



GENETIC AND ENVIRONMENTAL CONTRIBUTIONS
TO MORPHOLOGICAL VARIATION IN THE
HUMAN PERMANENT DENTITION
- A Study of Australian Twins

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Contents

Title Page	
Frontispiece	
Contents	
Declaration	
Abstract	
Acknowledgements	
Publications	
Abbreviations	
Chapter 1	Introduction to the Project 1
Chapter 2	Data Collection 50
Chapter 3	Exploring the Data 61
Chapter 4	Sexual Dimorphism in the Permanent Dentition 86
Chapter 5	The Role of Sex Chromosomes 103
Chapter 6	Sex Hormones, Twin Gestation and the Dentition 120
Chapter 7	Genetic Modelling of Tooth Crown Size - the Univariate Analyses 137
Chapter 8	Multivariate Modelling of Tooth Crown Size 199
Chapter 9	Final Synthesis 303
Appendices 317
References 348

Abstract

The aim of this thesis was to elucidate the nature and extent of genetic and environmental contributions to variation in permanent tooth crown size. Two crown diameters - the mesiodistal length (MD) and buccolingual breadth (BL) of 28 permanent teeth were recorded. Phenotypic variation among individuals for quantitative traits can be divided into additive and non-additive genetic factors, and individual and family environmental factors. The most common method used is the study of correlations among relatives, in particular, the classical twin method. In addition, twin studies may reveal evidence of contributions of sex-linked genes and sex hormones.

Sibling correlations were compared to find evidence of sex-linked genes contributing to tooth crown size. About half of the 56 crown diameters were in agreement with predictions. Alternative explanations were explored, and it was decided that the finding was consistent with a contribution of sex-linked genes to tooth crown size.

All 56 variables displayed significant sexual dimorphism, with males having larger teeth on average than females. The hypothesis that sex hormones contributed to sexual dimorphism was tested by comparing mean tooth size in female-male (opposite-sex or OS) twins with same-sex (SS) twins, and singletons. A multivariate ANOVA of 12 variables revealed a significant increase in tooth crown size of OS females, and no change in OS males. This is consistent with expectations if sex hormones diffused between twins in utero and influenced tooth size.

Most previous quantitative studies of tooth crown size have revealed a high degree of genetic determination. However, all of the statistical methods used had substantial difficulties in their application. Structural equation modelling analyses in this project revealed that most variation could be explained by additive genetic and unique environmental factors. In univariate analyses, canine and first premolar MD lengths showed substantial non-additive genetic variation, while common environmental variation was significant in the maxillary first molar. Multivariate analyses revealed several genetic and environmental factors applied to all variables in the analysis. Other additive genetic factors affected individual teeth or antimeric pairs of teeth, while non-additive genetic factors influenced groups of teeth. Common environment affected posterior teeth in the maxillary right quadrant. All findings were interpreted in the light of genetic, evolutionary and embryological principles.