TRADITIONAL TAXONOMY IN THE MOLECULAR AGE: CONTROVERSIES OR SYNERGIES?

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A sound species taxonomy of diatoms is of paramount importance, among other reasons because everything else – ecology, biogeography, evolution, stratigraphy, palaeoecology, biomonitoring, biotechnology, etc (all of which are rapidly expanding) – is underpinned by our ability to identify species and link data together via species names. The introduction of molecular data into diatom taxonomy has led to much discussion and even some antagonism. At their most extreme, opposing attitudes could perhaps be caricatured as (1) morphology is unreliable, subjective and should be abandoned as a source of data and replaced by modern molecular techniques; versus (2) the molecular approach is full of fake promises about improvements, and all it has done so far is reveal high genetic diversity whose relevance (if any) is unknown. However, increasingly there are examples that show that multiple sources of data (e.g. morphological and molecular but also physiological, reproductive behaviour, etc) provide different but complementary insights into species delimitation and identification. To illustrate this, I will mainly use our work on some *Nitzschia* sect. Lanceolatae species, but I will also make reference to other diatoms from time to time. *Nitzschia* is a large genus, notorious for its taxonomic difficulty, and members of the sect. Lanceolatae are particularly challenging, because most have small cells and delicate structure, and because they offer few diagnostic characters. However, these difficulties need to be overcome, for instance because the Lanceolatae are of great t importance from the (palaeo-) ecological point of view: they occur frequently and abundantly in all kinds of waters, and several of them are considered to be indicators of particular environmental conditions. I will explain how we have used culture experiments to investigate 1) how phenotypic plasticity (e.g. in relation to salinity) affects the reliability of morphological characters for taxonomy, 2) morphological changes associated with the life cycle, 3) reproductive biology, and 4) ecophysiology, and I will then explore how these results can be integrated with molecular phylogenetic data. Finally, I will provide a brief evaluation of the current status of DNA-based barcoding in diatoms and its potential and limitations in future characterizations of diatom communities.