

QUANTITATIVE VARIATION OF HAIR: SOME ASPECTS OF EVOLUTIONARY BIOLOGY

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ABSTRACT

Hair is a defining characteristic of mammals. Despite diverse micromorphology, the hair present same structural patterns throughout the class. The hair shaft is a keratinized cylindrical filament of different configurations. An important aspect of hair evolution is the considerable reduction in hair cover in adult humans during their recent history. The major structural proteins found in the hair shaft are the hair keratins and keratin-associated proteins. Contemporary study reported a predominant expression of the KRTAP/KAP2 proteins in the keratinizing zone of the human hair shaft cortex and the results further enhanced the crucial roles of KRTAP/KAPs in hair shaft keratinization in humans. The biophysical features of KRTAP/KAPs, however, have remained largely unknown. The present study attempted to understand histomorphological variation and evolutionary biology of hair shaft and medulla diameter as quantitative traits in humans and chimpanzees.

Keywords: Hair Shaft, Hair Medulla, Quantitative traits, Evolutionary Biology

INTRODUCTION

Hair is a defining characteristic of mammals that does not occur in other amniotes and their evolutionary origin is presumably one of the key steps that contributed significantly to the rapid radiation of mammals and their rise to become the dominant terrestrial vertebrate during late Triassic (Maderson, 2003). Hair might have arisen specifically within late Triassic therapsid lineage (ancestor of modern mammals/mammalian forms) approximately 200 million years ago (Meng and Wyss, 1997). The potential selective advantages that may be responsible for the origin of thick coat of hair, the pelage, include the heat-insulating function in primitive homeothermic mammals (Brink, 1956). Hair morphology differs considerably among closely related mammalian taxa and they are highly plastic in terms of adaptation to habitat condition (Noback, 1951). Despite diverse micromorphology, the hair present same structural patterns throughout the class. The hair shaft is a keratinized cylindrical filament of different configuration. The outer surface of the shaft is often covered with single or multilayer cuticle. Beneath the cuticle is the cortex, whereas medullary layer

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constitute the core of the hair. 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). Naked skin might have worked as body cooling system to facilitate efficient heat emission (prevent thermal damage) in response to establishment of bipedalism and large relative brain size in hominids (Wheeler, 1984).

In most mammals, the hair cover needs constant supply of new hairs to perform different functions. To produce new hair, primary hair follicles (established during early development) go through a cycle of activity divided into three phases, i.e. growth phase (anagen), destructive phase (catagen) and resting phase (telogen) (Alonso and Fuchs, 2006). A number of signaling pathways/molecules have been implicated in regulating different steps of hair follicle cycling (Alonso and Fuchs, 2006; Schneider *et al.*, 2009).

In the mammalian hair follicle (HF), the hair shaft is produced during the anagen or growth phase of the hair cycle, which continues in repeated cycles throughout life (Hardy, 1992). The hair shaft or hair fiber is the only part of the HF that protrudes above the skin surface and plays various physiological roles including protection of the skin and thermal insulation. The hair shaft consists of three concentric layers with a cuticle on the outside, a cortex, and a medulla on the inside. In humans, the cortex makes up the bulk of the hair shaft, with the size and shape of the medulla varying greatly depending on hair type (Jave-Suarez *et al.*, 2002). The production and assembly of the hair shaft layers are highly coordinated processes that involve very rapid proliferation of the matrix cells in the HF bulb, followed by a gradual cellular differentiation program that takes place within the funnel-shaped pre-cortex region (Langbein and Schweizer, 2005). The major structural proteins found in the hair shaft are the hair keratins and keratin-associated proteins (KAPs) (Lee *et al.*, 2006). Keratins constitute the intermediate filament cytoskeleton of both epidermal keratinocytes and the specialized hair shaft trichocytes, which is indispensable since these cells must withstand substantial and continuous mechanical stress (Rogers, 2004). To achieve this, the intermediate filaments or keratins form an intracellular network that links to the plaque proteins of cell-cell adhesion complexes called desmosomes. This intra- and inter-cellular network of keratins and desmosomes provides the hair fiber with its properties of a relatively high tensile strength as well as elasticity. Desmosomes are calcium dependent cell junctions that are prevalent in tissues that are subjected to continuous mechanical stress. Interestingly, mirroring the pattern of expression in the skin, DSG2 and DSG3 are expressed in the lower outer root sheath of the hair follicle, while DSG1 is expressed in the more differentiated inner root sheath (Kurzen *et al.*, 1998; Wu *et al.*, 2003). DSG1 is also expressed in the upper outer root sheath along with DSG2 and DSG3, and DSG3 is expressed in the medulla of the hair follicle (Kurzen *et al.*, 1998; Wu *et al.*, 2003). Hair medulation of nonhuman primates varies with different species. The structure of hair medulla, therefore, could be considered very useful in classifying of congeneric and intergeneric

primates. Studies revealed that examination of hair medulla structures may be useful for understanding evolutionary biology (Inagaki and Amashita, 1994.).

The availability of the rapidly increasing number of genome sequences provides opportunities for investigators to study evolutionary patterns that potentially account for morphological characteristics, and suggest the genetic basis for variation in phenotypes. In particular, gene families in which duplications, rate variation and pseudogenization occur frequently are likely involved in functional innovation and adaptation (Hughes, 1999). Examples of such gene families are those involved in the perception systems, for example, the odorant receptors (Niimura and Nei, 2007), and the sweet/umami and bitter receptors (Shi *et al.*, 2003). These studies facilitated understanding of the general evolutionary trends in genomic complexity and lineage-specific adaptation. Likewise, the study of the evolutionary patterns of the keratin associated protein (KRTAP/KAP) gene family, whose encoded proteins are major components of hair, revealing the underlying basis of phenotypic diversity. The major components of hair are alpha-keratins and keratin associated proteins, each of which are encoded by multigene families. In humans, the alpha-keratin gene family has been extensively studied demonstrating that there are 54 functional genes that are clustered on chromosomes 12q13.13 and 17q21.2 that show differing expression patterns during hair development (Rogers *et al.*, 2006). Furthermore, hair keratin-associated proteins (KRTAP/KAPs) are one of the major structural components of the hair shaft. A recent study (Fujikawa *et al.*, 2012) reported a predominant expression of the KRTAP/KAP2 proteins in the keratinizing zone of the human hair shaft cortex and the results further enhanced the crucial roles of KRTAP/KAPs in hair shaft keratinization in humans. The biophysical features of KRTAP/KAPs, however, have remained largely unknown. The present study attempted to understand histomorphological variation and evolutionary biology of hair shaft and medulla diameter as quantitative traits in humans and chimpanzees.

MATERIALS AND METHODS

Materials for the present study consist of the hair samples of human and non human primates. 125 scalp hairs from individuals from adult male Bengalee population and 125 hair strands from adult non human primate species (*Pan paniscus*) were taken for the present study. In adult human, 125 hair strands from each individuals were obtained by cutting a bunch of hair from as nearly possible as the root level from the occipital zone of the scalp. The collected hairs were kept in serially marked paper envelopes separately. The non-human primate hair samples (shaded hairs) were collected from Alipur Zoological Garden, Kolkata with the help of the staff members. Therefore, altogether 250 hair strands were analyzed for the present purpose.

The names of the species are as follows:

- *Pan paniscus* (Suborder: Anthropeida, Family: Pongidae - Ape).

- *Homo sapiens* (Suborder: Anthropeidea, Family: Hominidae).

Before microscopic scanning, each of the hair samples were cleaned following the standard technique (Banerjee and Das Chaudhuri 1965; Sen and Das Chaudhuri, 2001; Gaur et al., 2007) and subsequently, were dried at room temperature for the examination of the histomorphological characters. For microscopic study of histomorphological variables, i.e., hair medullation, each washed hair strand was mounted on microscopic glass slides with 10 x ocular microscope (Binoculour: Letiz, WETZLAR, Germany) with 0.65 objective resolutions. On the other hand for quantitative variables the above mentioned resolution was used and measurements have been obtained in mm by micrometer fitted with the microscope.

Data were analyzed for descriptive and inferential statistics in SPSS 10.0 (Windows) version and cut of point was set as $p < 0.05$.

RESULTS AND DISCUSSIONS

In the hair cortex, hair keratins are embedded in an interfilamentous matrix, which consists of hair keratin-associated proteins (KRTAP/KAP/KAP) (Powell *et al.*, 1991). KRTAP/KAP 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.*, 2006). Inventory of KRTAP/KAP genes on the basis of recent rapid increase in the availability of comparative genomic data is facilitating the illumination of evolutionary features of organisms. Primate data from human (International Human Genome Sequencing Consortium, 2001) and chimpanzee (The Chimpanzee Sequencing and Analysis Consortium, 2005) revealed excess high/ultrahigh cysteine (HS), and high glycine-tyrosine (HGT) KRTAP/KAPs in human (HS 12.6%, HGT 33.3%) in comparison to chimpanzee (HS 11.6%, HGT 24.0%) (Wu *et al.*, 2009). In other words, KRTAP/KAP is relatively small, hydrophobic proteins, and often has characteristic repeat structures. KRTAP/KAP is a major component of the matrix between the keratin intermediate filaments (KIF) and may be responsible for forming the rigid hair shaft through extensive disulfide bond cross-linking with the KIF (Powell and Rogers, 1997). To understand the biophysical features of KRTAP/KAP, which is remained largely unknown (Fujikawa *et al.*, 2012) and as well as the interaction of KIF and KRTAP/KAP (Shimomura and Ito, 2005), the present study compared the hair quantitative traits (hair shaft and medulla diameter) between human and chimpanzee for modeling of evolutionary aspects. Quantitative variables in terms of shaft and medulla diameter presented in Table-1, indicated significant difference ($p < 0.05$) indicating higher shaft diameter among the human compared to the chimpanzee. On the other hand, medulla diameter (Table-2) revealed also significant ($p < 0.05$) difference and discerned significantly ($p < 0.05$) absence

of medulla and as well as decreased medulla diameter in human than the chimpanzee. Examination on occurrence of medullation human hair samples (Table-3) revealed significant ($p < 0.05$) difference in terms of higher medullation in comparison to the chimpanzee. However, excess presence of medullation in human hair samples irrespective of hair forms had already been reported (Banerjee, 1965), but contemporary studies (Van Neste, 2004; Mistry *et al.*, 2010) demonstrated further evidence on the relationship medullation, increased shaft diameter and pigmentation of human hair. Furthermore, the analysis of mean shaft diameter for presence of medullation in both human and chimpanzee demonstrated significantly ($p < 0.05$) higher shaft diameter compared to absence of medullation. However, for absent medullation, human shaft diameter showed significantly ($p < 0.05$) less mean shaft diameter in comparison to chimpanzee. Although, the thickness of medullated hairs has been taken into consideration among the monkeys (Inagaki, 1986), but evolutionary approach for hair variation among the human and non human primates has recently been taken (Chatterjee and Bandyopadhyay, 2012) as imperative research domain in Anthropology. Since, inventory of KRTAP/KAP genes revealed a rather high HS and HGT in human, therefore, expression related to higher shaft diameter and lower medulla diameter might be that these size polymorphisms may have been generated by an intragenic deletion and/or duplication event of the repeat structures during evolution (Shimomura and Ito, 2005).

Table-1: Distribution of hair Shaft Diameter in Human and Chimpanzee

Suborder	Family	Species	Mean \pm SD (mm)
Anthropoidea	Pongidae(<i>Anthropoid ape</i>)	<i>Pan paniscus</i> (Chimpanzee)	29.68 \pm 3.10
Anthropoidea	Hominidae	<i>Homo sapiens</i>	31.23 \pm 4.47*

* $p < 0.05$

Table 2: Distribution of hair Medulla Diameter in Human and Chimpanzee

Suborder	Family	Species	Mean \pm SD(mm)
Anthropoidea	Pongidae(<i>Anthropoid ape</i>)	<i>Pan paniscus</i> (Chimpanzee)	9.96 \pm 1.95
Anthropoidea	Hominidae	<i>Homo sapiens</i>	4.23 \pm 1.52*

* $p < 0.05$

Table 3: Distribution of Shaft diameter according to the medullation

Species	N	Shaft diameter(Medulla Present) Mean \pm SD	N	Shaft diameter(Medulla Absent) Mean \pm SD (mm)
<i>Pan paniscus</i>	85	39.04 \pm 4.10	40	19.62 \pm 1.92*
<i>Homo sapiens</i>	115	52.12 \pm 4.84	10	09.98 \pm 1.84*

* $p < 0.05$

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REFERENCES

- Alonso, L. and E. Fuchs, 2006. The hair cycle. *J Cell Sci.*, 119(Pt 3):391-393.
- Banerjee A. R., 1965. On variation of human head hair: Hair form and medullation. *Z. Morph. Anthropol.* 57:56-69.
- Brink A. S., 1956. Speculations on some advanced mammalian characteristics in the higher mammallike reptiles. *Palaeontol. Afr.* 4:77-96.
- Chatterjee, M. and A.R. Bandyopadhyay, 2012. Some aspects of Evolutionary Biology of Primate hair. In: Dimensions of Anthropological Research in India. J. Sarkar, A. Basu and A. K. Singh (Eds.). The Indian Anthropological Society (ISBN: 81-85525-06-4), pp. 51-69.
- Fujikawa, H., Fujimoto, A., Farooq, M., Ito, M. and Y. Shimomura, 2012. Characterization of the human hair keratin-associated protein 2 (KRTAP/KAP2) gene family. *J Invest Dermatol.* 132(7):1806-1813.
- Gaur, R., Angrish, I. and S. R. Bansal, 2007, Age, Gender and Caste Variations in Scalp Hair Micro-Morphological Variables among Brahmins and Banias of Punjab, India. *Anthropologischer Anzeiger*, 65(2): 157-168.
- Hardy, M.H.,1992. The secret life of the hair follicle. *Trends Genet.* 8(2):55-61.
- Hughes, A.L.,1999. Adaptive evolution of genes and genomes. Oxford University Press US
- Inagaki, H., 1986. Morphological characteristics of the hair of Japanese monkeys (*Macaca fuscata fuscata*): Length, diameter and shape in cross-section, and arrangement of the medulla. *Primates*, 27: 115-123.
- Inagaki, H. and Y. Amashita, 1994. An investigation of intergeneric relations among Papionini monkeys based on fine hair medulla structures. *Primates*, 35:499-503.
- International Human Genome Sequencing Consortium, 2001. Initial sequencing and analysis of the human genome. *Nature*, 409:860-921.
- The Chimpanzee Sequencing and Analysis Consortium, 2005. Initial sequence of the chimpanzee genome and comparison with the human genome. *Nature*: 437:69-87.
- Jave-Suarez, L.F., Winter, H., Langbein, L., Rogers, M.A. and J. Schweizer, 2002. HOXC13 is involved in the regulation of human hair keratin gene expression. *J Biol Chem.*, 277(5):3718-26.
- Kurzen, H., Moll, I., Moll, R., Schafer, S., Simics, E., Amagai, M., Wheelock, M.J. and W.W. Franke, 1998. Compositionally different desmosomes in the various compartments of the human hair follicle. *Differentiation*, 63:295-304.
- Langbein, L. and J. Schweizer, 2005. Keratins of the human hair follicle. *Int Rev Cytol.*, 243:1-78.
- Lee, Y.J., Rice, R.H. and Y.M. Lee, 2006. Proteome analysis of human hair shaft: from protein identification to posttranslational modification. *Mol Cell Proteomics*, 5: 789-800.
- Maderson, P. F. A., 2003. Mammalian skin evolution and reevaluation. *Experimental Dermatology*, 12(3):233-236.
- Meng, J. and Wyss, A.R., 1997. Multituberculate and other mammal hair recovered from Palaeogene excreta. *Nature*, 385(6618):712-714.
- Mistry, S., Bandyopadhyay, A. R., Chakrabarti, N.K., Chatterjee, M., Roy, T. J. and J. R. Ghosh, 2010. Histomorphological and quantitative study on black and gray hair in Bengalee Population. *J Ind Acad For Sci.*, 42(1&2): 32-40.

- Niimura, Y. and M. Nei, 2007. Extensive gains and losses of olfactory receptor genes in mammalian evolution. *PLoS ONE*, 2(8):e708.
- Noback, C.R., 1951. Morphology and phylogeny of hair. *Ann NY Acad Sci.*, 53(3):476-492.
- Powell, B.C., Nesci, A. and G.E. Rogers, 1991. Regulation of keratin gene expression in hair follicle differentiation. *Ann NY Acad Sci.*, 642:1-20.
- Powell, B.C. and G.E. Rogers, 1997. The role of keratin proteins and their genes in the growth, structure and properties of hair. In: Formation and Structure of Human Hair. Jolles, P., Zahn, H., Höcker, H. (Eds). *Basel: Birkhäuser*, p 59–148.
- Rogers, G.E., 2004. Review Hair follicle differentiation and regulation. *Int J Dev Biol.*, 48:163-170.
- Rogers, M.A., Langbein, L., Praetzel-Wunder, S., Winter, H. and J. Schweizer, 2006. Human hair keratin-associated proteins (KAPs). *Int Rev Cytol.*, 251:209-263.
- Schwartz, G. G. and L. A. Rosenblum, 1981. Allometry of primate hair density and the evolution of human hairlessness. *Amer J Phys Anthropol.*, 55(1):9-12,
- Schneider, M.R., Schmidt-Ullrich, R. and R. Paus, 2009. The hair follicle as a dynamic miniorgan. *Curr Biol.*, 19(3):132-142.
- Shi, P., Zhang, J., Yang, H. and Y. Zhang, 2003. Adaptive diversification of bitter taste receptor genes in mammalian evolution. *Mol Biol Evol.*, 20(5):805-814.
- Shimomura, Y. and M. Ito, 2005. Human Hair Keratin-Associated Proteins. *J Inves Dermatol Symp Proc.*, 10: 230–233.
- Wheeler, P. E., 1984. The evolution of bipedality and loss of functional body hair in hominids. *J Hum Evol.*, 13 (1):91-98.
- Wu, D.D., Irwin, D.M. and Y.P. Zhang, 2009. Correction: Molecular evolution of the keratin associated protein gene family in mammals, role in the evolution of mammalian hair. *BMC Evol Biol.*, 8:241.
- Wu, H., Stanley, J.R. and G. Cotsarelis, 2003. Desmoglein isotype expression in the hair follicle and its cysts correlates with type of keratinization and degree of differentiation. *J Invest Dermatol.*, 120:1052–1057.
- Van Neste, D., 2004. Thickness, medullation and growth rate of female scalp hair are subject to significant variation according to pigmentation and scalp location during ageing. *Eur J Dermatol.*, 14:28-32.



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