



A73 Molar Crenulation Trait Definition and Population Variation

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After attending this presentation, attendees will better understand how molar crenulations vary in modern human populations and how this variation can be used to estimate the ancestry of individuals in a forensic context.

This presentation will impact the forensic science community by providing a standardized scoring system for molar crenulations that can be adopted by forensic anthropologists for use in the development of the biological profile. Additionally, this presentation outlines frequency data on molar crenulations in various modern human samples — data that has been lacking within forensic anthropology.

The condition of crenulated (i.e., wrinkled) molars has been described extensively in the paleontological and anthropological literature. Within forensic anthropology, molar crenulations have often been identified as being encountered at higher frequencies among samples of individuals of African ancestry.^{1,2} Despite the recognized importance of this trait to differentiate contemporary samples, very little data exist that document the distribution of molar crenulations. Part of the difficulty with implementing research programs investigating molar crenulations may stem from the fact that they are not well defined. In fact, they do not form a part of the standard suite of dental morphological characteristics that are described in the Arizona State University Dental Anthropology system.³ In this work, a clear and operational definition and scoring system for the trait is provided, as well as inter- and intra-observer error rates. Frequencies for modern groups are documented and the use of the trait for differentiating between these populations is explored.

Molar crenulations are defined here as curved fissures and ridges that surround the primary ridges (i.e., cristids) of each main molar cusp. These crenulations are found on the occlusal surface of all three molars of both the mandible and maxilla. The scoring system is: 0 = no crenulation; 1 = crenulations are shallow and do not involve all cusps; and, 2 = crenulations are deep and involve all major cusps. Data were collected on several modern skeletal collections ($n=420$). These samples include individuals from Japan ($n=98$), Hispanic migrants ($n=54$), American Whites ($n=111$), American Blacks ($n=17$), and casts of South African Bantu-speaking peoples ($n=140$). To test inter- and intra-observer error, data were again collected on the same set of individuals ($n=50$).

Inter- and intra-observer error rates were assessed using Cohen's Kappa. Rater agreement was moderate to high (<0.41) for all teeth, indicating the reliability of this scoring system.⁴ The frequency of molar crenulations was low among the Japanese, Hispanic, and American White samples. When the trait was observed, it was typically on the third molar and was a score of 1. Crenulation frequencies increased with the American Black sample and greatly increased with the South African sample. In these samples, the trait was present on all molars and scores of 2 were much more frequent. Univariate statistics (Chi-square) indicated a difference in crenulation presence between groups for all molars when raw scores were used. When data were dichotomized and the breakpoint set at one, this same pattern was found. When the breakpoint was set at two, all teeth show group differences except for the lower first molar.

Based on this research, it is argued that molar crenulations become part of a suite of traits that can be used to estimate ancestry. It is further advocated that crenulations (as well as other dental morphological traits) be included in statistical frameworks to improve accuracy rates of ancestry estimation as part of the biological profile.



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