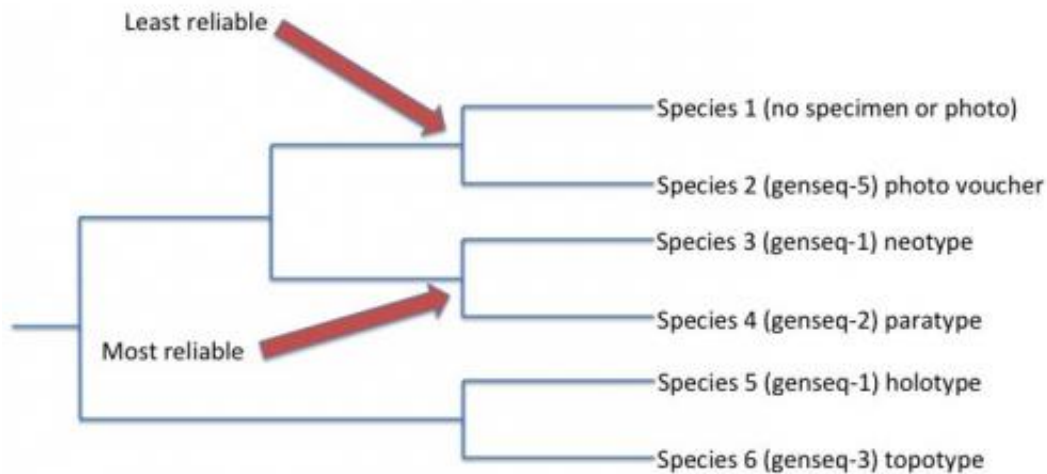


GenSeq: Updated nomenclature for genetic sequences to solve taxonomic determination issues

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The GenSeq nomenclature provides a way to determine the reliability of recovered evolutionary relationships based on how accurately the source specimen of the genetic sequences can be positively identified.

This image illustrates the logic of the GenSeq nomenclature. Credit: Prosanta Chakrabarty

An improved and expanded nomenclature for genetic sequences is introduced that corresponds with a ranking of the reliability of the

taxonomic identification of the source specimens. This nomenclature is an advancement of the "Genetypes" naming system, which some have been reluctant to adopt because of the use of the "type" suffix in the terminology. The study was published in the open access journal *Zookeys*.

The use of genetic sequences has been increasing with each passing year but unfortunately, the separation between voucher specimens and genetic sequences is similarly growing. With increasing frequency, the link between the genetic sequences being used in analyses and the organisms from which they came is not being reported. The taxonomic determination remains solely the responsibility of the submitter of the sequences. Erroneous identifications are difficult to discover, and the perpetuation of the error in subsequent uses of the sequence data is nearly impossible to stop.

In the new nomenclature, genetic sequences are labeled "genseq," followed by a reliability ranking (e.g., 1 if the sequence is from a primary type), followed by the name of the genes from which the sequences were derived (e.g., genseq-1 16S, COI). The numbered suffix provides an indication of the likely reliability of taxonomic identification of the voucher. Included in this ranking system, in descending order of taxonomic reliability, are the following: sequences from primary types – "genseq-1," secondary types – "genseq-2," collection-vouchered topotypes – "genseq-3," collection-vouchered non-types – "genseq-4," and non-types that lack specimen vouchers but have photo vouchers – "genseq-5."

To demonstrate use of the new nomenclature, the authors of the study review recently published news species descriptions in the ichthyological literature that include DNA data and apply the GenSeq nomenclature to sequences referenced in those publications.

"Use of the new nomenclature and [ranking](#) system will improve integration of molecular phylogenetics and biological taxonomy and enhance the ability of researchers to assess the [reliability](#) of sequence data," explains one of the authors Dr. Prosanta Chakrabarty, Museum of Natural Science, Louisiana State University. "We further encourage authors to update sequence information on databases such as GenBank whenever nomenclatural changes are made."

More information: Chakrabarty P, Warren M, Page LM, Baldwin CC (2013) GenSeq: An updated nomenclature and ranking for genetic sequences from type and non-type sources. *ZooKeys* 346: 29–41. [DOI: 10.3897/zookeys.346.5753](#)

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