

# Genetic Basis of the Crown-Size Profile Pattern

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Although genetic control of crown diameters has been documented by a number of workers (R. H. OSBORNE ET AL, *Amer J Hum Genet* **10**: 350-356, 1958; S. M. GARN ET AL, *J Dent Res* **44**:228-242, 1965; D. W. LEWIS and R. M. GRAINGER, *Arch Oral Biol* **12**:539-544, 1967; and D. H. GOOSE, *J Dent Res* **46**:959-962, 1967), genetic involvement in crown-size patterning has not been ascertained for the whole dentition.

To investigate the genetic and chromosomal basis of crown-size profile patterning, crown-size patterns of 960 pairs of subjects from southwestern Ohio were compared. After converting individual measurements into normalized  $T$  scores (W. A. MCCALL, *Measurement*, 1939, pp 505-508) by using a computer program (C. R. BLACK, *Ann NY Acad Sci* **134**: 538-540, 1966), dentitions of each pair of subjects were compared by the product moment correlation,  $r$ . The resulting correlation coefficients ( $r_T$ ), involving  $T$ -scored values of corresponding teeth, provided a simple expression of the degree of patterned similarity between any two individuals. The use of normalized  $T$  scores automatically corrected for sex made possible cross-sexed as well as like-sexed comparisons.

Sibling correlations for tooth-size similarity approximated 0.22 for 246 like-sexed and cross-sexed brothers and sisters (Table). Parent-child similarities in crown-size profile pattern approximated 0.20 as shown by 90 parent-child pairings. Similarly investigated, 58 pairs of cousins yielded a mean similarity coefficient value of 0.15. Finally, randomly paired, unrelated subjects had a pattern profile similarity value of 0.01, close to the theoretical 0.00 value. With profile-pattern similarity values ranging from 0.90 for monozygotic female twins through 0.20 for parents versus their children, 0.15 for cousins, and 0.00 for unrelated pairs, it is clear that crown-size profile patterns have a genetic basis.

The values in the table also show evidence for X-chromosomal involvement in the pattern of the total dentition. Sister-sister values of  $r_T$  exceeded the remaining sibling correlations.

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PARENT-CHILD, SIBLING, AND COUSIN RESEMBLANCES IN CROWN-SIZE PROFILE PATTERNS

Type of Comparison	N	Mean
		$r_T^*$
<i>Sibling</i>		
Sister-sister	67	0.256
Brother-brother	65	0.117
Brother-sister	114	0.219
All	246	0.218
<i>Parent-child</i>		
Father-daughter	29	0.256
Father-son	19	-0.045
Mother-daughter	28	0.310
Mother-son	14	0.162
All	90	0.195
<i>Cousin</i>		
Female cousins	23	0.168
Male cousins	8	0.119
Male-female cousins	27	0.148
All cousins	58	0.152
<i>Random pairings</i>		
Females	50	-0.011
Males	56	0.034
Male-female	66	0.007

\* Left side, except where a corresponding tooth on the right side was substituted because of missing data.

Moreover, father-daughter crown-size profile patterns were more alike ( $r_T=0.26$ ) than father-son correlations ( $r_T=-0.04$ ), again in accordance with the hypothesis of X-chromosomal mediation.

Taking twin, sibling, parent-child, and cousin similarities in crown-size profile patterning into account, using the statistic  $r_T$  throughout, it is estimated that 80% to 90% of patterned variance in crown size has a genetic basis, most of which can be attributed to a combination of autosomal genes and genes located on the X chromosome. Finally, from the excess of sister-sister over brother-brother values of  $r_T$  and the excess of father-daughter over father-son values, it would appear that a greater proportion of crown-size profile pattern variance is controlled by relatively few genes on the X chromosome than by the larger number on the remaining 22 pairs of autosomes.

Ova D. Goins of the Fels Computer Facility assisted in the computer programming for the statistic  $r_T$ , and Edmund Churchill made statistical studies.