

derived from individuals with FA (with unknown complementation group) for the absence of FAAP43 by Western blot using antibody against FAAP43. They found the mutation of *FAAP43* gene in a cell line derived from an individual with FA. Because of this mutation, this cell line could no longer produce FAAP43 protein. They could correct the cellular FA phenotype by introducing their wild type *FAAP43* gene back to the cell but this could not be done by introducing the ring-finger mutant FAAP3 that lacks the E3 ligase activity. Meetei *et al.* named the gene product FAAP43 as FANCL (complementation group L)<sup>11</sup>. An alternative name for the protein is PHF9 (PHD finger protein 9, HGNC ID: 20748) that was recommended by the Human Genome Nomenclature Committee.

One of the important implications of the discovery described here is the suggestion for a possible therapy of the hereditary disease FA. The expression of an enzymatic activity of the newly identified FA protein FANCL (PHF9) suggests that a small molecule could modulate its

activity. If such a molecule could stimulate the monoubiquitination of FANCD2 in the absence of the FA 'core complex', that compound may hold hope for preventing the disastrous consequences of genomic instability in individuals with FA<sup>10</sup>. An attempt can now be made to discover such a molecule or to design it after elucidating the specific binding site structure(s) of the enzyme. Besides, inhibitors of the enzyme activity would probably create a FA-like phenotype and would sensitize cells to DNA cross-linkers. DNA cross-linkers such as cisplatin are already among the best currently available cancer chemotherapy agents<sup>10</sup>. As such, inhibitors of the enzyme activity, if discovered or designed, may serve as good cancer drug candidates.

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## COMMENTARY

### The biodiversity bandwagon: the splitters have it

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The accurate estimation of biodiversity has become one of the most important biological and conservation concerns of the 21st century. An unbiased estimate of biodiversity requires an unambiguous measurement unit. The most commonly used unit is the 'species', and though it is implicitly accepted as valid, consistent and appropriate, there has been little consensus over the many different species concepts proposed over the years<sup>1</sup>. Among these, the Biological Species Concept<sup>2</sup> has been widely used, but it has come under fire due to the arbitrariness of the genetic distance or morphological divergence that is generally used to assign species status<sup>3,4</sup>. Recently, the phylogenetic species concept<sup>5</sup>, which recognizes diagnosably distinct taxa, has been used extensively for some groups. In the context of conservation, 'management units'

and 'evolutionary significant units' have been proposed<sup>6,7</sup>, but most studies still use species as the basic unit without examining or explaining which definition of 'species' they are using.

The core of the species debate revolves around questions over its significance as an evolutionary unit<sup>6</sup>, its utility as a taxonomic unit<sup>8</sup> and its place in the phylogenetic tree<sup>9</sup>. These debates have been largely restricted to systematists and evolutionary biologists while conservation biologists have participated little in the debate<sup>10</sup> even though it has direct bearing on the IUCN Red List or through the designation of biodiversity hotspots<sup>11,12</sup>. Recent conservation paradigms have made species lists paramount, though the biology on which they rest may be suspect. Currently, much of the focus in conser-

vation is on the extinction of described species<sup>13</sup>, and the most 'funded' species today are those listed as 'threatened' in the IUCN Red List while the best funded regions are those designated as biodiversity hotspots, namely those with the most numbers of endangered species.

Recent interest in the herpetofauna of southern India and Sri Lanka has resulted in many field studies and publication of results in various forms, including theses<sup>14,15</sup>, papers<sup>16–20</sup> and reports<sup>21–23</sup>. In particular, three of these<sup>16,21,22</sup> have announced dramatic increases in species richness in the Western Ghats and Sri Lanka. Given the importance of consistency and precision in assessments of diversity, we examine these publications, in particular, the paper in *Science*<sup>16</sup>, which 'describes' more than 100 new species of amphibians to stake the claim that Sri

Lanka is a new amphibian hotspot. We do not dispute the claim that there are several undescribed taxa of amphibians in Sri Lanka and the Western Ghats (and surely in many other unexplored areas in the region such as the Andaman and Nicobar Islands and the eastern Himalaya). Rather, we suggest that the evidence presented is incomplete, and examine the impact of these publications.

### Diversity leapfrogs in Sri Lanka

The discovery of around 200 new species from Sri Lanka was first reported<sup>21</sup> in 1998, following which taxonomic and phylogenetic studies were initiated, leading to the recent paper in *Science*<sup>16</sup>. We found several discrepancies in the data presented in Meegaskumbura *et al.*<sup>16</sup>, in which the authors report about 100 new species. The phylogenetic tree in this paper lists 62 species (45 sequenced by authors and 17 from online databases)<sup>24</sup>. Among these 45 samples, only 32 samples were from Sri Lanka, of which three are known species. Hence, the maximum number of new species that can be inferred from these data is 29. Furthermore, no justification is provided for the sample subset, many of the so-called species nodes do not have bootstrap support to suggest separation, and the level of genetic distance used to delineate species is inconsistent. Thus, it is neither clear that all the terminals in the tree represent unique species nor how the data presented is extrapolated to arrive at '> 100 new species'.

In fact, the identities of many species mentioned in the paper and in GENBANK (<http://www.ncbi.nlm.nih.gov>) do not match, which leads to further confusion. The authors claim to have examined 1500 specimens across the globe<sup>24</sup>, but the details of specimens examined are not given. Since the conclusions in Meegaskumbura *et al.*<sup>16</sup> depend on the description of several new species, it is critical to understand how species were identified. The authors state that they used (i) morphological, (ii) ecological, (iii) bioacoustic, and (iv) molecular data for discriminating species. In this paper, phylogenetic trees are based only on molecular data (12S and 16S of mitochondrial DNA). No mention is given in the text of how morphological, biological or bioacoustic characters were used to identify species,

and instead one is referred to the online supplement<sup>24</sup> for details of the analysis. The supplement contains 76 pages of material, which mostly contains information on 186 sequences, which represent 12S and 16S sequences for 62 samples, many already available in GENBANK. The authors state that only 32 Sri Lankan samples were analysed genetically, and only 20 were subjected to acoustic analysis. The acoustic data are neither presented nor even peripherally discussed in the paper. There is some mention of having collected ecological parameters, but once again the data are not presented.

Clearly, the authors primarily relied on morphological data for the recognition of species, and provide a list of 38 morphological characters in the paper. The authors state that they followed methods detailed in refs 25, 26. However, in ref. 26 an analysis of morphological characters is not evident. On the contrary, the authors<sup>26</sup> emphasize the limitations of morphological characters in rhacophorid taxonomy because of high intraspecific variability. In ref. 25, only around 20 species of rhacophorids were used to produce a key and, Pethiyagoda and Manamendra-Arachachi<sup>21</sup> themselves claim that this key is insufficient to identify Sri Lankan rhacophorids. Unfortunately, few variable morphological characters exist for the identification of rhacophorids<sup>27</sup> and standardized methods for character selection and use in taxonomic classification are needed. The absence of this information is a major lacuna which makes comparisons with other datasets impossible. An initial claim of about 200 undescribed species in Sri Lanka<sup>21</sup> was altered<sup>16</sup> to ca.120, which may change again when species descriptions occur.

The taxonomy of the amphibian fauna of the oriental region is of great interest to systematists and evolutionary biologists due to affinities with other biogeographic regions<sup>27</sup>. However, there has been no revision in the taxonomic status of different groups in 80 years<sup>27</sup>. In the past three years, three major papers have addressed the taxonomy and phylogeny of oriental frogs<sup>16,28,29</sup>. This work indicates a growing global interest in the systematics and biogeography of oriental frogs that show high levels of endemism. Amphibians exemplify ambiguity in taxonomy, with a high level of conservatism in body plan but extreme intra-specific variation<sup>27</sup>. An unequivocal method of combining ecological, bioacoustic and

morphological data is essential for field biologists and taxonomists. Ongoing and future research on taxonomy and diversity needs to evaluate carefully the correspondence between various methods.

### The frog in the well

A substantial part of conservation funding is directed towards areas with high biodiversity. For example, recent programmes such as the Critical Ecosystem Partnership Fund (CEPF), a joint initiative of major conservation funding agencies, provide millions of dollars to support conservation efforts in biodiversity hotspots<sup>30</sup>. The criterion for designating hotspots is species richness of IUCN 'Endangered' species. Hence, many studies may be inclined to use methods that inflate species richness<sup>31,32</sup> or increase the conservation importance of recorded species. Further, descriptions of one or more new species are easily published and results that assign taxa to existing species are of less interest. Species 'splitters' benefit in other ways: when an existing species is divided into two, it reduces the population and distribution of each one, and inflates the richness of the region. Populations of many of these species may thus fall below certain thresholds, according them higher risk status under IUCN criteria. For example, of the primates added to list of threatened species, 17 were due to new descriptions based on the Phylogenetic Species Concept (PSC) compared to seven from an actual change in the status<sup>31,32</sup>. There has been a 27% increase in threatened species of birds across the globe because of the application of the PSC in the identification and delineation of species<sup>33</sup>.

The recent discovery of a relic frog family Nasikabatrachidae<sup>17,18</sup> has reinforced the notion that Sri Lanka and the Western Ghats have a large number of amphibian species. However, given the political and financial baggage of biodiversity, biologists have an even greater responsibility to be careful and consistent in the use of methods, and in their presentation of results. For example, Meegaskumbura *et al.*<sup>16</sup> compare the amphibian diversity of Sri Lanka with Madagascar, Borneo and New Guinea when it is not clear that comparable approaches and criteria have been used to delineate species at all locations. Similarly, Biju<sup>22</sup> reports new

genera and species, in particular ~ 100 new 'species' of *Philautus*, but does not provide any support apart from references to unpublished manuscripts.

Perhaps Meegaskumbura *et al.*<sup>16</sup> and Biju<sup>22</sup> have substantial data which support their findings, but that is still hidden from the public. The publication of such findings in high impact journals<sup>16</sup>, and the reporting of such findings as important research news<sup>34</sup> exert influence on conservation policy and the allocation of funds. That influential reports and papers can be published without transparency in methodology cannot be good for the growth of herpetology in particular and conservation in general in this region. After all, a flood of poorly substantiated reports cannot contribute to scientific knowledge or benefit species conservation. In contrast, they can reduce the credibility of scientific research in conservation biology at a time when many countries are (for the first time) making an attempt to protect their native biodiversity using scientific means.

Effective conservation requires reliable and repeatable methods for estimating diversity that are consistent across taxa and allow accurate measurement of inter-specific variability without being influenced by inconsistent species concepts<sup>35</sup>. Biodiversity conservation may not be well served when planning is centered around a single taxonomic level, especially one as contentious as the 'species'<sup>1</sup>. Phylogenetic diversity is emerging as an important component in the measurement and assessment of biological diversity<sup>36-38</sup>. However, the PSC will have more impact on some taxa and some regions than others and comparisons of lists are seriously undermined<sup>37</sup>. Significant operational difficulties in phylogenetic theory must be resolved before it can be used to reliably estimate species richness or evolutionary history<sup>39</sup>. In essence, studies must attempt to establish concordance between molecular, morphological or other methods of classification to ensure proper characterization and conservation of biodiversity. We stress that biologists and taxonomists must display caution in describing species and diversity, so that these issues do not become an endless bone of contention amongst herpetologists to the detriment of the conservation of the species and their habitats.

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