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Gary Skiba
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Dear Mr. Skiba:

This letter is to address your request for my comments on Dr. R. R. Ramey's report "Testing the taxonomic validity of Preble's Meadow Jumping Mouse (*Zapus hudsonius preblei*)". I am not an expert on genetic analyses, so am not able to comment on the specifics of the analyses presented in the report. Likewise, I am not an expert on morphometric analyses, so cannot comment on these measurements.

I will comment on the conclusions provided in the report based on the logic presented. Namely, this report concludes that there is no basis to distinguish between *Z. h. campestris* and *Z. h. preblei* because the authors did not find a difference with the tools they used. This conclusion is equivalent to stating that a Chevy 4-door wagen is equivalent to a Corvette because both use gasoline, both are shiny, both have windows, and both run on rubber tires. Both vehicles share many, many similar qualities, but are still very different vehicles.

The problem is that it is logically much easier to state that two items are different if the proper metric is measured. In contrast, one can never state that 2 items are identical, even if many, many measurements are taken, because the one critical difference between the two items was not measured or detected in the analysis. This report concludes that the two subspecies are the same, based on a limited suite of measurements. In reality, the report should conclude that no differences were detected given the measurements conducted, and should not jump to the unfounded conclusion that the two subspecies are identical. The conclusions presented in the report are much too strong given the necessarily limited set of measurements used.

Most importantly are the limited inferences that can be drawn from genetic measurements concerning important differences. Mitochondrial DNA sequence data could not distinguish a miniature dachshund from a Saint Bernard. Likewise mitochondrial DNA sequence data cannot distinguish a fall run salmon stock from a spring run salmon stock of the same species, even though this behavioral trait is critical to the survival of each stock. Wayne and Morin (2004) emphasize that the vast majority of conservation genetic evaluations are based on neutral markers which are influenced by genetic drift. Quoting Wayne and Morin (2004:93-94):

Specifically, neutral markers may often be poor surrogates for levels of variation in fitness traits (Reed and Frankham 2001). Furthermore, measures of population differentiation based on the analysis of quantitative traits, such as life history

characteristics, may not be well correlated with measures based on neutral markers (McKay and Latta 2002; Merila and Crnokrak 2001). Conservation units based on historical isolation alone may not capture the adaptive variation necessary for populations to thrive in the short and long term, given changing environmental conditions (Crandall et al. 2000). Consequently, conservation genetic surveys should include neutral markers to assess population history and demography, as well as assays of fitness-related traits to preserve adaptive diversity.

Wayne and Morin (2004) provide further justification for why additional metrics than mitochondrial DNA and morphometric measurements are needed, such as analysis of natural history, functional aspects of the genotype and phenotype, and habitat data.

In summary, the conclusions in the Ramey et al. report are an example of a basic statistical misinterpretation. They were unable to reject the null hypothesis of no differences between *Z. h. campestris* and *Z. h. prebleii* based on either genetic or morphometric procedures, so they concluded that the null hypothesis of no difference between *Z. h. campestris* and *Z. h. prebleii* is true. As discussed above, such a conclusion is not supported by the data, and in fact can never be made with certainty.

Sincerely,

Gary C. White
Professor

Literature Cited

Wayne, R. K., and P. A. Morin. 2004. Conservation genetics in the new molecular age. *Frontiers in Ecology and the Environment* 2(2):89-97.

Literature Cited in quote from Wayne and Morin (2004)

Crandall, K. A., O. R. P. Bininda-Emonds, G. M. Mace, and R. K. Wayne. 2000. Considering evolutionary processes in conservation biology. *Trends in Ecology and Evolution* 15:290-295.

McKay, J. K., and R. G. Latta. 2002. Adaptive population divergence: markers, QTL and traits. *Trends in Ecology and Evolution* 17:285-291.

Merila, J., and P. Crnokrak. 2001. Comparison of genetic differentiation at marker loci and quantitative traits. *Journal of Evolutionary Biology* 14:892-903.

Reed, D. H., and R. Frankham. 2001. How closely correlated are molecular and quantitative measures of genetic variation? A meta-analysis. *Evolution* 55:1095-1103.