

Whither Taxonomy?

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Opinion

In order to collate and interpret observations - experimental or observational - it is vital to know the identity of the subject organism.

To achieve this, a taxonomic system was devised over several hundred years.

Descriptions of species range from a few words in Latin, to modern treatments with a full morphological description of a type specimen, supported by tables of measurements, line drawings to scale, and sometimes electron micrographs. But however inadequate the original description, the species name cannot be changed. It can be superseded by a published re-description of the original type specimen, or if that is lost or damaged, of a formally designated replacement type. Generic names, which define the group to which that species belongs, represent a particular expert's opinion and can be changed by publishing a reasoned argument.

These two names, the Generic first (with a capital letter) then the specific (in lower case), define the species. At intervals it is necessary to revise a genus or higher taxon, to bring the descriptions of all species up to the same high standard, and to tease out those pesky synonyms that arise when the same species has accidentally been described more than once.

A revision is hugely worthwhile, as it enables everyone working on that taxon to be confident that they are really reporting on the same species.

Great advances have been made in recent years in the use of molecular sequencing in taxonomy, but the data is used very differently. Each sequence represents an individual organism, but it is not a type specimen.

The study subjects are (provisionally) identified by their morphology, as before. Sequence data from many individuals can be used to formulate a new definition of a species. It can also be used to construct a phylogeny, the equivalent of a family tree for each species, including its relationships to other species and to higher taxa, and the relative evolutionary time separating them.

However, for work on populations in the field, it is not possible to sequence every single individual organism. Morphological taxonomy is still essential, and the two approaches complement each other. But there is now a great disproportion in the resources available. The exciting new molecular studies get the research funding, but morphological taxonomy is regarded as old-fashioned and expendable. If we allow them to get too far out of step, we may regret it.

Fungus-growing termites (Macrotermitinae) provide an example of what problems the current state of taxonomy can throw up. They are a monophyletic group that originated in African forests and later spread to the African savannas and to the tropical forests of SE Asia. There are 322 described species overall, of which 172 belong to the genus *Odontotermes* [1]. That genus has never been revised since it was set up in 1912. Species show great variation in morphology, and the genus clearly needs to be split. Preliminary work on molecular sequencing carried out at Cambridge [2,3] indicated a split into two major groups. Several discrete groups were given provisional or doubtful species names, and several synonymies were suspected. No funding could be obtained to continue the work. Although it is a large, widespread and ecologically important group, very little work has ever been done on it because so many species cannot be securely identified, and that makes it difficult to publish results.

This example also illustrates how important it is to collect and keep voucher specimens from the field, so that the species identity can be verified when a group is revised. Otherwise hundreds of hours and many years of work might be under-valued or wrongly applied, or even lost to science. Fully labelled voucher specimens should be deposited in a permanent, well-maintained collection such as that of a specialist Museum or University.

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Conflict of Interest

No conflict of interest.

References

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