

PRIMATES OF THE ORIENTAL NIGHT

Edited by:

Myron Shekelle
Ibnu Maryanto
Colin Groves
Helga Schulze
Helena Fitch-Snyder



**RESEARCH CENTER FOR BIOLOGY
THE INDONESIAN INSTITUTE OF SCIENCES
AND
THE INDONESIAN BIOLOGICAL SOCIETY**

© 2008 Indonesian Institute of Sciences (LIPI)
Research Center for Biology*

Cataloging-in-Publication Data

Primates of The Oriental Night/Myron Shekelle, Ibnu Maryanto, Colin Groves, Helga Schulze, Helena Fitch-Snyder (Eds.). – Jakarta : LIPI Press, 2008.
ix + 145 pp.; 17,6 x 25 cm

ISBN 978-979-799-263-7

1. Primates 2. Tarsiers 3. Slow loris

599.83

Publisher : **LIPI Press, member of Ikapi**



* Indonesian Institute of Sciences (LIPI)
Research Center for Biology
Cibinong Science Center
Jl. Raya Bogor km. 46, Cibinong
West Java
Telp: 021-8765056, 8765057

A METHOD FOR MULTIVARIATE ANALYSIS AND CLASSIFICATION OF TARSIER TAIL TUFTS

Myron Shekelle¹, Collin Groves², Sharon Gursky³, Irene Neri-Arboleda, & Alexandra Nietsch⁴

¹Center for Biodiversity Studies and Conservation, Faculty of Mathematics and Science
University of Indonesia, Depok 16421, Indonesia Email: shekelle@tarsier.org

²School of Archaeology and Anthropology, Australian National University, Canberra, ACT 0200 Australia

³Department of Anthropology, Texas A&M University, College Station TX 77843, USA

⁴Freie Universität Berlin, Institut für Verhaltensbiologie, Haderslebener Str. 9, 12163 Berlin, Germany

ABSTRACT

Several independent studies of acoustics, DNA, and morphology support the hypothesis of numerous cryptic sibling taxa within *Tarsius tarsier* (=spectrum), but direct comparison among studies is often hindered by the relative incomparability of specimens (e.g. those that measure acoustic form versus those that measure crania). Tail tufts have been used for taxonomic identification both among and within tarsier species groups, but traditional univariate measures of tail tuft have yielded disappointing results. We used an ordinary ruler to assess 105 museum specimens and captive animals for overall tail length and five measurements of tail tuft fur length. We used a discriminant function analysis for 2 sets of analyses, one on all 105 tarsiers specimens grouped by tarsier species groups, and another on 37 Eastern tarsiers grouped by taxon. To accommodate for possible changes in tail length due to preservation method, separate analyses were conducted for both using: a) all variables, and b) all variable except tail length. In the analysis of all tarsiers grouped by species group with all variables, 96.2% of the original grouped cases were correctly classified, and 93.3% of cross-validated cases were correctly classified, while the respective values were 91.4% and 89.5% when the variable, tail length, was excluded. In the analysis of Eastern tarsiers grouped by taxon with all variables, 86.5% of the original cases were correctly classified, and 67.6% of the cross-validated cases correctly classified, while the respective values were 78.4% and 45.9% when the variable tail length was excluded. This method clearly has utility for diagnosing tarsier species groups, and it shows strong potential for assisting in the diagnosis of fine scale taxonomic variation within the Eastern tarsier species group, and perhaps within other tarsier species groups, as well. It is applicable for a great variety of specimen types, requires almost no cost and very little training, and takes very little time. We expect that this method will find utility for studies of both tarsier taxonomy as well as wildlife monitoring. We intend to extend our examinations of tarsier tail tufts.

Keywords: *Tarsius*, Taxonomy, Wildlife Monitoring

INTRODUCTION

There is a growing body of evidence that supports the hypothesis of numerous cryptic sibling species within *Tarsius tarsier* (=spectrum) as predicted by MacKinnon and MacKinnon (1980). In addition to MacKinnon and MacKinnon, results of several other field surveys show geographically-structured variation in the duet call (Niemitz 1984, Niemitz *et al.* 1991, Nietsch and Niemitz 1993, Shekelle *et al.* 1997, Nietsch and Kopp 1998, Nietsch 1999, Nietsch and Babo 2001, Nietsch and Burton 2002, Shekelle 2003). Groves (1998, 2001, 2003) found that multivariate analysis of cranio-skeletal material in museum collections partially corroborates the classification based upon duet form. Shekelle (2003) found that DNA sequence data offered robust support

for the taxonomic separation of insular island populations from Sangihe and the Togian Islands of Malenge and Batudaka, but the bootstrap tree showed poor resolution among populations from Sulawesi proper. Shekelle *et al.* (this volume) found that the most parsimonious tree in Shekelle (2003) was not significantly shorter than a tree constrained by the hypothesis that forces monophyly based upon duet form and showed that the distribution of tarsier acoustic groups (=duet forms) formed a nearly one-to-one match with a 'hybrid biogeographic hypothesis' that layered prior hypotheses based upon empirical biological and geological data. Merker *et al.* (2007) examined mtDNA and nDNA sequence information from a total of 139 specimens from a short transect connecting two putative tarsier species identified by acoustic data and found limited hybridization, with a

pattern of genetic diversity consistent with the hypothesis that acoustic groups are separate taxa. Thus, several independent studies of morphology, genetics, and biogeography are all broadly consistent with the hypothesis that tarsier duet forms identify distinct taxa.

One problem that has proven vexing for tarsier taxonomy and evolutionary biology is that specimens that can be scored for cranio-skeletal variation are not typically scorable for acoustic variation, and vice versa. A second set of problems is that current methods for surveying tarsier populations, principally analysis of DNA sequence data and acoustic surveys, are labor intensive, expensive, and require technological sophistication. For the purposes of conservation and monitoring, what is needed is an inexpensive, low-tech method that can be applied to living animals, both captive and wild, as well as deceased specimens. At a workshop in Jakarta in January 2003, several specialists in tarsier biology held a brainstorming session on this topic and the decision was made to try using a multivariate technique to glean taxonomic information from the tail tuft.

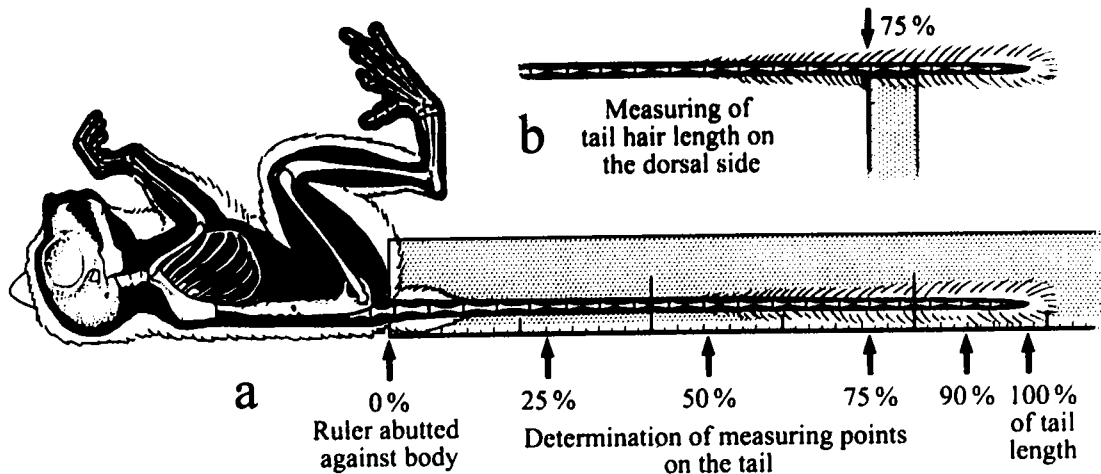
Hill (1953, 1955) identified systematic differences in the tail tufts of tarsiers from the Philippines, Sundaland, and Sulawesi, and classified these animals as *Tarsius syrichta*, *T. bancanus*, and *T. spectrum*, respectively. Tarsier taxonomy is currently in a state of flux, and these species are referred to herein as Philippine, Western, and Eastern tarsiers, respectively (see Shekelle, this volume). More subtle differences have been noted in some tarsier populations, offering some hope that this feature can be used for fine-scale taxonomic identification. Meyer (1897) described a new species, *Tarsius sangirensis*, from Greater Sangihe Island and from Siau Island, both in the Sangihe Island chain between Sulawesi and Mindanao, based in part on reduced furriness of the tail tuft. Meyer (1897) further noted that a tarsier in the Dresden museum collected from Selayar Island, south of Sulawesi, also had a less extensive tail tuft. Groves (1998) found a second specimen of a Selayar tarsier to have the same condition and recommended taxonomic separation of the Selayar population. Shekelle *et al.* (1997) surveyed wild tarsier populations

on Greater Sangihe Island and also noted differences in the tail tuft, consistent with what Meyer had noted for *T. sangirensis*. Field surveys corroborated the observation by Meyer and Groves that the Selayar Island tarsier population has a less extensive tail tuft (M.S., personal observation), and three specimens from that expedition are included in this study. Thus, several authors have used tail tuft variation to show pronounced differences among species groups and subtle differences within the Eastern tarsiers using non-quantitative observations.

Efforts to quantify these differences have had limited success using univariate statistics, such as "tail tuft length" (C.G. unpublished data). This is partly because, under close examination, very fine hairs are visible along the length of the tail, and determination of where the tail tuft begins is arbitrary and repeatability of this measurement is questionable. Additionally, univariate statistics fail to capture some of the subtle complexity of the tail tuft's structure. Therefore, we elected to try a multivariate approach that was methodologically simple and inexpensive, but which would capture some aspects of tail tuft shape.

METHODS

The length of the tarsier tail was measured using a scaled ruler. One end of the ruler butted into the spot where the tail articulates with the body, and tail length was measured to the limit of the fleshy portion of the tail (i.e. the length of the fur on the end of the tail was not included in this measurement) (Figure 1). The shape of the tail tuft was estimated by measuring the length of fur at certain relative points along the tail. For consistency, the dorsal surface was arbitrarily chosen for measuring fur length. Quartiles were chosen for the original method, and the length of the fur was measured at 100%, 75%, 50%, and 25% of the length of the tail. For example, if a tarsier tail measured 200 mm, the length of the tail fur was measured at the extreme distal end, 150 mm from the base, 100 mm from the base, and 50 mm from the base. Preliminary results indicated that quartiles would not adequately capture the variation in those



Helga Schulze © 2008

Figure 1: Diagram illustrating how to collect the measurements discussed in this paper.

populations with relatively small tail tufts, (i.e., *T. bancanus* and *T. syrichta*) and one additional measurement, 90%, was arbitrarily chosen. Thus, the measurements in this study include tail length (TAILLENG, or TL), and the length of tail fur at 100% (FULL), 90% (NINETY), 75% (SEVFIVE), 50% (FIFTY), and 25% (TWFNVE) of total tail length.

All measurements were estimated to the nearest millimeter. Fur that appeared to be less than about 0.5 mm was scored as 0.0 mm. Where fur length varied at a given point, efforts were made to measure the longest *hairs* (but not necessarily the longest *hair*, such as in cases when one, possibly aberrant, hair is much longer than other hairs around it). The search for the longest hairs at a given point was by no means exhaustive, and typically entailed several seconds of examination at most. All of the measurements on a given animal could be completed in no more than five or ten minutes, usually much less.

The original data set was collected on tarsiers in the *Museum Zoologicum Bogoriense* (MZB), including several live specimens, by the entire group of authors. Subsequent data were collected by M.S. at the Field Museum of Natural History (FMNH), the Smithsonian (USNM), and the Raffles Museum of Biodiversity Research (ZRC).

Data were analyzed using the discriminant function analysis in SPSS 11.0 for Macintosh. Prior probabilities were calculated using the 'all groups

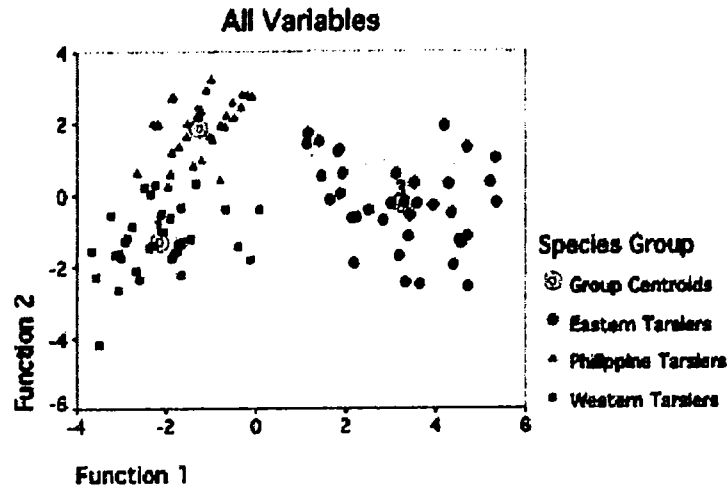
equal' option. In each analysis, the 'enter independents together' option was used.

Only adult specimens were included in the analyses reported here. These amounted to 105 specimens: 37 Western tarsiers, 31 Philippine tarsiers, and 37 Eastern tarsiers. We speculate that the tail length changes after an animal dies and is preserved. To examine the possibility of error introduced by this, separate analyses were conducted, both with and without using the variable tail length. In all analyses, the robustness of the results was tested using a jack-knife approach with the 'leave one out' option in SPSS (referred to as "cross-validated" results).

RESULTS

The first set of two analyses consisted of 105 specimens grouped by species group, i.e. Philippine ($n=31$), Western ($n=37$), and Eastern ($n=37$), analyzed first with all variables (Analysis 1a) and secondly without the variable "tail length" (Analysis 1b). Graphical results of analyses 1a and 1b are presented in Figure 2, with function 1 plotted against function 2. The three species groups appear as two well-defined clusters, with Eastern tarsiers clearly separated from a second Philippine-Western cluster. Philippine and Western tarsiers are, themselves, distinct clusters with very slight overlap. In analysis 1a, 96.2% of the original grouped cases were correctly classified, and 93.3% of cross-validated cases were

Canonical Discriminant Functions
All Cases, Grouped by Species Group



Canonical Discriminant Functions
All Cases, Grouped by Species Group

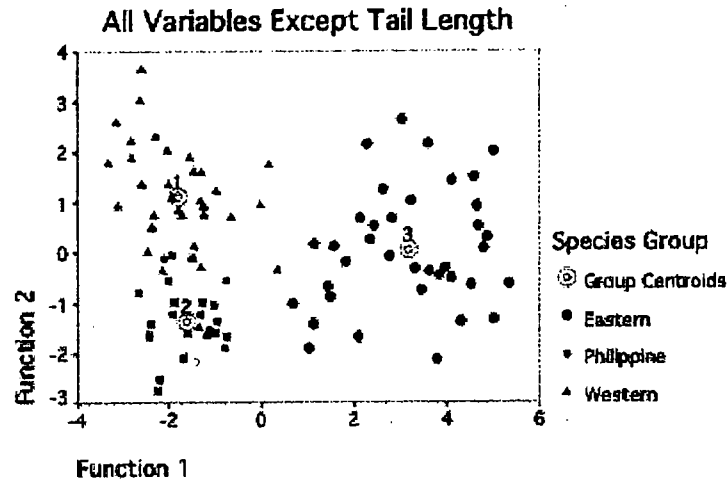


Figure 2: Results of DF analysis of three tarsier species groups. Analyses 1a, with tail length, (above) Analyses 1b, without tail length, (below)

correctly classified, while the respective values for analysis 1b were 91.4% and 89.5% (Table 1).

A second set of two analyses was performed on the Eastern tarsiers in our data set. Cases were grouped by taxon as follows: those taxa of Eastern tarsiers recognized by Brandon-Jones *et al.* (2004), i.e. *T. sangirensis* (n=3), *T. pelengensis* (n=5), *T. dentatus* (=dianae) (n=6), *T. pumilus* (n=2). Other taxa included in the analysis included: *T. spl* (from

Selayar Island, see Groves 1998) (n=3), and *T. lariang* (i.e. the Palu acoustic form, Merker and Groves 2006) (n=3). Brandon-Jones *et al.* (2004) list numerous other populations that may be undescribed taxa that warrant further taxonomic research (see Shekelle and Leksono 2004), but these were all lumped into *T. tarsier sensu lato* (n=15), following Groves (2001). Graphical results of analyses 2a and 2b are presented in Figure 3, with function 1 plotted against function 2. In analysis 2a

Table 1: Results of Analyses 1a (above) and 1b (below)

| | | Predicted group membership | | | | |
|-----------------|-------|----------------------------|---------|------------|---------|-------|
| | | | Western | Philippine | Eastern | Total |
| Original | Count | Western | 36 | 1 | 0 | 37 |
| | | Philippine | 1 | 30 | 0 | 31 |
| | | Eastern | 0 | 2 | 35 | 37 |
| | % | Western | 97.3 | 2.7 | 0 | 100 |
| | | Philippine | 3.2 | 96.8 | 0 | 100 |
| | | Eastern | 0 | 5.4 | 94.6 | 100 |
| Cross-validated | Count | Western | 35 | 2 | 0 | 37 |
| | | Philippine | 2 | 29 | 0 | 31 |
| | | Eastern | 0 | 3 | 34 | 37 |
| | % | Western | 94.6 | 5.4 | 0 | 100 |
| | | Philippine | 6.5 | 93.5 | 0 | 100 |
| | | Eastern | 0 | 8.1 | 91.9 | 100 |

96.2% of original grouped cases correctly classified

93.3% of cross validated grouped cases correctly classified

| | | Predicted group membership | | | | |
|-----------------|-------|----------------------------|---------|------------|---------|-------|
| | | | Western | Philippine | Eastern | Total |
| Original | Count | Western | 32 | 5 | 0 | 37 |
| | | Philippine | 2 | 29 | 0 | 31 |
| | | Eastern | 0 | 2 | 35 | 37 |
| | % | Western | 86.5 | 13.5 | 0 | 100 |
| | | Philippine | 6.5 | 93.5 | 0 | 100 |
| | | Eastern | 0 | 5.4 | 94.6 | 100 |
| Cross-validated | Count | Western | 32 | 5 | 0 | 37 |
| | | Philippine | 3 | 28 | 0 | 31 |
| | | Eastern | 0 | 2 | 35 | 37 |
| | % | Western | 86.5 | 13.5 | 0 | 100 |
| | | Philippine | 9.7 | 90.3 | 0 | 100 |
| | | Eastern | 0 | 8.1 | 91.9 | 100 |

96.2% of original grouped cases correctly classified

93.3% of cross validated grouped cases correctly classified

(including tail length), the seven taxa appear as four partially distinct clusters. One cluster on the left-hand side of the graph is formed by *T. sangirensis* and *T. sp.* (Selayar)—both insular forms isolated on small, remote islands. A second cluster, in the middle is *T. pelengensis*—another insular form, this one from Peleng Island. A third cluster, in the lower right, is composed of *T. lariang*, *T. pumilus*, and *T. dentatus*—all from the central core of Sulawesi. A fourth cluster,

T. tarsier sensu lato, spreads across the upper right corner—most of which come from the northern peninsula. In analysis 2b (excluding tail length), the results are similar except that the centroid of *T. pumilus* has moved away from the centroids of *T. lariang*, and *T. dentatus*, with commensurately clearer separation of *T. pumilus*. In analysis 2a, 86.5% of the original cases were correctly classified, and 67.6% of the cross-validated cases correctly classified, while the

respective values for analysis 2b were 78.4% and 45.9% (see Table 2).

DISCUSSION

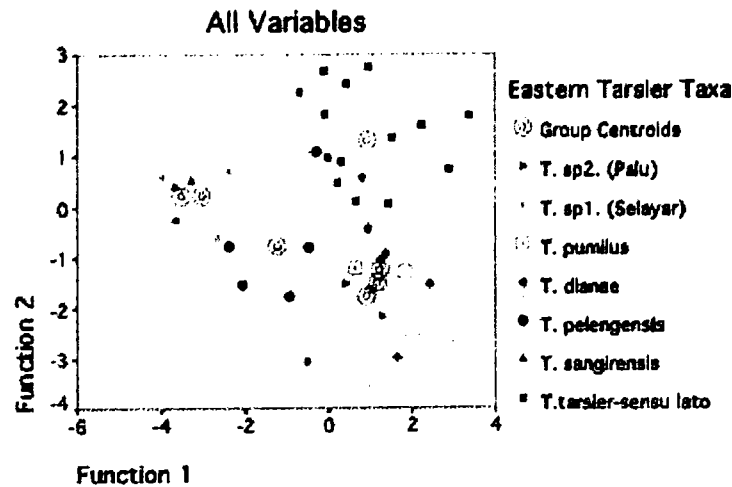
The three tarsier species groups, Philippine, Western, and Eastern tarsiers, can easily be distinguished by this method. More than 95% of the cases were correctly classified (101 of 105). Indeed, two of the misclassified cases (on the upper left-hand side of the Eastern tarsier cluster, see figure 1a) were clearly well within the Eastern tarsier cluster, but happened to be slightly closer to the Philippine tarsier centroid. Furthermore, checking the provenance of those two misclassified cases, it turns out that they are themselves part of a three-case cluster of *T. sangirensis* (again, visible on the upper left-hand side of the Eastern tarsier cluster, see Figure 2, analysis 1a). Thus, those two cases were misclassified as a result of an over-simplified taxonomy that examines species groups, as opposed to species. If we ignore them, more than 98% of the cases are correctly classified (103 out of 105). This leaves two misclassified cases, one each of Western and Philippine tarsiers, which were misclassified as one another. Therefore, the amount of overlap between Eastern tarsiers and other tarsiers is effectively zero, while the overlap between Philippine and Western tarsiers is 2 out of 68.

The cross-validated classification results found slightly less than 90% of the cases correctly classified (94 out of 105). In the cross-validated analysis, all three of the *T. sangirensis* cases occasionally cluster with Philippine tarsiers, but the Eastern tarsier cluster is, nevertheless, clear-cut (Figure 2, analysis 1b, the three *T. sangirensis* cases are visible in the lower left-hand side of the Eastern tarsier cluster). Ignoring these, 92.4% of cases were correctly classified, with 8 misclassified cases, five Western and 3 Philippine tarsiers, which were misclassified as each other. The cross-validated analysis is designed to estimate how likely this method will be to correctly classify other cases, not yet included in this data set, and the answer is that the amount of overlap between Eastern tarsiers and

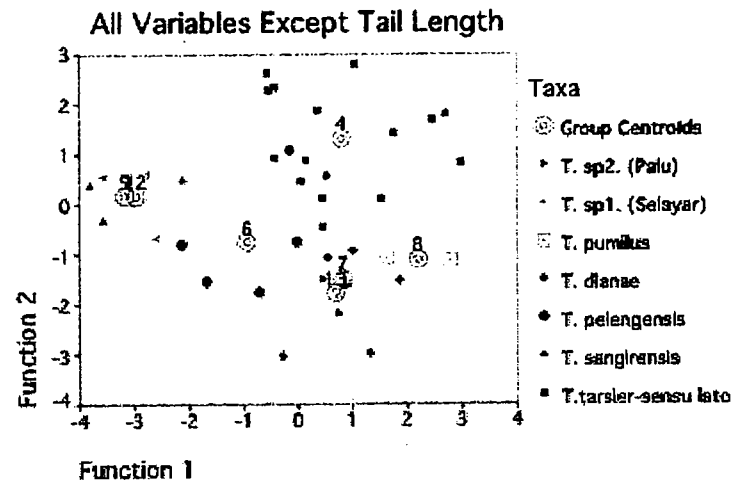
other tarsiers is, again, zero, while the overlap between Philippine or Western tarsiers is 8 out of 68 (or 88.2% correctly classified). In other words, if an otherwise unskilled wildlife monitor were to confiscate a tarsier and use this method, we would expect that he or she would could correctly classify Western and Philippine tarsiers 88% of the time, while Eastern tarsiers could be correctly classified essentially 100% of the time—*using multivariate analysis of tail tuft only.*

The applicability of this method for use within the Eastern tarsier species group is less clear cut. Two insular island populations, those from Sangihe and Selayar, both of which have reduced furriness of the tail tuft, are clearly separated from all other tarsiers, but overlap with each other. This is ironic because Sangihe Island is at the extreme northern end of the distribution of Eastern tarsiers, while Selayar Island is at the extreme southwestern end. Thus, the first working hypothesis is that the similarity is convergent, and does not indicate a close phylogenetic relationship. Future DNA studies will address that more definitively. A third insular island population, from Peleng, with a tail tuft that is intermediate in furriness between the mainland tarsiers and the Sangihe-Selayar cluster, is partially separated from all other tarsiers. Four out of five cases were correctly classified, while a fifth was misclassified as *T. tarsier sensu lato*. Interestingly, the *T. pelengensis* centroid appears to lie more-or-less halfway between the centroids of those populations from Sulawesi proper (e.g. *T. lariang*, *T. pumilus*, *T. dentatus*, and *T. tarsier sensu lato*) and the centroids of the other insular island populations (i.e. *T. sp.* (Selayar) and *T. sangirensis*). Once again, our first working hypothesis would not be to suspect a special phylogenetic relationship between the Peleng Island population, which lies at the extreme eastern end of the distribution of Eastern tarsiers, with the Sangihe (extreme north), Selayar (extreme southwest) populations. Our first best guess is that these populations are convergent, which in turn implies two hypotheses, a) chance or, b) directional evolution of tail tuft shape for insular island populations. An alternative hypothesis is that a lightly furred tail is a primitive retention, but this goes against the principle of global polarity, which predicts

Canonical Discriminant Functions Eastern Tarsiers, Grouped by Taxon



Canonical Discriminant Functions Eastern Tarsiers, Grouped by Taxon



Notes: *T. sp2* (Palu) = *T. lariang*, *T. dianae* is a junior synonym of *T. dentatus*, and *T. tarsier sensu lato* is a wastebasket of all specimens not classified as something other than *T. tarsier* and almost certainly contains cryptic taxonomic diversity.

Figure 3: Results of DF analysis within the Eastern tarsier species group. Analyses 1a, with tail length, (above), Analyses 1b, without tail length, (below)

that the primitive condition is like other primates, i.e. relatively furry. We intend to investigate this curious phenomenon further.

Fewer than 50% of the cases were correctly classified in the cross-validated analysis within the Eastern tarsier species group. This is unsatisfactory, but does not necessarily indicate that this method is

not practical for Eastern tarsier taxonomy. First, the sample sizes are low, and the number of putative taxa are many. The only group that exceeds the minimum sample size requirements of the statistical model is *T. tarsier sensu lato*, itself a wastebasket assemblage of everything that fit nowhere else. Even so, if we investigate the misclassified cases, patterns emerge.

Table 2: Results of Analyses 2a (above) and 2b (below)

| | | Predicted group membership | | | | | | | | |
|-----------------|-------|---|------------------------------|-----------------------|-----------------|-------------------|-------------------------|----------------------|-------|-----|
| | | <i>T. tarsier sensu lato</i> | <i>T. sangirensis</i> | <i>T. pelengensis</i> | <i>T. danae</i> | <i>T. pumilus</i> | <i>T. sp1 (Selayar)</i> | <i>T. sp2 (Pulu)</i> | Total | |
| Original | Count | <i>T. tarsier sensu lato</i> | 14 | 0 | 0 | 1 | 0 | 0 | 15 | |
| | | <i>T. sangirensis</i> | 1 | 2 | 0 | 0 | 0 | 1 | 3 | |
| | | <i>T. pelengensis</i> | 1 | 0 | 4 | 0 | 0 | 0 | 5 | |
| | | <i>T. danae</i> | 1 | 0 | 0 | 4 | 0 | 0 | 6 | |
| | | <i>T. pumilus</i> | 0 | 0 | 0 | 0 | 2 | 0 | 2 | |
| | | <i>T. sp1 (Selayar)</i> | 0 | 0 | 0 | 0 | 0 | 3 | 3 | |
| | | <i>T. sp2 (Pulu)</i> | 0 | 0 | 0 | 0 | 0 | 3 | 3 | |
| | | % | <i>T. tarsier sensu lato</i> | 93.3 | 0 | 0 | 6.7 | 0 | 0 | 100 |
| | | | <i>T. sangirensis</i> | 0 | 66.7 | 0 | 0 | 0 | 33.3 | 100 |
| | | | <i>T. pelengensis</i> | 20 | 0 | 80 | 0 | 0 | 0 | 100 |
| | | <i>T. danae</i> | 16.7 | 0 | 0 | 66.7 | 0 | 16.7 | 100 | |
| | | <i>T. pumilus</i> | 0 | 0 | 0 | 0 | 100 | 0 | 100 | |
| | | <i>T. sp1 (Selayar)</i> | 0 | 0 | 0 | 0 | 0 | 100 | 100 | |
| | | <i>T. sp2 (Pulu)</i> | 0 | 0 | 0 | 0 | 0 | 100 | 100 | |
| Cross-validated | Count | <i>T. tarsier sensu lato</i> | 12 | 0 | 0 | 1 | 0 | 0 | 15 | |
| | | <i>T. sangirensis</i> | 0 | 1 | 0 | 0 | 0 | 2 | 3 | |
| | | <i>T. pelengensis</i> | 1 | 0 | 4 | 0 | 0 | 0 | 5 | |
| | | <i>T. danae</i> | 1 | 0 | 0 | 4 | 0 | 0 | 6 | |
| | | <i>T. pumilus</i> | 0 | 0 | 1 | 0 | 1 | 0 | 2 | |
| | | <i>T. sp1 (Selayar)</i> | 0 | 1 | 0 | 0 | 0 | 2 | 3 | |
| | | <i>T. sp2 (Pulu)</i> | 0 | 0 | 0 | 2 | 0 | 0 | 3 | |
| | | % | <i>T. tarsier sensu lato</i> | 80 | 0 | 0 | 6.7 | 0 | 13.3 | 100 |
| | | | <i>T. sangirensis</i> | 0 | 33.3 | 0 | 0 | 0 | 66.7 | 100 |
| | | | <i>T. pelengensis</i> | 20 | 0 | 80 | 0 | 0 | 0 | 100 |
| | | <i>T. danae</i> | 16.7 | 0 | 0 | 66.7 | 0 | 16.7 | 100 | |
| | | <i>T. pumilus</i> | 0 | 0 | 50 | 0 | 50 | 0 | 100 | |
| | | <i>T. sp1 (Selayar)</i> | 0 | 33.3 | 0 | 0 | 0 | 66.7 | 100 | |
| | | <i>T. sp2 (Pulu)</i> | 0 | 0 | 0 | 66.7 | 0 | 33.3 | 100 | |
| | | 36.5% of original grouped cases correctly classified 67.6% of cross validated grouped cases correctly classified | | | | | | | | |
| | | Predicted group membership | | | | | | | | |
| | | <i>T. tarsier sensu lato</i> | <i>T. sangirensis</i> | <i>T. pelengensis</i> | <i>T. danae</i> | <i>T. pumilus</i> | <i>T. sp1 (Selayar)</i> | <i>T. sp2 (Pulu)</i> | Total | |
| Original | Count | <i>T. tarsier sensu lato</i> | 14 | 0 | 0 | 1 | 0 | 0 | 15 | |
| | | <i>T. sangirensis</i> | 0 | 2 | 0 | 0 | 0 | 1 | 3 | |
| | | <i>T. pelengensis</i> | 1 | 0 | 3 | 1 | 0 | 0 | 5 | |
| | | <i>T. danae</i> | 1 | 0 | 0 | 3 | 1 | 0 | 6 | |
| | | <i>T. pumilus</i> | 0 | 0 | 0 | 0 | 2 | 0 | 2 | |
| | | <i>T. sp1 (Selayar)</i> | 0 | 0 | 0 | 0 | 0 | 3 | 3 | |
| | | <i>T. sp2 (Pulu)</i> | 0 | 0 | 0 | 1 | 0 | 0 | 3 | |
| | | % | <i>T. tarsier sensu lato</i> | 93.3 | 0 | 0 | 6.7 | 0 | 0 | 100 |
| | | | <i>T. sangirensis</i> | 0 | 66.7 | 0 | 0 | 0 | 33.3 | 100 |
| | | | <i>T. pelengensis</i> | 20 | 0 | 60 | 20 | 0 | 0 | 100 |
| | | <i>T. danae</i> | 16.7 | 0 | 0 | 50 | 16.7 | 0 | 100 | |
| | | <i>T. pumilus</i> | 0 | 0 | 0 | 0 | 100 | 0 | 100 | |
| | | <i>T. sp1 (Selayar)</i> | 0 | 0 | 0 | 0 | 0 | 100 | 100 | |
| | | <i>T. sp2 (Pulu)</i> | 0 | 0 | 0 | 33.3 | 0 | 66.7 | 100 | |
| Cross-validated | Count | <i>T. tarsier sensu lato</i> | 8 | 1 | 1 | 1 | 1 | 0 | 15 | |
| | | <i>T. sangirensis</i> | 0 | 1 | 0 | 0 | 0 | 2 | 3 | |
| | | <i>T. pelengensis</i> | 1 | 0 | 2 | 0 | 0 | 0 | 5 | |
| | | <i>T. danae</i> | 1 | 0 | 2 | 2 | 2 | 0 | 6 | |
| | | <i>T. pumilus</i> | 0 | 0 | 2 | 0 | 0 | 0 | 2 | |
| | | <i>T. sp1 (Selayar)</i> | 0 | 0 | 0 | 0 | 0 | 3 | 3 | |
| | | <i>T. sp2 (Pulu)</i> | 0 | 0 | 2 | 0 | 0 | 0 | 3 | |
| | | % | <i>T. tarsier sensu lato</i> | 53.3 | 6.7 | 6.7 | 6.7 | 6.7 | 0 | 100 |
| | | | <i>T. sangirensis</i> | 0 | 33.3 | 0 | 0 | 0 | 66.7 | 100 |
| | | | <i>T. pelengensis</i> | 20 | 0 | 40 | 0 | 0 | 0 | 100 |
| | | <i>T. danae</i> | 16.7 | 0 | 33.3 | 33.3 | 33.3 | 0 | 100 | |
| | | <i>T. pumilus</i> | 0 | 0 | 100 | 0 | 0 | 0 | 100 | |
| | | <i>T. sp1 (Selayar)</i> | 0 | 0 | 0 | 0 | 0 | 100 | 100 | |
| | | <i>T. sp2 (Pulu)</i> | 0 | 0 | 66.7 | 0 | 0 | 33.3 | 100 | |
| | | 78.4% of original grouped cases correctly classified 45.9% of cross validated grouped cases correctly classified | | | | | | | | |

Notes: *T. sp2 (Pulu)* = *T. lariang*, *T. danae* is a junior synonym of *T. dentatus*, and *T. tarsier sensu lato* is a wastebasket of all specimens not classified as something other than *T. tarsier* and almost certainly contains cryptic taxonomic diversity.

Of the cluster composed of *T. sp. (Selayar)* and *T. sangirensis*, all six cases are correctly classified within the cluster. Thus, even with very low samples sizes, we would expect our hypothetical wildlife monitor to correctly classify 100% of confiscations of *T. sp (Selayar)* or *T. sangirensis* as having originated from one of those two islands. Likewise, with the cluster of populations from the central core of Sulawesi (*T. lariang*, *T. pumilus*, and *T. dentatus*), 10 out of 11

cases were correctly classified within the cluster, with a lone specimen of *T. dentatus* being classified together with the wastebasket *T. tarsier sensu lato*. Of the two remaining clusters, there is no clear pattern to the misclassified cases of *T. tarsier sensu lato* and *T. pelengensis* in the cross-validated analysis, and perhaps this should not be surprising. As mentioned, the former is a wastebasket taxon, while the latter appears to be morphologically midway between the

very clearly isolated island populations of Sangihe and Selayar, on the one hand, and Sulawesi proper, on the other.

In summary, we are encouraged by the results of this pilot study, the product of a brainstorming session by several experienced tarsier biologists. Our results show that this method clearly has utility for diagnosing tarsier species groups, and it shows strong potential for diagnosing finer scale taxonomic variation within the Eastern tarsier species group. It is applicable for a great variety of specimen types, including wild, captive, and deceased specimens. It requires almost no cost and very little training, and scoring an individual animal, whether alive or deceased, takes a matter of a few minutes at most. We expect that this method will find utility for studies of both tarsier taxonomy as well as wildlife monitoring.

We intend to further our examinations. We plan to increase the data set by sampling other museum specimens, by adding this method to our field protocol, and by encouraging other tarsier biologists to take these measurements. We have begun a study to examine the utility of analyzing deciles versus quartiles, as well as identifying which measurements have the greatest influence on the classification. We intend to examine both intra and inter observer repeatability. The pattern of decreased furriness of the tail tuft among insular island populations opens a window for future studies of character evolution and biogeography that we intend to explore.

ACKNOWLEDGEMENTS

This material is based grants to MS from the National Science Foundation (No. INT 0107277), the Margot Marsh Biodiversity Foundation, and the Gibbon Foundation. For access to museum collections we thank Dr. Siti Prijono (MZB) Dr. Robert Martin and Michi Schulenberg (FMNH), Dr. Richard Thorington and Linda Gordon (USNM), Dr. Peter Ng and Kelvim Lim (ZRC), and Paula Jenkins in the NHM (London). We thank Willie Smits and the Schmutzer Primate Center, and Dr. SN. Prijono, Research Centre in Biology (LIPI) for sponsoring the workshop at which this work was conducted.

REFERENCES

- Brandon-Jones, D, AA. Eudey, T. Geissmann, CP. Groves, DJ. Melnick, JC. Morales, M. Shekelle & CB. Stewart. 2004. Asian Primate Classification. *International Journal of Primatology*. 25:97-164.
- Groves, CP. 1998. Systematics of tarsiers and lorises. *Primates*, 39:13-27.
- Groves, C. 2001. Primate Taxonomy. Washington D.C.: Smithsonian Institution Press. 350 p.
- Groves, C. 2003. The tarsiers of Sulawesi. In *Tarsiers: Past, Present, and Future*. Wright PC, Simons EL, Gursky S. (eds) pp:179-195. New Brunswick: Rutgers UP.
- Hill, WCO. 1953. Caudal cutaneous specializations in *Tarsius*. *Proceedings of the Zoological Society of London* 123:17-25.
- Hill, WCO. 1955. *Primates: Comparative Anatomy and Taxonomy. II. Haplorhini: Tarsioida*. Edinburgh: Edinburgh University Press.
- MacKinnon, J. & K. MacKinnon K. 1980. The behavior of wild spectral tarsiers. *International Journal of Primatology* 1:361-379.
- Merker, S, & CP. Groves. 2006. In Press. *Tarsius lariang*: A New Primate Species from Western Central Sulawesi. *International Journal of Primatology* 27:
- Merker, S, C. Driller, D. Perwitasari-Farajallah, & H. Zischler. 2007. Hybridisation in tarsiers. Prosimians 2007. Ithala Game Reserve, KwaZulu-Natal, 15-19 July 2007
- Meyer, AB. 1897. Säugethiere vom Celebes- und Philippinen-Archipel, I. *Abhandlungen und Berichte der Kaiserlich Zoologische und Anthropologische-Ethnologische Museum zu Dresden*, 6:I-VIII, 1-36.
- Niemitz, C. 1984. Vocal communication of two tarsier species (*Tarsius bancanus* and *Tarsius spectrum*). In *Biology of Tarsiers*. Niemitz C. (ed) pp:129-142. New York: Gustav Fischer Verlag.
- Niemitz, C, A. Nietsch, S. Warter, & Y. Rumpler. 1991 *Tarsius diana*: A new primate species from

- Central Sulawesi (Indonesia). *Folia Primatologica* 56:105-116.
- Nietsch, A. 1999. Duet vocalizations among different populations of Sulawesi tarsiers. *Int. J. Primatol.* 20:567-583.
- Nietsch, A, & C. Niemitz. 1993. Diversity of Sulawesi tarsiers. *Deutsches Gesellschaft fur Säugetierkunde* 67:45-46.
- Nietsch, A, & ML. Kopp. 1998. Role of vocalization in species differentiation of Sulawesi Tarsiers. *Folia primatologica*, 68(suppl.1):371-378.
- Nietsch, A, & N. Babo. 2001. The tarsiers of South Sulawesi. In *Konservasi Satwa Primata*. pp:114-119. Yogyakarta: Fakultas Kedokteran Hewan dan Fakultas Kehutanan Universitas Gajah Mada University - Yogyakarta.
- Nietsch, A, & J. Burton. 2002. Tarsier species in southwest and southeast Sulawesi. *Abstracts*, The XIXth Congress of the International Primatological Society (IPS), 4-9 Aug. 2002, Beijing, China: 20-21.
- Shekelle, M. 2003. Taxonomy and Biogeography of Eastern Tarsiers. Doctoral thesis. Washington University, St. Louis.
- Shekelle, M, SM. Leksono, LLS. Ichwan, & Y. Masala. 1997. The natural history of the tarsiers of North and Central Sulawesi. *Sulawesi Primate Newsletter*, 4(2):4-11.
- Shekelle, M, & SM. Leksono. (2004) "Rencana Konservasi di Pulau Sulawesi: Dengan Menggunakan Tarsius Sebagai 'Flagship Taxon'". *Biota* IX(1):1-10.
- Shekelle, M, JC. Morales, C. Niemitz, LLS. Ichwan & DM. Melnick. (this volume). The distribution of tarsier mtDNA haplotypes for parts of north and central Sulawesi: a preliminary analysis. In *Primates of the Oriental Night*. Shekelle M, Maryanto I, Groves C, Schulze H, Fitch-Snyder H. (eds). (This volume). Indonesian Institute of Sciences, Bogor, Indonesia.

Appendix I: DF Statistics

Table A-1: Results for Analysis 1a "All Variables, by Species Group"

Eigenvalues

| Function | Eigenvalue | % of Variance | Cumulative % | Canonical Correlation |
|----------|--------------------|---------------|--------------|-----------------------|
| 1 | 6.001 ^a | 77.8 | 77.8 | .926 |
| 2 | 1.716 ^a | 22.2 | 100.0 | .795 |

^a: First 2 canonical discriminant functions were used in the analysis.

Wilks' Lambda

| Test of Function(s) | Wilks' Lambda | Chi-square | df | Sig. |
|---------------------|---------------|------------|----|------|
| 1 through 2 | .053 | 293.043 | 12 | .000 |
| 2 | .368 | 99.406 | 5 | .000 |

Standardized Canonical Discriminant Function Coefficients

| Function | Tail Length | 100% | 90% | 75% | 50% | 25% |
|----------|-------------|-------|-------|-------|------|------|
| 1 | .269 | .028 | -.577 | 1.147 | .238 | .175 |
| 2 | .625 | -.371 | -.854 | .308 | .286 | .023 |

Structure Matrix

| Function | 75% | 50% | 25% | 90% | 100% | Tail Length |
|----------|-------------------|-------------------|-------------------|--------------------|--------------------|-------------------|
| 1 | .881 ^a | .637 ^a | .363 ^a | .489 | .400 | .167 |
| 2 | -.421 | -.153 | -.076 | -.713 ^a | -.648 ^a | .521 ^a |

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions
Variables ordered by absolute size of correlation within function

^a: Largest absolute correlation between each variable and any discriminant function

Table A-2: Results for Analysis 1b "All Variables except Tail Length, by Species Group"

Eigenvalues

| Function | Eigenvalue | % of Variance | Cumulative % | Canonical Correlation |
|----------|--------------------|---------------|--------------|-----------------------|
| 1 | 5.643 ^a | 84.8 | 84.8 | .922 |
| 2 | 1.015 ^a | 15.2 | 100.0 | .710 |

^a First 2 canonical discriminant functions were used in the analysis.

Wilks' Lambda

| Test of Function(s) | Wilks' Lambda | Chi-square | df | Sig. |
|---------------------|---------------|------------|----|------|
| 1 through 2 | .075 | 259.424 | 10 | .000 |
| 2 | .496 | 70.062 | 4 | .000 |

Standardized Canonical Discriminant Function Coefficients

| Function | 100% | 90% | 75% | 50% | 25% |
|----------|------|-------|-------|-------|-------|
| 1 | .074 | -.514 | 1.144 | .183 | .169 |
| 2 | .390 | 1.173 | -.664 | -.274 | -.043 |

Structure Matrix

| Function | 75% | 50% | 25% | 90% | 100% |
|----------|-------------------|-------------------|-------------------|-------------------|-------------------|
| 1 | .929 ^a | .662 ^a | .377 ^a | .545 | .450 |
| 2 | .303 | .023 | -.001 | .787 ^a | .728 ^a |

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions. Variables ordered by absolute size of correlation within function.

^a Largest absolute correlation between each variable and any discriminant function.

Table A-3: Results for Analysis 2a "Eastern Tarsiers Only: All Variables, by Taxon"

Eigenvalues

| Function | Eigenvalue | % of Variance | Cumulative % | Canonical Correlation |
|----------|--------------------|---------------|--------------|-----------------------|
| 1 | 3.316 ^a | 55.1 | 55.1 | .877 |
| 2 | 1.804 ^a | 30.0 | 85.0 | .802 |
| 3 | .611 ^a | 10.2 | 95.2 | .616 |
| 4 | .254 ^a | 4.2 | 99.4 | .450 |
| 5 | .035 ^a | .6 | 100.0 | .183 |
| 6 | .001 ^a | .0 | 100.0 | .034 |

^a. First 6 canonical discriminant functions were used in the analysis.

Wilks' Lambda

| Test of Function(s) | Wilks' Lambda | Chi-square | df | Sig. |
|---------------------|---------------|------------|----|------|
| 1 through 6 | .039 | 95.342 | 36 | .000 |
| 2 through 6 | .170 | 52.205 | 25 | .001 |
| 3 through 6 | .478 | 21.790 | 16 | .150 |
| 4 through 6 | .770 | 7.715 | 9 | .563 |
| 5 through 6 | .965 | 1.041 | 4 | .904 |
| 6 | .999 | .035 | 1 | .852 |

Standardized Canonical Discriminant Function Coefficients

| Function | 100% | 90% | 75% | 50% | 25% | Tail Length |
|----------|-------|-------|--------|-------|-------|-------------|
| 1 | .646 | -.070 | .210 | .948 | -.670 | .486 |
| 2 | -.971 | 1.546 | -1.487 | .880 | .192 | .040 |
| 3 | -.390 | -.109 | .627 | -.141 | .151 | 1.058 |
| 4 | -.428 | .907 | .275 | -.491 | .393 | -.117 |
| 5 | .389 | -.847 | .334 | .073 | .872 | .096 |
| 6 | .406 | 1.007 | -1.385 | -.021 | .135 | .070 |

Structure Matrix

| Function | 50% | Tail Length | 90% | 75% | 25% | 100% |
|----------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| 1 | .584 ^a | .045 | .441 | .463 | -.035 | .518 |
| 2 | .462 | -.051 | .002 | -.108 | .191 | -.406 |
| 3 | -.287 | .873 ^a | -.112 | -.108 | -.031 | -.245 |
| 4 | .084 | -.278 | .872 ^a | .765 ^a | .415 | .362 |
| 5 | .424 | -.041 | -.061 | .116 | .886 ^a | .283 |
| 6 | -.419 | .392 | .172 | -.405 | .071 | .544 ^a |

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions. Variables ordered by absolute size of correlation within function.

^a - Largest absolute correlation between each variable and any discriminant function

Table A-4: Results for Analysis 2b "Eastern Tarsiers Only: All Variables except Tail Length, by Taxon"

Eigenvalues

| Function | Eigenvalue | % of Variance | Cumulative % | Canonical Correlation |
|----------|--------------------|---------------|--------------|-----------------------|
| 1 | 2.853 ^a | 57.6 | 57.6 | .861 |
| 2 | 1.802 ^a | 36.4 | 93.9 | .802 |
| 3 | .258 ^a | 5.2 | 99.1 | .453 |
| 4 | .039 ^a | .8 | 99.9 | .195 |
| 5 | .003 ^a | .1 | 100.0 | .058 |

^a First 5 canonical discriminant functions were used in the analysis

Wilks' Lambda

| Test of Function(s) | Wilks' Lambda | Chi-square | df | Sig. |
|---------------------|---------------|------------|----|------|
| 1 through 5 | .071 | 79.528 | 30 | .000 |
| 2 through 5 | .272 | 39.059 | 20 | .007 |
| 3 through 5 | .762 | 8.149 | 12 | .773 |
| 4 through 5 | .959 | 1.260 | 6 | .974 |
| 5 | .997 | .100 | 2 | .951 |

Standardized Canonical Discriminant Function Coefficients

| Function | 100% | 90% | 75% | 50% | 25% |
|----------|-------|-------|--------|-------|-------|
| 1 | .743 | -.031 | .014 | .871 | -.692 |
| 2 | -.946 | 1.551 | -1.507 | .899 | .173 |
| 3 | -.475 | .894 | .350 | -.498 | .388 |
| 4 | .442 | -.717 | .159 | .063 | .878 |
| 5 | .379 | 1.099 | -1.438 | -.032 | .052 |

Structure Matrix

| Function | 50% | 100% | 90% | 75% | 25% |
|----------|-------|-------|-------|-------|-------|
| 1 | .634* | .579* | .479 | .504 | -.037 |
| 2 | .483 | -.387 | .017 | -.093 | .191 |
| 3 | .054 | .326 | .856* | .753* | .394 |
| 4 | .407 | .357 | -.015 | .106 | .898* |
| 5 | -.443 | .530 | .193 | -.399 | -.005 |

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions. Variables ordered by absolute size of correlation within function.

* Largest absolute correlation between each variable and any discriminant function