

Letters to the Editor

Letters (~300 words) discuss material published in *Science* in the previous 6 months or issues of general interest. They can be submitted through the Web (www.submit2science.org) or by regular mail (1200 New York Ave., NW, Washington, DC 20005, USA). Letters are not acknowledged upon receipt, nor are authors generally consulted before publication. Whether published in full or in part, letters are subject to editing for clarity and space.

Revisiting the Taxonomic Impediment

WE READ WITH SOME FRUSTRATION THE RECENT Editorial and Letters concerning the “taxonomic impediment” (Q. D. Wheeler *et al.*, “Taxonomy: Impediment or expedient?”, Editorial, 16 Jan. 2004, p. 285; “Taxonomists and the CBD,” R. Geeta *et al.*, Letters, 20 Aug. 2004, p. 1105; “Museum collections and taxonomy,” D. Causey *et al.*, Letters, 20 Aug. 2004, p. 1106). Geeta *et al.*'s claim that “developing nations... produce far fewer taxonomists than developed countries” is not true in much of Latin America, where a large proportion of research biologists are systematists. For example, Brazil has more systematic ichthyologists, entomologists, and botanists than most countries, due to a federal directive in the 1980s that trained new generations of specialists in cladistics. Undergraduate biology courses in Brazil emphasize not only zoology and botany but also cladistics and biogeography, more so than in American universities, which consequently produce fewer new systematists. But with meager employment prospects in morphological systematics in U.S. institutions and in the developed world generally, how could this be otherwise? This bleak prognosis has also affected U.S. collections (1), representing a “broader trend away from organismal biology” (2); the number of doctorates awarded yearly in botany and zoology is decreasing in the United States.

Unfazed, Geeta *et al.* further suggest that the United States must help overcome the taxonomic ignorance and “dearth of taxonomists” in biodiversity-rich countries. A globalization of taxonomy, like its economic cousin, may negatively affect taxonomic research where it is most needed—in developing nations, which should have a greater stake in biodiversity-related profits. This, in turn, depends on an efficient legal framework that discriminates basic research from biopiracy (3, 4). Developing countries should take the lead in funding research on their biodiversity (5); it will be their burden to protect it.

Wheeler *et al.*'s argument that taxonomists are not capable of efficiently providing species “identities” for ecologists, conservationists,

and politicians is fallacious. This static, atheoretical view of species ignores their phylogeny and biogeography, and thus fails to consider relevant conservation priorities (6). Our notions of species and their relationships (taxa) are based on scientific theories subject to change; the identification of a species is also open to falsification. This is trivialized by conservationists, some molecular systematists (7, 8), and even by Wheeler *et al.*, who affirm that current taxonomic practices “are clearly inadequate for the challenge at hand.” Descriptions of new taxa require theoretical, empirical, and epistemological rigor and seldom follow a time-frame judged appropriate to curtail the biodiversity crisis. This is not a “failure” of systematists but of those who regard taxonomy as only a “biodiversity-naming” service.

“ A globalization of taxonomy, like its economic cousin, may negatively affect taxonomic research where it is most needed—in developing nations, which should have a greater stake in biodiversity-related profits.”

—DE CARVALHO ET AL.

A disregard for long-established taxonomic practice, not considered cyber-enhanced enough (7–10), underscores our angst. We concur that “informatics... is not a substitute for science” (11), and that the “Big Machine” of molecular taxonomy may “do little to address the real problem” (12). Speeding up the pace of taxonomy through the Internet and technology, although desirable, is not enough to stimulate a growing taxonomic foundation. For this, systematics needs theoretical training, more professionals, a lasting commitment to collections, and recognition as a robust science by peers and policy-makers, without which taxonomy itself may fall victim to extinction.

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A Clue to the Origin of the Bilateria?

IN THEIR REPORT “ORIGINS OF BILATERAL symmetry: *Hox* and *Dpp* expression in a sea anemone” (28 May 2004, p. 1335), J. R. Finnerty *et al.* deduce from expression patterns of *Hox* genes during development of the planula larva (their fig. 3) that the oral-aboral axis in the adult sea anemone *Nematostella vectensis* is homologous to the anterior-posterior axis (A-P axis) of adult arthropods and craniates. In his accompanying Perspective, “The ups and downs of a sea anemone” (p. 1255), P. Holland points out that a homolog of an “anteriorly” expressed *Hox* gene in the

LETTERS

anthozoan *Nematostella* is expressed posteriorly in the planula of the hydrozoan *Podocoryne* (1). This conflicting evidence may be resolved by assuming a “developmental reversal of spatial polarity” during hydrozoan metamorphosis (Finnerty *et al.* SOM).

Concerning this discrepancy, we want to point out that in acoel flatworms, which are regarded by some to represent the most basal extant bilaterians (2–4), the anterior pole of the A-P axis in the developing brain is separate from the developing mouth (5), as is the case in most bilaterians (6). The developing anterior pole and the A-P axis of the acoel *Convoluta pulchra* can be deduced from the formation of the primary muscle grid consisting of circular and longitudinal fibers (7, 8). The mouth becomes visible after the primary muscle grid is established on the ventral side in the posterior third of the animal. The separate spatial origin of the mouth and anterior pole of the A-P axis is consistent with the planula concept for the origin of the Bilateria, in which triploblasts are derived from larval diploblasts (9, 10), but is in conflict with the co-localization of the mouth and anterior pole as indicated by Finnerty *et al.*

However, the new *Hox* gene information from *Nematostella* brings into focus the

opposing hypotheses, in which triploblasts are either derived from larval or from adult diploblasts (11–13). Spatial expression of homolog *Hox/ParaHox* genes (14) in embryos of acoel flatworms and similar data on basal scalidophorans (e.g., priapulids) with the brain encircling the mouth may bring us closer to solving the puzzle of the origin of the Bilateria, summarized by Hyman in the closing sentence of her famous “Retrospect”: “Anything said on these questions lies in the realm of fantasy” [(15), p. 754].

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Response

RIEGER *ET AL.* FOCUS ON TWO QUESTIONS that are not directly addressed by the data in our Report: first, the evolutionary relationship of the mouth to the anterior-posterior axis, and second, the derivation of bilaterians from either a larval or an adult diploblastic ancestor.

On the basis of broad similarities in *Hox* and *TGF- β* expression between *Nematostella* and bilaterian metazoans, we argued that the bilateral symmetry exhibited by anthozoan cnidarians (corals, anemones, and their allies) is homologous to the bilateral symmetry exhibited by bilaterians. Our hypothesis implies a direct correspondence between the oral-aboral axis of cnidarians and the anterior-posterior axis of bilaterians. Furthermore, because *Nematostella* homologs of “anterior” *Hox* and *ParaHox* genes are expressed near the mouth, we suggest a correspondence between the oral end of cnidarians and the anterior end of bilaterians (1).

However, as Rieger *et al.* point out, a different relationship is suggested by the expression of an anterior *Hox* gene in the hydrozoan jellyfish *Podocoryne*: *cnox1-Pc* is expressed in a region of the planula larva corresponding to the future aboral end of the adult polyp (2). The evolutionary significance of this finding is unclear because (i) the expression patterns of *Hox* and *Hox*-related genes vary among hydrozoans (1, 2), and (ii), in one instance, a *Hox*-related gene undergoes an axial reversal during the course of development in *Podocoryne* itself (3). This variability within and between hydrozoan cnidarians makes it difficult to reconstruct the spatial expression of *Hox*-related genes in the ancestral hydrozoan. It is therefore impossible to reliably extrapolate these hydrozoan data to the ancestral cnidarian or the cnidarian-bilaterian ancestor. In contrast, orthologous genes in *Nematostella* and the coral *Acropora*, two anthozoan cnidarians, tend to exhibit highly similar and presumably conserved patterns of spatial expression [our Report, (4)].

We argue that the mouth of most bilaterians is formed "in a region" close to the anterior end of the adult body plan. On the basis of paleontological evidence, an anterior terminal mouth is likely to be the ancestral condition for all ecdysozoans (5), and a compos-

ite circum-oral "brain" is a feature of virtually all invertebrate animals (6). With regard to the position of the mouth in acoels, the development of the primary muscle grid may or may not be associated with the position of the anterior pole. The only way to make such a statement about the embryological origin of any structure is to perform a detailed fate map, but such a fate map has been performed only for a single species of acoelomorph (7).

Finally, it is not clear if our data can distinguish whether triploblastic bilaterians arose from larval or adult diploblasts. Diploblasts (cnidarians and ctenophores) do not generate feeding larvae and the adult mouth arises only once, at the animal pole (also the site of first cleavage). In cnidarians, the mouth arises at the posterior pole of the swimming stage (planula). If *Nematostella* reflects the ancestral condition for the cnidarian-bilaterian ancestor, then most descendant organisms modified an axial system in which the mouth forms at the anterior pole.

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CORRECTIONS AND CLARIFICATIONS:

Essays: "The scientific consensus on climate change" by N. Oreskes (3 Dec. 2004, p. 1686). The final sentence of the fifth paragraph should read "That hypothesis was tested by analyzing 928 abstracts, published in refereed scientific journals between 1993 and 2003, and listed in the ISI database with the keywords 'global climate change' (9)." The keywords used were "global climate change," not "climate change."

News of the Week: "Science agencies caught in postelection spending squeeze" (3 Dec. 2004, p. 1662). The article contains an incorrect reference to Michael Marx's institutional affiliation. He is a professor of physics at Stony Brook University in New York.