J Mol Evol (1998) 46:378–381

JOURNAL OF MOLECULAR EVOLUTION

Point Counter Point

Is There Sufficient Evidence to Elevate the Orangutan of Borneo and Sumatra to Separate Species?

Recently, Xu and Arnason (1996) proposed that the orangutan of Borneo and Sumatra be assigned separate species status. The proposed taxonomic change is based on comparison of a single Sumatran mtDNA sequence to a single mtDNA sequence found in Genbank (D38115). Two partial sequences were also included in their analysis.

Xu and Arnason's proposal is not the only proposal for separate species status for the orangutan populations. Jancewski et al. (1990) alluded to such a notion and Zhi et al. (1996), in a paper published concurrently with that of Xu and Arnason, also propose that the subspecies be elevated to species status based on 2-D gel data, mtDNA RFLP data, and an RFLP assessment of a single minisatellite locus.

We do not agree with the taxonomic conclusions made by either group but will, for the purposes of this letter, concentrate on the conclusions of Xu and Arnason. We find their conclusions to be untenable for a number of reasons. These include their choice of species definition, the sample size employed, and the reliance on a maternally inherited character for assessing gene flow. Since changes in the taxonomy of the orangutan are likely to have implications for their conservation, it is particularly important to not base these changes on flawed arguments.

Xu and Arnason note that their proposal is at odds with the biological species concept (BSC) championed by Mayr (1965). The BSC has been widely criticized both on philosophical grounds and because it is directly testable in only a very limited number of cases (see Mallet 1995). The orangutan is one of those cases. Not only do Bornean/Sumatran crosses result in viable and fully fertile offspring, but there are anecdotal reports that, at least in the captive setting, the orangutan prefers to ''outcross.'' According to the Species Survival Plan orangutan ''Stud Book,'' of the 304 captive orangutans in North American zoos, 88 are Bornean/Sumatran crosses (L. Perkins, personal communication).

Xu and Arnason did not actually state which species definition they used, but referenced Mallet (1996). Mallet concludes that the genetic cluster method (GC) best meets the requirements that a method be applicable in the broadest possible range of cases and yield natural groupings of organisms. His approach seems reasonable but requires identification of genetically definable clusters of individuals and the absence of intermediates. The samples employed by Xu and Arnason clearly do not fit these criteria: One individual from Sumatra (plus a partial from another) is compared to one from Borneo (plus partials from two others). All sequences were derived from zoo animals, and no geographic information is provided beyond ''Sumatra'' and ''Borneo.'' It is quite possible that the two ''Sumatran'' representatives were connected by a short, uninterrupted maternal lineage. Since the partial sequence was identical to the homologous region of the complete Sumatran sequence, they base their conclusions on the single complete sequence. A single individual cannot represent a population. To make matters worse, deBoer (1982) asserts that there are at least two separate populations of orangutan in Sumatra.

There are similar problems with the Bornean samples. According to the work of Zhi et al. (1996) and Muir et al. (1994), there is a significant substructure to the Bornean population. The Bornean orangutan could not possibly be represented by two partial and one complete mtDNA sequences of unknown geographic origins. There is no question that sequence divergence exists between individuals from the two islands, but Xu and Arnason have made no attempt to assess the range of variation in the populations on either of these islands.

Mallet's genetic cluster method clearly cannot be applied to this data set. So what definition did Xu and Arnason use? They seem to rely entirely on the idea of ''species level of divergence'' (SLD) for their argument. Zhi et al. (1996) used the same notion. SLD is a term that

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does not really apply to anything. The term implies that a certain amount of divergence is diagnostic of speciation, and in our view, betrays a fundamental misunderstanding of speciation. Jolly et al. (1995) pointed out that there is a 200-fold range of sequence divergence among sibling vertebrate species. This range can only increase as more sequences become available. Although it seems worthwhile to quantify speciation, everything we know about it suggests that speciation is not an algorithmically definable process. That a proportionality exists between speciation and the rate of acceptance of mutations remains unsupported.

We believe sequence divergence is an inadequate basis for defining species. But even if one holds the view that sequence divergence can define species, mtDNA cannot provide the information necessary. The mtDNA genome is inherited as a single genetic locus in a strictly maternal manner. A maternally inherited molecule is a poor choice for assessing total gene flow in an organism with two sexes. The inability of mtDNA to provide information about gene flow in males is particularly problematic with the orangutan since male and female home ranges are often significantly different (Galdikas 1985a,b).

Zhi et al. (1996) recognize the need to include nuclear loci to understand gene flow in the orangutan. However, their attempt to address this need by employing an RFLP analysis of a single minisatellite locus falls short. Given the high rate of acceptance of mutations for minisatellites, in addition to increased likelihood for size homoplasy in populations which have been isolated for a significant period (Garza and Freimer 1996), we suggest minisatellites are not a good choice either.

A number of studies have pointed out that changing taxonomy has implications for conservation (Zhi et al. 1996; Mallet 1996; Uchida 1996). Here lies the danger in creating taxonomy which may have an influence on conservation strategy. It is a seductive argument that orangutan populations in Borneo and Sumatra should be maintained and conserved *because* they are separate species, but using this argument, the populations become vulnerable if an expanded dataset argues against species-level designation. Utilizing this argument also facilitates the prioritization of conservation efforts based on species status. It is essential that conservation issues be removed from the vagaries of academic systematics arguments. Are we basing global conservation and endangered species legislation on a term which we have been unable to define for two centuries? In terms of conservation of the orangutan and other endangered species, a better more permanent case can be made for preserving diversity without tying the argument to ephemeral species definitions.

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Response

The topic of Xu and Arnason's (1996) study was clearly expressed in their Introduction: "In the present study we address the systematic status of the Sumatran and Bornean orangutans by quantifying their molecular difference on the basis of comparison of complete mitochondrial DNA (mtDNA) molecules." They then compared this difference with the differences between "all closely related mammalian species pairs currently represented by complete mtDNAs." Xu and Arnason (1996) sequenced the complete mtDNA of one Sumatran specimen and the complete control region of another Suma-