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The sponge genetree server—providing a phylogenetic backbone for poriferan evolutionary studies

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Unravelling the phylogenetic relationships of sponges (Phylum Porifera) is an important as well as challenging task. It helps the understanding of character evolution among early branching metazoans but also aids in bioprospecting for valuable bioactive sponge compounds. However, the phylogenetic relationships among Porifera are largely unsolved, because the simple poriferan bauplan frequently prevents unambiguous taxonomic species assignment and a clear definition of morphological synapomorphies is difficult (see e.g. Boury-Esnault 2006). DNA sequence markers are frequently employed to overcome morphological shortcomings in phylogeny (e.g. Kelly Borges *et al.* 1991) and taxonomy (e.g. DNA barcoding, see Wörheide & Erpenbeck 2007). However, some DNA markers suffer from insufficient phylogenetic signal (see e.g. Duran *et al.* 2004 and Wörheide 2006 on CO1 in population studies) and unequal evolutionary rates among taxa (see e.g. Erpenbeck *et al.* 2004 on 28S in Haplosclerida). Therefore, a careful evaluation and selection of molecular markers for each individual project is required.

The Sponge Genetree Server (www.spongegenetrees.org, SGS hereafter) aims to summarize and visualize DNA sequence information on sponges that has accumulated in the past years in public databases. Its up-to-date phylogenetic gene trees use publicly available data to provide a phylogenetic backbone for evolutionary and phylogenetic studies. The genetic distances among sponge taxa and the phylogenetic signal contained in the different gene fragments used for sponge phylogenies to date can be estimated based on those trees. Gene trees presented on the SGS are calculated under different phylogenetic reconstruction methods by using the most frequently used DNA markers currently available in public databases such as Genbank (http://www.ncbi.nlm.nih.gov/). The phylogenies are updated regularly when new sequences are published.

The SGS applies datasets with reasonable taxonomic sampling. Markers that are too variable to serve the purpose of SGS (e.g. the internal transcribed spacer regions of the nuclear rRNA cistron, ITS) are not considered. Due to the fact that different studies employed different partitions of a gene, for some markers several different datasets are analysed separately. The SGS is easily scalable to accommodate phylogenies from additional gene regions with sufficiently large taxon sampling in the future (e.g. ribosomal proteins).

The phylogenetic trees of the SGS are reconstructed under Bayesian- and Maximum-Likelihood methods. Evolutionary models for the individual gene fragments, such as secondary structure specific models for ribosomal RNA genes, are implemented where possible. To assess incompatibilities due to different reconstruction methods, phylogenetic analyses are performed under different reconstruction methods and approaches (e.g. nucleotide data against amino acid data for protein coding genes).

Material and methods

The phylogenetic trees of the Sponge Genetree Server are updated in regular time intervals. Automatization of this process is in development. Trees are presented for each of the major sponge lineages (Demospongiae, Calcarea, Hexactinellida and Homoscleromorpha) separately, and are rooted by sequences from a different sponge group. The matrix is derived from a master alignment for every gene from which the individual partitions are extracted separately. When possible for individual markers, sequences from identical specimens were concatenated. To save calculation time and to

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