Hair Ultrastructure: A comparative study on Old world and New world monkey

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ABSTRACT

Hair is unique to mammals. Keratin associated proteins (KRTAPs) are one of the major components of hair and play essential roles in the formation of rigid and resistant hair shafts. The important aspect of hair evolution is the considerable reduction in hair cover in adult humans during their recent history (after humans-African apes split) but, humans actually have a similar density of hair follicles to that seen in apes. Evolutionary patterns that potentially account for morphological characteristics suggest the genetic basis for variation in phenotypes. Under this circumstance, the present paper attempted to understand the variation of primate hair with regard to cross sectional character of ultrastructure on the basis of Scanning Electron Microscopy (SEM). To achieve the purpose hair strands (125 each) from adult male non-human primates Papio hamadryas [representing Catarrhine (OWM)] and Cebus albifrons [representing Platyrrhine (NWM)] was taken for SEM using standard technique. Examination on ultrastructure revealed significantly (p<0.05) higher values for major axis, minor axis, cross section area and hair index in accordance with higher phylogenetic position among the primates. Furthermore, the present study also found more flattened elliptical pattern in Cebus comparison to Papio ~~on the basis of~~ in terms of hair index.

Keywords: *New world monkey, Old world monkey, Cebus albifrons, Papio hamadryas, Scanning Electron Microscopy, Hair*

INTRODUCTION

Mammalian appendages such as hair has a unique structure composed of a cuticle, a cortex and a medulla. Keratin associated proteins (KRTAPs) are one of the major components of hair and play essential roles in the formation of rigid and resistant hair shafts. In the hair cortex, hair keratins IFs are embedded in an in interfilamentous matrix, which consists of hair keratin-associated proteins (KATAP, usually abbreviated as KAP) (Powell and Rogers, 1991). KRTAP contains two major groups: high/ultrahigh cysteine (HS) and high glycine-tyrosine (HGT) that are considered to have originated independently, and are essential for the formation of rigid and resistant hair shafts through their extensive disulfide bond cross-linking with the abundant cysteine residues of hair keratins or hydrophobic interactions with keratins (Rogers *et al.,* 2007*; Powell and Rogers,* 1997*,* Shibuya *et al.,* 2004*,* Yahagi *et al*., 2004).On the issue of human hair, world wide variation in the hair form is observable and perhaps Haddon (1925) made a maiden attempt to utilize hair forms for ethnic classification as, Ulotrichous, Cymotrichous and Leiotrichous. On the contrary, non human primates, for example the apes however, hardly demonstrate such kind of hair variation throughout the entire body. An important aspect of hair evolution is the considerable reduction in hair cover in adult humans during their recent history (after humans-African apes split) (Schwartz and Rosenblum, 1981). Evolutionary patterns that potentially account for morphological characteristics suggest the genetic basis for variation in phenotypes. Literature review, however, indicate that the phenotypic differences have genetic predisposition and protein evolution hypothesis proposes that the key changes occurred in coding regions might result in apparent modifications to the encoded proteins. In contrast, the gene regulatory evolution model suggests that the changes are not due to the changes in the coding region sequence but due to the pattern and timing of turning of gene expression. Last but not least, the 'less-is-more hypothesis' suggests that gene loss has driven important evolutionary changes in humans.Hair samples have also been subjected to Scanning Electron microscopy (Sato *et al.,*, 1982*,* Hess *et al.,*, 1990*,* Pavlov *et al.,* 2000) in order to obtain some fine structural information. Studies accentuate the significance of the cortex and medulla structural patterns for taxon identification and adaptation to environmental conditions (Chernova, 2003).

Literature review also suggests utilization of advanced technology like Scanning Electron Microscopy (SEM) might be useful to understand the relationship between cuticle and hair

cortex (Kim *et al.,* 2010) with regard to the cortical filaments and hair shaft (Cao *et al.,* 2006) and thereby could be utilized for hair evolutionary biology. In this circumstance, the present study attempted to understand the evolutionary pattern by comparison of quantitative variables obtained by SEM among the New world and Old world monkey

MATERIALS AND METHODS

The present study consisted of a total of 250 hair strands. Out of 250 hair strands, 125 each were taken from two groups of male adult monkey- *Cebus albifrons* (New world monkey) and *Papio hamadryas* (Old world monkey). Prior to SEM all the hair samples were washed using standard technique (Sen and Das Chaudhuri, 2001) by first dipping into the solution of carbon tetra chloride (CCl_4) for at least 24 hours and subsequently dried at room temperature. Then the hair samples were further dipped into the solution of Ether and Alcohol (1:1 proportion) for at least 30 minutes and subsequently, dried at room temperature. To obtain the Ultrastructure, the microtomed hair samples were placed on carbon tape for fixing on a slide. Then the slides containing the hair samples were loaded into the Scanning Electron Microscope (Carl Zeiss, EVO 18 special edition - Germany) under vacuum condition (Reimer, 1998). The Ultrastructure regarding the cross section of hair measured (Major Axis and Minor Axis) in *μm*. Descriptive statistics and inferential statistics for hair quantitative variables were analyzed using SPSS(Version 10) and the cut off point was set as $p<0.05$.

RESULTS AND DISCUSSION

Examination of Major and Minor axis obtained by SEM revealed significantly ($p<0.05$) higher value for the cross section in *Papio hamadryas* (Fig. 1) in comparison to *Cebus albifrons* (Fig. 2)**.** Since the area of the cross section has the relation with the major and minor axis, therefore a similar trend of significantly ($p<0.05$) higher area has been observed in *Papio* compared to *Cebus***.** The hair index also showed higher value in *Papio* due to higher major and minor axis in comparison to *Cebus*. Interestingly, the hair index also indicates that the hair cross section of *Cebus* has more flattened elliptical pattern than *Papio*. Increased cross section area in *Papio* hair vindicated more thickness in course of human evolution (Chatterjee *et al.*, 2012). Present study corroborates with ~~recent~~ contemporary studies (Abbasi, 2011; Alibardi, 2012) on hair evolution which hypothesize that, the medulla has been obliterated or replaced by cortical cells while the

external part of the cortex formed a cuticular surface due to the different growth rate with inner root sheath cells.

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Table 1. Distribution of Major axis and minor axis in *C. albifrons* and *P. hamadryas*

Genus	Sex	No	Mean ±SD	
			Major axis (μm)	Minor axis (μm)
Cebus	M	125	50.62±11.99*	34.62±13.02
Papio	M	125	83.44±15.24*	65.15±14.70*

(*p<0.05)

Table 2. Distribution of Hair area and hair index of *C. albifrons* and *P. hamadryas*

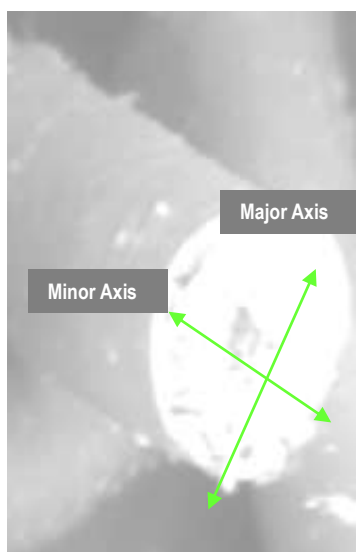| Genus	Sex	No	Mean ±SD	
			Hair area (μm^2)	Hair index
Cebus	M	125	1458.02± 820.68	67.21± 14.70
Papio	M	125	4392.28± 1579.33*	77.97± 9.88*

(*p<0.05)

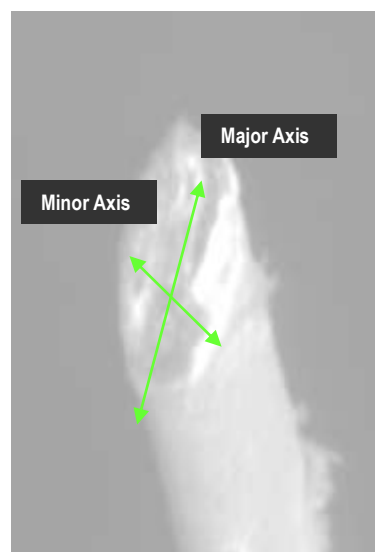

Figure 1
Papio hamadryous

Figure 2
Cebus albifrons

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