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Patterns of variation in canal and root number in human post-canine teeth

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Abstract

Descriptive morphology of tooth roots traditionally focuses on number of canals and roots. However, how or if canal and root number are related is poorly understood. While it is often assumed that canal number is concomitant with root number and morphology, in practice canal number and morphology do not always covary with external root features. To investigate the relationship between canal and root number, fully developed, adult post-canine teeth were examined and quantified from computerized tomography scans from a global sample of 945 modern humans. We tested the hypotheses that root and canal number do not follow a 1:1 ratio, that canal to root ratios differ between teeth, and that canal to root ratios differ across major human geographical groups. Results indicate that not only is root number dependent on canal number, but that this relationship becomes more variable as canal number increases, varies between individual teeth and by major geographical group, and changes as these groups increase in geographical distance from Sub-Saharan Africa. These results show that the ratio of canal number to root number is an important indicator of variation in dental phenotypes.

KEYWORDS
dental anthropology, human dental evolution, root canals, tooth roots

1 | INTRODUCTION

Tooth root anatomy varies in canal and root number, and canal number does not always covary with root number. Various aspects of this have been studied in modern humans (Ackerman et al., 1973; Ahmed et al., 2017; Hsu & Kim, 1997; Kovacs, 1971; Vertucci & Gegauff, 1979; Zorba et al., 2014), extant hominoids (Emonet et al., 2012; Kupczik et al., 2005; Moore et al., 2013, 2015), and fossil hominins (Kupczik et al., 2009; Kupczik & Hublin, 2010; Le Cabec et al., 2013; Moore et al., 2016; Plavcan & Daegling, 2006; Wood & Engleman, 1988). However, the numerical relationship between canals and roots is poorly understood. This study uses CT scans to investigate the relationship and variability between canal and root number of fully developed, adult post-canine teeth in a global

sample of modern humans ($n = 945$ individuals) from several archaeological/osteological collections. Specifically, we asked (1) what is the relationship between root number and canal number; (2) does this relationship vary by tooth type and (3) does the relationship between canal and root number vary in global groups?

1.1 | Root and canal formation

Tooth canal and root formation are comprised of a series of reciprocal cellular interactions in the dental papilla of the developing tooth (Jernvall & Thesleff, 2000). Central to the process, is Hertwig's epithelial root sheath (HERS), which is derived from the cervical loop of the enamel organ and is thought to be responsible for root number,

shape and length (Luder, 2015; Miller, 2013). Following crown formation, mesenchyme cells form the blood vessels, nerves and connective tissue of the pulp cavity and root canals (Wright, 2007). Simultaneously, the HERS extends apically, interacting with the mesenchyme cells of the developing canal structures, and differentiating into odontoblasts responsible for dentin and cementum production (Li et al., 2017).

During root morphogenesis, the HERS produces inter-radicular processes (IRPs), finger-like protrusions to adjacent the cervical foramen of the tooth crown. The extension and fusion of opposing IRPs across the cervical foramen create multiple secondary foramina which, in turn, form multiple tooth roots (Kovacs, 1971; Orban & Bhaskar, 1980); and it may be that number and orientation of IRPs are responsible for the variation in canal and root forms (Figure 1). While molecular regulation and tooth morphogenesis have been extensively studied in tooth crowns, the mechanisms responsible for variation in canal and root structures are poorly understood. Because of its extensive role in root formation, HERS has been an area of focus; and several studies have shown that disturbances in the formation of the HERS result in abnormalities in root number and shape (see Luder, 2015 for a review).

Though morphogenesis of internal and external root structures are concurrent processes, the completed structures do not always covary. There is great variation and complexity in root canals. While it is easy to conceptualize canals as round holes which taper towards the roots' apex, in reality, many teeth have multiple canals of differing shape and orientation within a single root. These canals can join and separate in unpredictable places and the more ovoid the cross-section the greater the propensity for complexity (Ahmed et al., 2017; de Pablo et al., 2010; Vertucci & Gegauff, 1979). Possible causes of divergence in canal and root number have been attributed to uneven deposition of dentin on the walls of the canal

(Manning, 1990), trauma to the HERS by radiation or chemical interference (Fischischweiger & Clausnitzer, 1988), and/or failure of the HERS to fuse on different sides of the root (Miller, 2013; Nelson & Ash, 2010).

In this paper we (1) test the hypothesis that there is no difference between canal and root number in the pooled post-canine teeth in our sample; (2) test the relationship between canal and root number in the individual post-canine teeth of the jaws and (3) test the relationship between canal and root number in pooled and individual teeth, by geographical regions.

2 | MATERIALS AND METHODS

2.1 | Dental formula

Categorically, premolars in this study are shortened to P, and molars to M. Tooth numbers are labelled with super- and subscripts to differentiate the teeth of the maxilla and mandible, respectively. For example, M^1 indicates the 1st maxillary molar while M_1 indicates the 1st mandibular molar. Through the course of evolution, apes and Old World monkeys have lost the first and second premolars of their evolutionary ancestors (Novacek, 1986; White et al., 2012), thus the remaining two premolars are numbered 3 and 4.

Using a tooth root phenotyping method developed by Gellis and Foley (2021), we classify roots and canals in a way that captures and combines internal and external numbers across all teeth. For example, a single root (R) with a single canal (C) would be classified as R1-C1, while R1-C2 is classified as a single root with two canals. Using this method, identification of a tooth root's phenotype and its permutations are easy to classify and compare both descriptively and statistically.
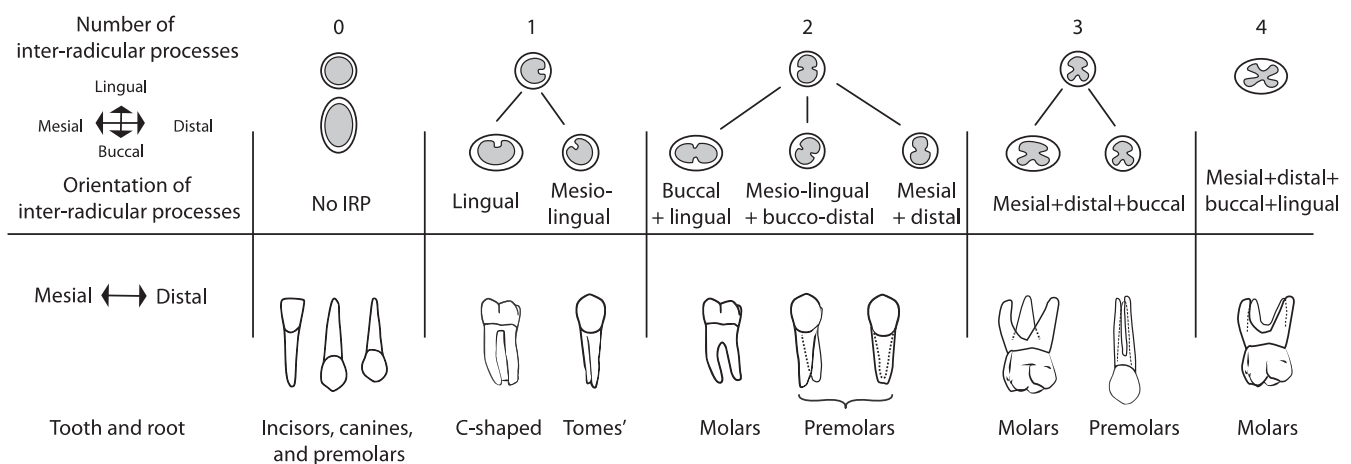
FIGURE 1 Top: The location on the apical foramen of the tooth crown where the inter-radicular processes (IRPs) form determines the number and orientation of each tooth root/tooth roots. For example, in a tooth with mesial and distal roots, two inter-radicular processes arise from the buccal and lingual borders of the apical foramen, forming mesial and distal secondary apical foramina upon fusion. Grey = apical foramina of the developing tooth crown. Bottom: Fully developed roots of different types of teeth with the same number, but different orientation of IRPs. From left to right: single-rooted teeth, single-rooted teeth in which IRP did not fuse with opposing side of apical foramen, two rooted teeth in which two opposing IRPs fused, three rooted teeth in which three opposing IRPs fused, four rooted teeth in which four opposing IRPs fused.

2.2 | Human samples

The 945 individuals used in this study were recovered from archaeological sites across the globe. These individuals are stored in osteological collections at the Smithsonian National Museum of Natural History, Washington D.C., USA (SI), American Museum of Natural History, New York, USA (AMNH) and the Duckworth Laboratory (DW) at the University of Cambridge, England (summarized in Figure 2). Only adult individuals, based on the eruption, occlusion and closed root apices of M^3s/M_3s (or M^2/M_2s in the case of congenitally absent M^3s/M_3s), were used in this study.

2.3 | American Museum of Natural History

The 186 individuals from the AMNH collection are comprised of humans from Point Hope, Alaska, North America (Figure 2, right). These individuals are attributed to the Ipiutak (500 BCE to 500 CE) and Tigara (1300–1700 CE) cultures (Larsen & Rainey, 1948; Rainey, 1941; Rainey, 1947, 1971). Information on sex (Figure 3) and antiquity come from the AMNH archives and publications associated with the collection (ibid).

2.4 | Duckworth laboratory

The majority of individuals ($n = 621$) used in this study come from the DW Laboratory collections (Figure 2, left). The DW is composed of several private collections as well as research collections from the University of Cambridge Departments of Zoology, Anatomy and Museum of Archaeology and Anatomy (Mirazón-Lahr, 2011). The oldest individuals used in this study come from the archaeological sites of Badari, Egypt (4000–3200 BCE), Jebel Moya, Sudan (100 BCE to 500 CE) and Ngada, Egypt (4400–4000 BCE), in North-East Africa. The majority of the remaining individuals are ~200 years old. In many cases information on the exact locality, age and age of death is unavailable. Information on sex (Figure 3) comes from DW archives. A complete list of the DW individuals used in this study, their collection information, antiquity, sex and locality based on available records are listed in Supplementary Materials Table A.

2.5 | Smithsonian National Museum of Natural History

The 138 individuals from the SI collection are from Oceania, Southeast Asia and Greenland. Individuals from Oceania belong ($n = 67$) to four different populations: Australia (Aboriginal), New Zealand (Maori), the Philippines and Papua New Guinea (Figure 2, right). Individuals from Southeast Asia ($n = 19$) are from Indonesia. Inuit individuals come from the North-West coast of Greenland ($n = 52$). While all SI individuals were recovered from archaeological sites, information on exact locality, age and age of death, is

unavailable. However, information on sex is taken from archives at the SI (Figure 3) as reported in Copes (2012).

The populations in this study have been, at their broadest level, grouped into five major human geographical groups: Sub-Saharan Africa, West-Eurasia, Sahul-Pacific, Sunda-Pacific and Sino-Americas (Table 1, Figure 4). Though Table 1 reports information for sex, this is for descriptive purposes. All analyses and reported results are for pooled sex samples. A complete list and description of individuals included in this study are listed in the Supplementary Materials Table A.

These groups are derived from two major works. The first is Cavalli-Sforza's *The History and Geography of Human Genes* (1994), a synthesis of global genetics with nearly half a century's worth of geographical, ecological, linguistic, archaeological and paleoanthropological research. Among the author's many conclusions are that all available evidence points to (1) an African origin for *H. sapiens*; and (2) the fact that a series of dispersal and admixture events can classify and map where major human geographical groups (as listed above) and their subsequent populations originated and dispersed through the ancient world. The volume (1994:317) also recognises that dental data "on northern Asia, southeast Asia and the Americas are generally in excellent agreement with those from single genes." The dental data they refer to are crown and root trait frequencies collected and analysed by Christy Turner and others (Busse & Carpenter, 1976; Nichol et al., 1984; Turner, 1987; Turner II, 1989). These data, along with later core collected works on dental crown traits and biogeography utilizing the ASUDAS (Hanihara, 2013; Irish, 1998; Scott, 1988; Scott et al., 2018; Stringer et al., 1997; Turner II et al., 1991), form the second basis for major human geographical groups presented here. These researchers (ibid) have shown that teeth are effective for identifying the same prehistoric population identities and movements discussed by Cavalli-Sforza (1994), as well as capturing the dental phenotypic diversity within populations, and the differences that arise between them after extended periods of isolation. The most current collections of dental anthropological research (Rathmann et al., 2017; Rathmann & Reyes-Centeno, 2020; Scott et al., 2018) are increasingly in accordance with the most recent genomic studies (Fu et al., 2016; Pickrell & Reich, 2014; Posth et al., 2018; Rathmann et al., 2017; Reich, 2018; Skoglund et al., 2016), further reinforcing the utility of teeth as phenotypic records of human biogeography and evolutionary history.

2.6 | Use of computed tomography for visualizing internal and external features of tooth roots

In clinical settings (e.g. dental, hospital, etc.), and particularly for endodontics, varying forms of computed tomography (CT) — cone beam computed tomography (CBCT), spiral computed tomography (SCT) and micro CT (μCT) — are widely utilized to visualize internal and external structures of the crown and root(s) with varying degrees of resolution (Martins & Versiani, 2019). An important parameter supporting the reliability of visualization for the study of root and
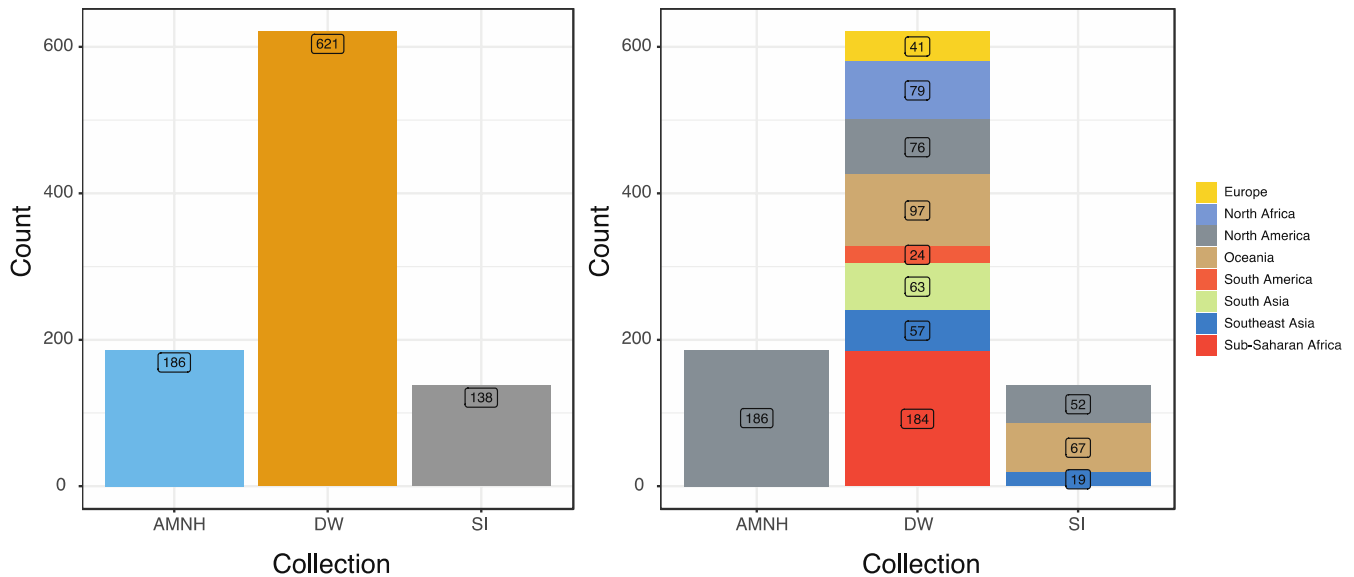
FIGURE 2 Sample sizes by collection. Left: Bar plot of counts for entire sample (*n* = 945). Right: Counts of samples divided up by collection, and geographic locations given by collection records. A complete list of the individuals used in this study, their collection information, antiquity, sex and locality based on available records is listed in Supplementary Materials Table A.
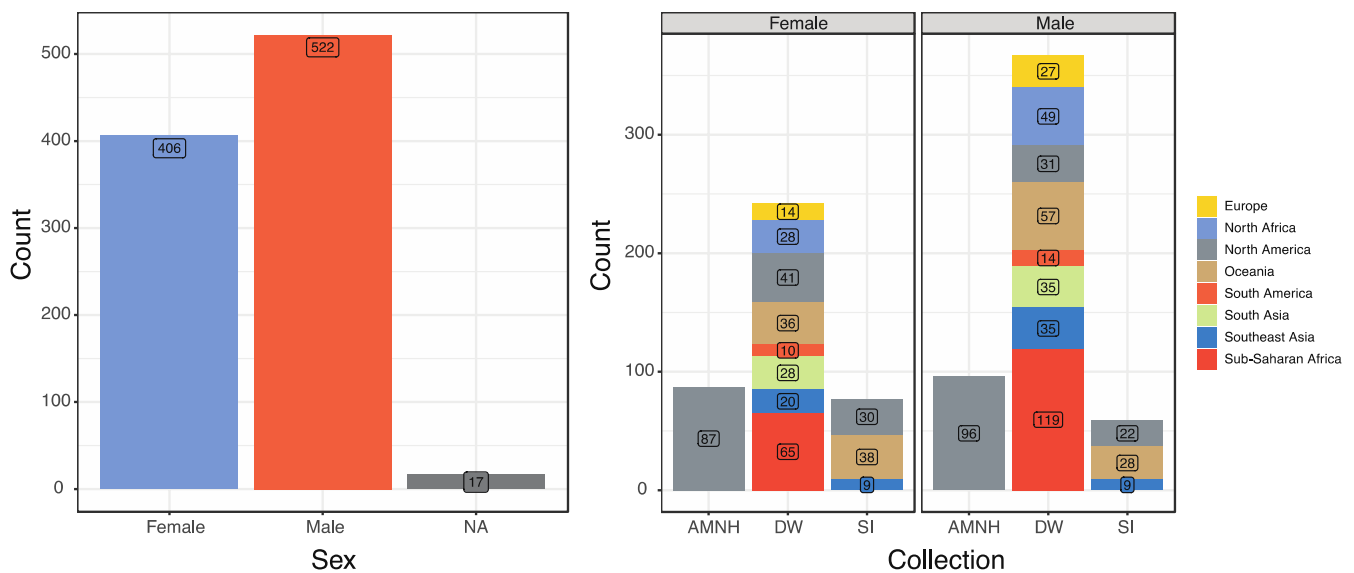
FIGURE 3 Human population sample sizes by location and sex. Left: Bar plot of sex for entire sample (*n* = 945). Right: Sex divided up by collection and geographic locations given by collection records. Individuals of undetermined sex ('NA') are not included in the plot on the right to improve readability. They are: AMNH (NA = 3), DW (NA = 12) and SI (NA = 2). A complete list of the individuals used in this study, their collection information, antiquity, sex and locality based on available records is Supplementary Materials Table A.

canal anatomy is voxel size. The smaller the voxel size relative to the volume of 3D CT, the greater the resolution. Compared to micro-CT (μCT) which operates on the micron scale (a thousandth of a millimetre) for increased resolution, CBCT and SCT use larger voxel sizes at the millimetre scale which results in a relatively decreased resolution. However, while μCT has proven invaluable for visualizing the microstructures of teeth, multiple studies have shown that CBCT and SCT are generally in agreement with μCT for detecting major structures such as root number, canal number configuration of main root canal systems in specific teeth or individual roots (Blattner et al., 2010; De Souza et al., 2017; Domark et al., 2013; He et al., 2010; Michetti

et al., 2010; Pecora et al., 2013; Sousa et al., 2017; additionally, see Martins & Versiani, 2019; Martins et al., 2019 for meta-analyses of CBCT and μCT on root canal anatomy by tooth). For example, Candeiro et al. (2021) successfully used CBCT to visualize canal configurations of 14,413 tooth roots at 0.14 mm (140 μM) voxel size; while Maret et al. (2014) compared CBCT images of different voxel sizes (0.076, 0.2 and 0.3 mm) with μCT (41 μm) and observed discrepancies of hard tissue morphology (i.e. cervical margins, cusp tips and incisal edges) were only significant at 0.3 mm (*p* = 0.01, Wilcoxon test). The use of SCT, especially for the study of hard tissues, has been confirmed to successfully and precisely visualize internal canal

anatomy. For example, Robinson et al. (2002) correctly diagnosed canal numbers and configurations in 188 P_3s at a slice thickness of 1.5 mm. Chandra et al. (2009) used SCT to diagnose a rare incidence of three canals in the distal root of an M_1 at a slice thickness of 1.5 mm, despite the thin dentinal tissues dividing canal structures. These studies (additionally, see Martins & Versiani, 2019; Martins et al., 2019 for meta-analyses of CBCT and μCT on root canal anatomy by tooth) have shown that CBCT and SCT can clearly and accurately detect the main internal and external structures of tooth roots at varying resolutions and slice thicknesses.

2.7 | Imaging of osteological collections

Following the method developed by Gellis and Foley (2021), we used CT scans to analyse 4366 post-canine teeth (Table 2) from the right sides of the maxillary and mandibular dental arcades of individuals ($n = 945$) from a global sample of humans (Table 1). Full skulls of specimens from the SI and AMNH were scanned by Dr Lynn Copes (2012) using a Siemens Somatom Spiral scanner (70 μA, 110 kV, slice thickness 1.0 mm, reconstruction at 0.5 mm, voxel size mm^3: 0.5 ×0.5 ×0.3676, 0.09 mm). Full skulls from the DC were

scanned by Professor Marta Miraźon-Lahr and Dr Frances Rivera (Rivera & Mirazón Lahr, 2017) using a Siemens Somatom Definition Flash Spiral scanner at Addenbrookes Hospital, Cambridge England (80 μA, 120 kV, slice thickness 0.6 mm, voxel size mm^3: 0.3906×0.3906×0.3, 0.05 mm). For all collections, crania and mandibles were oriented on the rotation stage, with the coronal plane orthogonal to the x-ray source and detector. Permission to use the scans has been granted by Dr Copes, Professor Miraźon-Lahr and Dr Rivera.

2.8 | Analysis of CT images

Transverse CT cross sections of roots and canals were assessed in the coronal, axial and sagittal planes across the CT stack, using measurement tools in the Horos Project Dicom Viewer (Figure 5) version 3.5.5 (https://www.horosproject.org 2016). Only permanent teeth with completely developed roots and closed root apices were

TABLE 1 The five major human geographical groups used in this study

Group	Male	Female	Unknown	Total
Sahul-Pacific	84	74	9	167
Sunda-Pacific	42	28	3	73
Sub-Saharan Africa	119	65	—	184
West Eurasia	111	70	2	183
Sino-Americas	163	168	7	338
Total	519	405	21	945

TABLE 2 Tooth counts of the right side of the maxillary and mandibular dental arcades

Tooth	n	Tooth	n	
Maxilla		**Mandible**		**Total**
P^3	515	P_3	343	858
P^4	467	P_4	313	780
M^1	697	M_1	410	1107
M^2	596	M_2	385	981
M^3	362	M_3	278	640
Total	**2637**	—	**1729**	**4366**

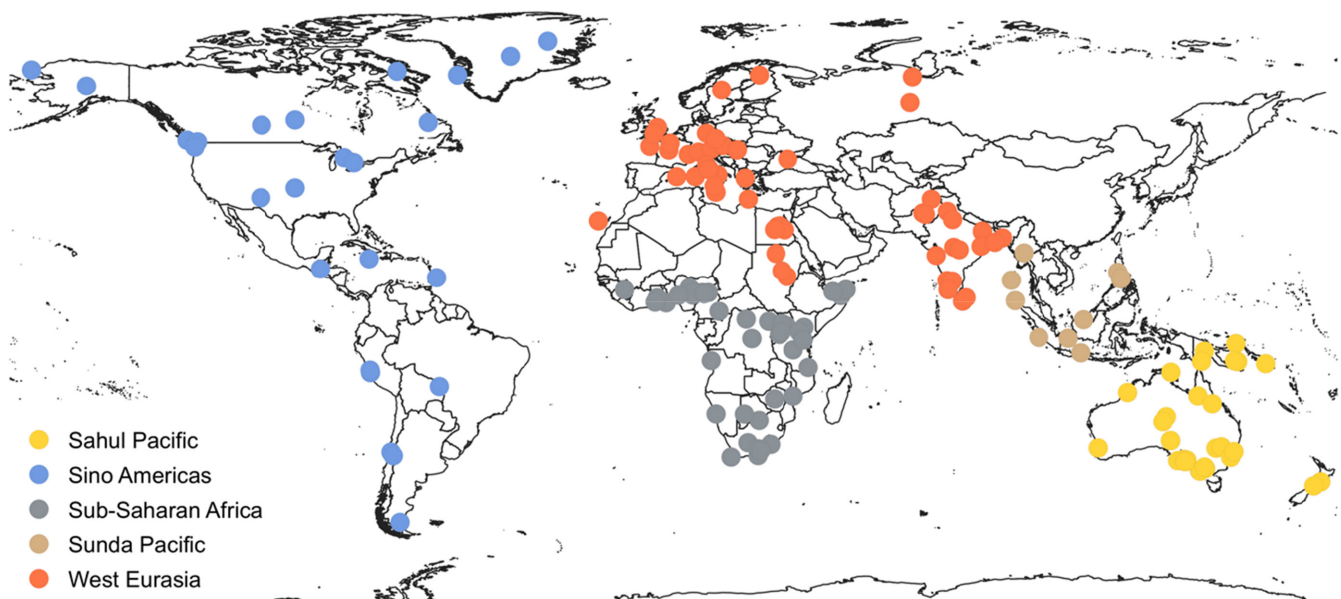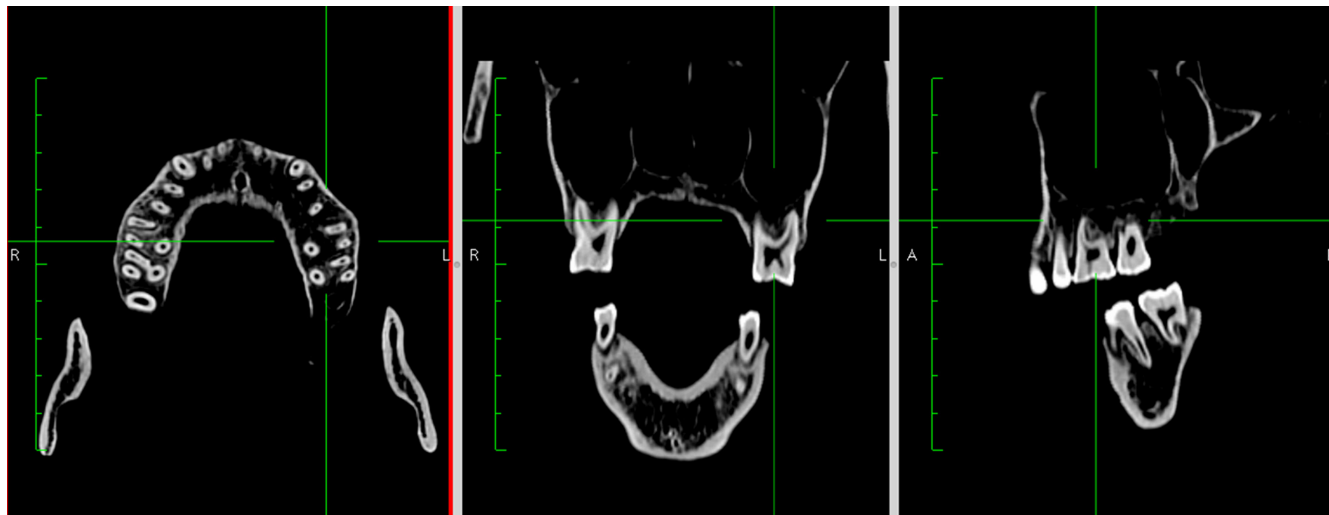*Note*: Superscript = maxilla, subscript = mandible. P = premolar, M = molar.

FIGURE 4 Map of individuals used in this study adapted to show the five major human geographical groups.

FIGURE 5 Horos Dicom Viewer 2D orthogonal view used to assess root and canal morphologies. Left: Coronal view at mid-point of roots (see Figure 6 for measurements). Centre: Anterior view. Right: Saggital view.

used for this study. While information for all teeth from both sides of the maxillary and mandibular arcades was recorded, only the right sides were analysed to avoid issues with asymmetry and artificially inflated sample size.

2.9 | Determination of root and canal number

In multi-rooted teeth, the portion of the root from the CEJ to the point of bifurcation is called the trunk, while the structures extending from the point of bifurcation are called radicals. Each radical contains one or more canals in differing configurations (Versiani et al., 2019). The radicals of multi-rooted teeth may be incompletely divided so that root number is difficult to determine. In the case of incompletely divided radicals, such as those whose division result in a bifid apex, root number was determined by applying the Turner Index (Turner, 1981; Turner II et al., 1991), which compares the point of bifurcation relative to root length (Figure 6). When bifurcation is greater than one-third (33%) of the total root length, the root is classified as multi-rooted. When the ratio is less than one-third (33%) the root is considered single rooted, or with a bifid apical third. Individual root number for analysis is recorded as a simple numerical count (e.g. 1,2,3, etc.).

Gellis and Foley (2021) modified the Turner Index for use with canals. Here, a single root canal is defined as a canal which extends from the pulp chamber within the crown and exits at a single foramen. Accessory canals (any branch of the main root canal/s that communicate with the periodontal ligament) and lateral/secondary canals (accessory canals located at the cervical and middle third of the main root canal/s) are not included in this study. Canals with greater than one-third (33%) furcation of the total canal structure length are classified as multi-canaled, even in the case where two canals briefly join in the root (Figure 6). This method is congruous with canal configurations and types described in the literature (Abbott, 1984; Ahmed et al., 2017; Vertucci & Gegauff, 1979); but

are here simplified into a system of thirds. It is by these methods that data were acquired for the analyses described and carried out in this study.

2.10 | Statistical analyses

Data were analysed with the R Project for Statistical Computing (R Core Team, 2017). Because the osteological materials used in this study were recovered from excavation sites, many of the individuals comprising our sample are missing one or more teeth. As the mechanism causing these missing data are unrelated to the values of any variables used in analysis (missing completely at random), our observed values are essentially a random sample of the full data set and not biased (Sterne et al., 2009). Thus, multiple imputations—the replacement of missing data with substituted values, here iteratively calculated using principal component regression and ridge regression (Josse et al., 2012)—is appropriate for our data set (Garson, 2015; Zhang et al., 2017). Using the missMDA package (Josse & Husson, 2016), we performed multiple imputations on missing root and canal number data in preparation for analysis as Generalized Estimating Equations (discussed below) cannot be applied to missing or "NA" values. Counts for imputed values used in analyses are provided in Supplementary Materials Tables B.

Because the Poisson distribution is typically used for count data, a Poisson general linear model (PGLM) was used to test the association between canal and root number at the $p = 0.05$ significance level (Zeileis et al., 2008). A key assumption underlying PGLM is the independence of observations (Hoffmann, 2004). Thus, the inclusion of multiple teeth from the same individuals may violate assumptions of independence for the PGLM used in this study. To account for this, we fit our PGLM with Generalized Estimating Equations (GEE). GEE estimates group-averaged parameters and their standard errors based on a number of assumptions: (1) The response variables are correlated or clustered; (2)
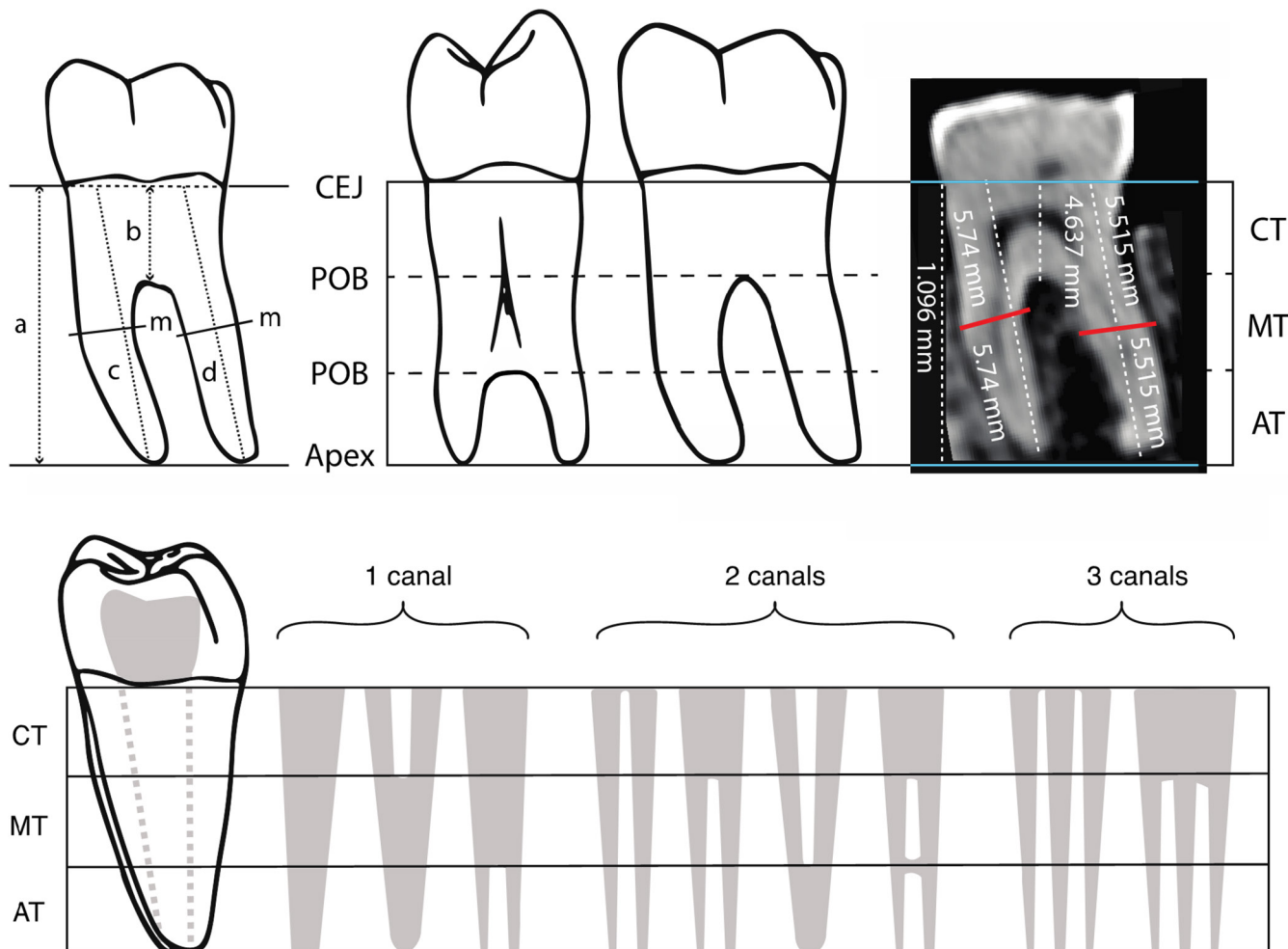
FIGURE 6 Measurement and identification of root and/or canal number. Top left: Locations of measurements taken in Horos Dicom Viewer of (a) Absolute length of root - CEJ to parallel position at apex of roots(s); (b) bifurcation length; (c & d) root length(s) along the axis of the root(s); (m) mid-point between CEJ and root apex along the long axis of the root. Top right: Application of measures to CT slice of a mandibular molar. Bottom: Determination of canal numbers from Gellis and Foley (2021). Illustration of a distal root of a double-rooted mandibular molar with examples of canal counts in solid grey. Dotted grey lines indicate canal/s position in root. CEJ, Cemento-enamel junction; POB, Point of bifurcation; Solid grey, canals; CT, cervical third; MT, middle third; AT, apical third.

There is a linear relationship between the covariates and a transformation of the response and (3) within-subject covariance has a correlation structure (Diggle et al., 2002; Zeger & Liang, 1986). In order to determine our correlation structure and how root and canal number correlated within and between teeth we conducted a Pearson correlation analysis of canal and root number. We selected an Auto Regressive Order 1 (AR1) correlation structure for our GEE covariance matrix. While GEE estimates of model parameters are valid regardless of the specified correlation structure, the AR1 correlation structure is appropriate because it (a) has no distributional assumptions (Zuur et al., 2009); (b) can accurately model covariance for cross-sectional individual and clustered studies (Müller et al., 2009; Muoka et al., 2021); (c) accurately model within-subject correlation decreasing across time and/or space (Agresti, 2002); and (d) assumes observations within and individual are non-independent (Zeger & Liang, 1986). Thus, AR1 is appropriate at the individual and group levels, and for the temporospatial distances within and between individuals and groups within our

sample. GEE was caried out using 'geepack: Generalized Estimating Equation Package' version 1.3.2 (Halekoh et al., 2006). Tukey's multiple comparison test of estimated marginal means (means extracted from the PGLM analysis) were used for pair-wise analysis of major human geographical groups (Full statistical output is presented in Supplementary Materials Table N). PGLM extended with GEE was also used to test for association between root and canal number by tooth and geographical groups. Tukey's multiple comparison test was used for pair-wise analysis of groups.

3 | RESULTS

3.1 | Number of teeth, roots and canals

Tables 3 and 4 report counts for number of roots and canals from post-canine teeth belonging to the right side of the maxilla and mandible. The number of roots in teeth from the sample are

TABLE 3 Number of roots in teeth of the maxilla and mandible by tooth

Tooth	Root number	n	Total roots	% of teeth[a]	Tooth	Root number	n	Total roots	% of teeth[a]
Maxilla					**Mandible**				
P^3	1	295	739	57.28	P_3	1	341	345	99.42
	2	216		41.94		2	2		0.58
	3	4		0.78					
P^4	1	405	530	86.72	P_4	1	313	313	100.00
	2	61		13.06					
	3	1		0.22					
M^1	1	2	2060	0.29	M_1	2	336	894	81.95
	2	28		4.02		3[b]	74		18.05
	3	666		95.55					
	4	1		0.14					
M^2	1	56	1561	9.39	M_2	1	49	727	12.73
	2	117		19.63		2	330		85.71
	3	421		70.64		3	1		0.26
	4	2		0.34		3[b]	5		1.30
M^3	1	89	831	24.59	M_3	1	20	563	7.19
	2	82		22.65		2	231		83.09
	3	186		51.38		3[a]	16		5.76
	4	5		1.38		3[c]	11		3.96

Note: Values in this table are not based on imputed data.

[a]Counts of teeth are from Table 2. Congenitally absent teeth are not included in the statistics of this table.

[b]Entomolaris.

[c]Paramolaris.

TABLE 4 Number of canals per tooth in the maxilla and mandible by tooth

Tooth	Canal number	n	Total Canals	% of teeth[a]	Tooth	Canal number	n	Total Canals	% of teeth[a]
Maxilla					**Mandible**				
P^3	1	82	959	15.92	P_3	1	254	433	74.05
	2	422		81.94		2	88		25.66
	3	11		2.14		3	1		0.29
P^4	1	233	708	49.89	P_4	1	300	326	95.85
	2	228		48.82		2	13		4.15
	3	5		1.07					
	4	1		0.22					
M^1	2	4	2430	0.57	M_1	2	27	1421	6.58
	3	355		50.93		3	168		40.98
	4	334		47.92		4	212		51.71
	5	3		0.43		5	3		0.73
	6	1		0.14					
M^2	1	8	1910	1.34	M_2	1	2	1093	0.52
	2	21		3.52		2	105		27.27
	3	408		68.46		3	231		60.0
	4	159		26.68		4	47		12.21
M^3	1	32	1065	8.84	M_3	1	10	747	3.60
	2	24		6.63		2	86		30.94
	3	239		66.02		3	163		58.62
	4	67		18.51		4	19		6.84

[a]Counts of teeth are from Table 2. Congenitally absent teeth are not included in the statistics of this table. Values in this table are not based on imputed data.

between one and four (Table 3). In this sample, teeth with four roots are limited to maxillary molars and appear with a relatively low frequency compared to 2 and 3 rooted teeth. Premolars, especially P_3 and P_4, are predominantly single-rooted, while the majority of mandibular molars in this sample are double-rooted. Entomolaris (En), or three-rooted molars, appear in 18.05% M1s, 1.23% of M2s and 5.94% of M_3s, and three-rooted paramolaris (Pa) appears in 3.63% of M_3s.

Teeth from this sample contain between one and six canals, and canal number often exceeds root number (Table 4). Many teeth contain two or more canals, especially in the molars. Molars have the greatest number of canals per tooth, with M^1s showing the most variation in canal number.

3.2 | Inter-trait correlations and independent observations

Tooth crown dimensions of adjacent teeth are strongly correlated with one another (Stanley M. Garn et al., 1965, 1968; Harris & Lease, 2005), as are eruption sequences (Ash, 2013; Fleagle, 2013; Smith, 1991), timing of mineralization (Miller, 2013; Nelson & Ash, 2010; Reid et al., 1998) and agenesis (Garn et al., 1963; Nieminen, 2009). Conversely, non-metric crown and root traits of adjacent teeth are usually expressed independently of one another (Corruccini, 1976; Markowski, 1995; Scott et al., 2018). To avoid violations of statistical independence and to test the relationship between adjacent teeth from the same individual, Pearson product–moment correlation coefficients (Figure 7) were computed to assess linear correlation and trait independence between root number (RN) and canal number (CN) within and between teeth, in preparation for PGLM.

The majority of variables have negligible to weak positive or negative correlation coefficient strength values of $0.01–\pm0.30$ (Akoglu, 2018). Within the same teeth, moderate to strong correlation coefficient values of $0.31–\pm0.69$ (ibid) are found in P^4 RN:P^4 CN (0.46), M^3 RN:M^3 CN (0.47), M_2 RN:M_2 CN (0.35) and M_3 RN:M_3 CN (0.50). With the exception of P^3 RN:P^4 CN (0.46), P^3 RN:P^4 CN (0.65), P_3 CN:P_4 CN (0.43), M^3 RN:M^2 CN (0.31) and M_2 CN:M_3 CN (0.31), there are no significant correlations of RN to CN across different teeth.

3.3 | PGLM of the relationship between canal and root number in individual teeth

While independent variables are uncorrelated, uncorrelated variables are not always independent. To address this, we fit PGLM with GEE to account for low levels of correlation between some traits (Figure 7), and to account for using multiple teeth from the same individuals, which may violate assumptions of variable independence. PGLM fitted with PGEE was used to directly test the linear relationship of root to canal number by tooth - in other words, to see how the relationship between canal and root number varies across different tooth types. PGLM of individual teeth reveal that for M^1–M^3, and M_1–M_3, as canal count increases, so does root count (Table 5). In the maxilla, the greatest increase in root to canal number is found in M^1 (99.99%), and similar relationships are found in M^2 and M^3. Maxillary premolars remain relatively stable, with a minimal increase (0.03%) in P^3, and no increase in root number in P^4. Mandibular molar (M_1–M_3) roots are comparatively similar to one another in their odds ratios, especially M_1 and M_2; while surprisingly, mandibular premolars (P_3–P_4) show that as canal number increases root number does not.

Prediction curves differ for each tooth, and the maxilla and mandible as a whole (Figure 8). Similar tooth groups have similar prediction curves—P_3, P_4 and P^4; M_3, M_2 and M_1; and M^1, M^2, M^3; and these differ between the maxilla and mandible. There is a slight overprediction in the number of roots for single canaled M^1–M^3s owing to (1) very small sample of individuals with one root to one canal for these teeth (see Table 3 for counts); and (2) because we have used a fixed non-parametric model to capture the non-linearity between canal and root number.

Figure 9 plots proportions of root and canal number phenotype permutations for individual teeth within the sample following the method developed by Gellis and Foley (2021). Different patterns are clearly evident across all teeth and between the maxilla and mandible and help to visualize and explain groupings of individual tooth prediction curves in Figure 8. Variation in canal to root number decreases in the premolars while increasing in the molars, though this variation does not covary between opposing individual maxillary and mandibular teeth. The greatest variation is found in the maxillary molars (M^1-M^3) while the least is found in P_4.

Tukey pair-wise comparisons of estimated marginal means from PGLM of root to canal number by tooth (Figure 10) show that patterns in prediction curves and canal-to-root proportions plotted in Figures 9 and 10 reflect significant differences between teeth (Full statistical output is presented in the Supplementary Materials Table M).

3.4 | PGLM of the relationship between canal and root number in major human geographical groups

We used PGLM fitted with GEE to test the linear relationship of root to canal number by tooth across major human geographical groups (Table 6). To avoid emphasizing results against one geographical region or tooth, we fitted the model without an intercept.

Individual teeth within major geographical groups are relatively similar in their odds ratios and prediction curves (Table 6 and Figure 11). Prediction curves for Sub-Saharan Africa are closest to the 1:1 canal-to-root ratio, while Sino-Americans are the furthest.

Marginal effects quantify how groups vary differently in their canal to root ratios when the explanatory variable (canals) changes by one unit (Figure 12). For all teeth, the Sino-American groups have the lowest degree of change in root number as canal number increases/decreases, while Sub-Saharan Africans show a higher percentage of root number change as canal number increases.

Differing canal and root number phenotype permutations are complex (Figure 13) but help clarify prediction curves and marginal effects in geographical groups (Table 6, Figures 12 and 13).

Tukey pair-wise comparisons for PGLM of canal to root number by major geographical group show that patterns in prediction curves, marginal effects and canal and root proportions (Figures 12–14) reflect significant differences between Sub-Saharan Africa and all other groups (Figure 14). Significant differences are also shown between Sahul-Pacific and Sino-America. Full statistical out is provided in Supplementary Materials (Table N).

4 | DISCUSSION

In the analyses presented above, we have been able to show that canal and root count are not correlated between adjacent teeth (Figure 7). However, because uncorrelated random variables are not always independent, we extended our PGLM with GEE to develop a predictive model of the relationship between canal and root number, globally and by geographical group, and we show that this relationship is not perfectly linear. We have found that canal number predicts root number, and that the greater the number of canals the more complex, and less predictable the number of roots. This relationship varies by maxillary and mandibular teeth and tooth row (Table 5). These results raise a number of issues: what does the complexity of canal to root number relationships mean developmentally? Why does this complexity vary across particular tooth types? How do canal and root number vary between maxillary and

FIGURE 7 Pearson correlation of root number (RN) to canal number (CN). Significance level = 0.05. Significant positive correlation coefficients in blue. Significant negative correlation coefficients in red. Blank cells in P_4 RN:P_4 RN due to all P_4s having the same level (i.e. one root; see Table 3). Counts for imputed values used in analyses are provided in Supplementary Materials Table B.

TABLE 5 Regression parameters for PGLM and GEE-fitted regression of the association between canal-to-root number by tooth, ranked by odds ratios from greatest to least[a]

	Estimate	Odds ratio	Std. error	Wald	*p*-value
Canal number	0.117	1.124	0.007	251.300	<0.0001
Maxilla					
M^1	0.693	1.999	0.025	750.400	<0.0001
M^3	0.650	1.916	0.025	683.700	<0.0001
M^2	0.648	1.911	0.025	651.900	<0.0001
P^3	0.000	1.000	0.018	0.000	0.990
P^4	−0.091	0.913	0.011	69.100	<0.0001
Mandible					
M_3	0.356	1.428	0.022	264.800	<0.0001
M_2	0.324	1.382	0.025	207.100	<0.0001
M_1	0.287	1.330	0.028	106.700	<0.0001
P_4	−0.119	0.887	0.008	248.000	<0.0001
P_3	−0.127	0.881	0.008	236.100	<0.0001

[a]Model fitted without intercept. Counts for imputed values used in analyses are provided in Supplementary Materials Table B.

mandibular teeth in total, by major human geographical groups, and individually?

4.1 | Differences in root and canal number

Currently, there is no consensus as to why canals and roots should differ in number, given that canal formation precedes root formation. Clusters of blood vessels entering the dental papilla early in tooth formation co-incide with the positions where roots will eventually form (Miller, 2013). The HERS and expanding dental pulp form around these nerves and blood vessels before dentin formation. Thus, each root must contain at least one canal for the pulp, and the nerve and blood supply that precede the formation of the surrounding root structure. It is possible that number, size and configuration of blood and nerve supplies is, in part, responsible for variation in canal number with the roots, and not variation in the number and orientation of the interradicular processes alone.

4.2 | Variance across teeth and between the maxilla and mandible

Why canal and root number should vary both within and between teeth of the maxilla and mandible is also unknown. Prediction curves and proportions of canal to root number phenotype permutations show that the relationship between canals and roots within tooth types are similar to one another, that is, maxillary molars are alike, while being significantly different from other tooth types, such as premolars and mandibular molars. Similar estimates (Table 5) and PGLM curves of tooth types (Figure 8) seem to lend support to the morphogenetic field model in which teeth within a field are more similar to one another than to teeth of another field (Butler, 1937, 1963; Dahlberg, 1945); especially for molar fields in both jaws. These results suggest that the number of canals and roots within tooth

types are relatively "fixed" with little intra-tooth type variation. We propose two possible explanations, the first functional and the second spatial.

Megadonty is a hallmark of early hominin evolution (Reed, 1997; Robinson, 1956; Wood & Abbott, 1983; Wood & Constantino, 2007); and heavy chewing requires large teeth. The majority of chewing actions occur on the broad occlusal surfaces of the post-canine teeth where, compared to anterior teeth, masticatory movements are complex combinations of antero-posterior, vertical and lateral movements (Ledogar et al., 2016; van Eijden, 1991). Chewing pressures on the maxillary teeth result from absorption of shearing and compressive forces generated by the active movement of the mandible (Ledogar et al., 2016). During mastication, maxillary molars are subjected to greater medio-lateral directed loads than mandibular molars (Dempster et al., 1963; Spears & Macho, 1998). These medio-lateral forces are dissipated into the jaws via the tooth roots (Baragar & Osborn, 1987; Zwemer, 1985); and in humans are strongest at, and decrease posteriorly from M^1/M_1s (Gordon, 1984; Macho & Spears, 1999). Consequently, as root surface area decreases in M^2 and M^3, so does root number (Dempster et al., 1963; Table 3).

It is possible that where increased masticatory loadings are a selective pressure for larger teeth, an increased blood supply required for developing a larger tooth will result in an increase in canal number. This will, in turn, result in more roots. The increased mesio-distal and bucco-lingual dimensions of premolars tooth crowns belonging to megadontic "robust australopiths" (*Paranthropus boisei*, *P. robustus*, *P. aethiopicus*), support such as hypothesis. These "hyper-robust" hominins regularly had multi-rooted/canaled premolars (Brook et al., 2014; Kupczik et al., 2018; Moore et al., 2016; Robinson, 1954, 1956; Wood & Engleman, 1988), and the ancestral hominin phenotype has been proposed as three-root maxillary premolars, and two-root mandibular premolars. In modern humans, molars withstand the heaviest masticatory loadings while premolars are subjected to the least (Demes & Creel, 1988; Ledogar et al., 2016). That
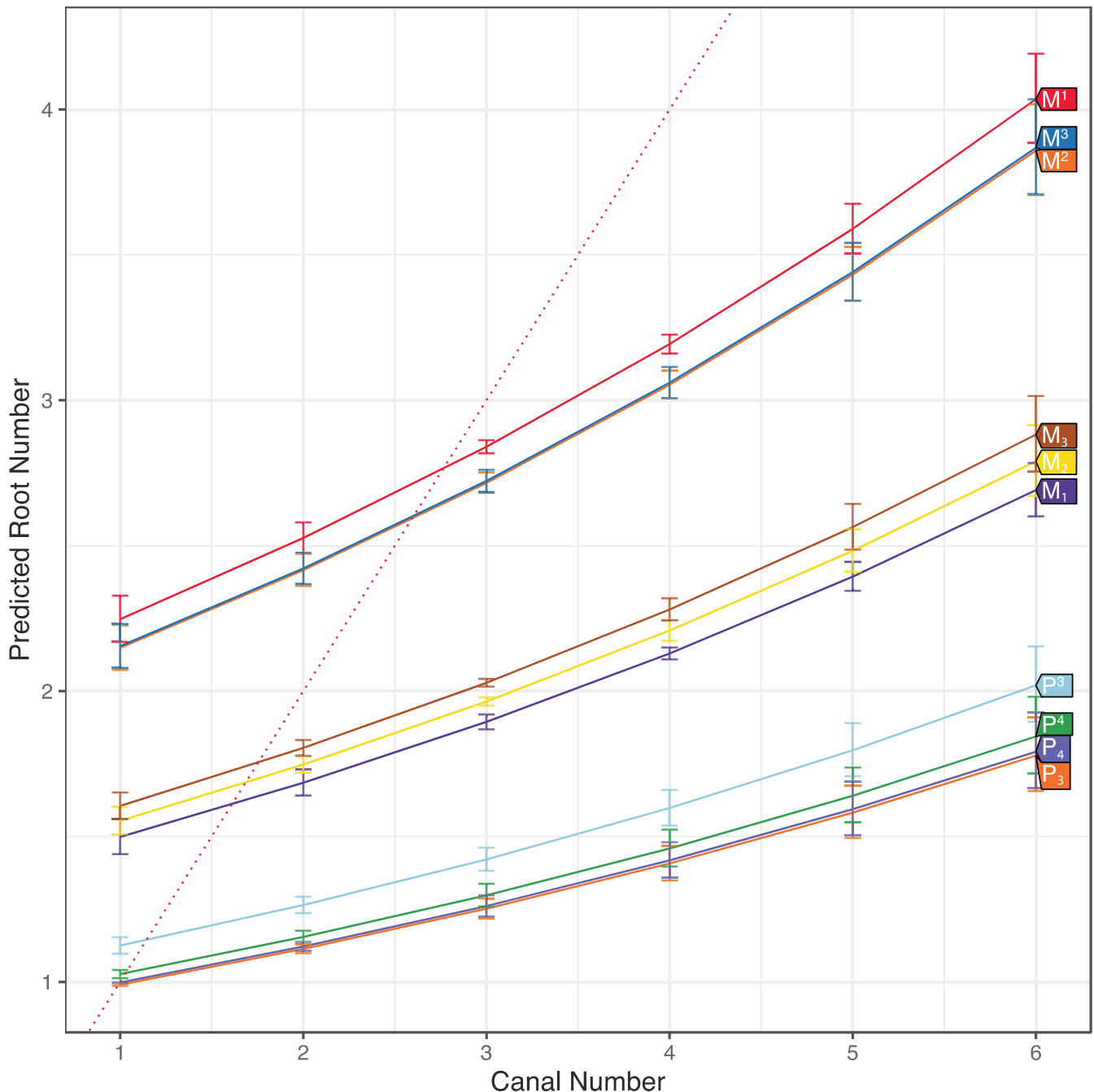
FIGURE 8 PGLM prediction curves with error bars for canal to root number for individual teeth. Dotted red line represents 1:1 canal to root relationship (i.e. what would be observed if there was a simple 1:1 relationship between roots and canals). Over prediction in the number of roots for single canaled M^1/M_1s-M^3/M_3s is owing to very small sample of individuals with one root to one canal (see Table 3 for counts). Counts for imputed values used in analyses are provided in Supplementary Materials Table B.

masticatory stresses produce high strains in the alveolar margin of the anterior maxilla (Ledogar et al., 2016) may act to increase canal and root number in the maxillary premolars compared to mandibular premolars. Developmentally, Shields (2005) proposed that tooth germ size influenced the number and development of IRPs. However, multiple studies have noted that tooth crown size (used as proxy for tooth germ size) does not always covary with root number and size in humans and hominoids (Abbott, 1984; Moore et al., 2013, 2016; Shields, 2005).

Different masticatory forces resulting from dietary demands have been shown to increase tooth root surface area, and thus size, in primates (Kovacs, 1971; Kupczik & Dean, 2008; Ledogar et al., 2016; Spencer, 2003). A possible selective mechanism to increase tooth root surface area would be to increase the number of roots, which would in turn enlarge the cervical base area of the crown (Kupczik et al., 2005). A study of *Gorilla gorilla*, *Pan troglodytes*, as well as 26 fossil gracile and robust hominins from South Africa concluded that dietary adaptations produced mesio-distal expansion at the base
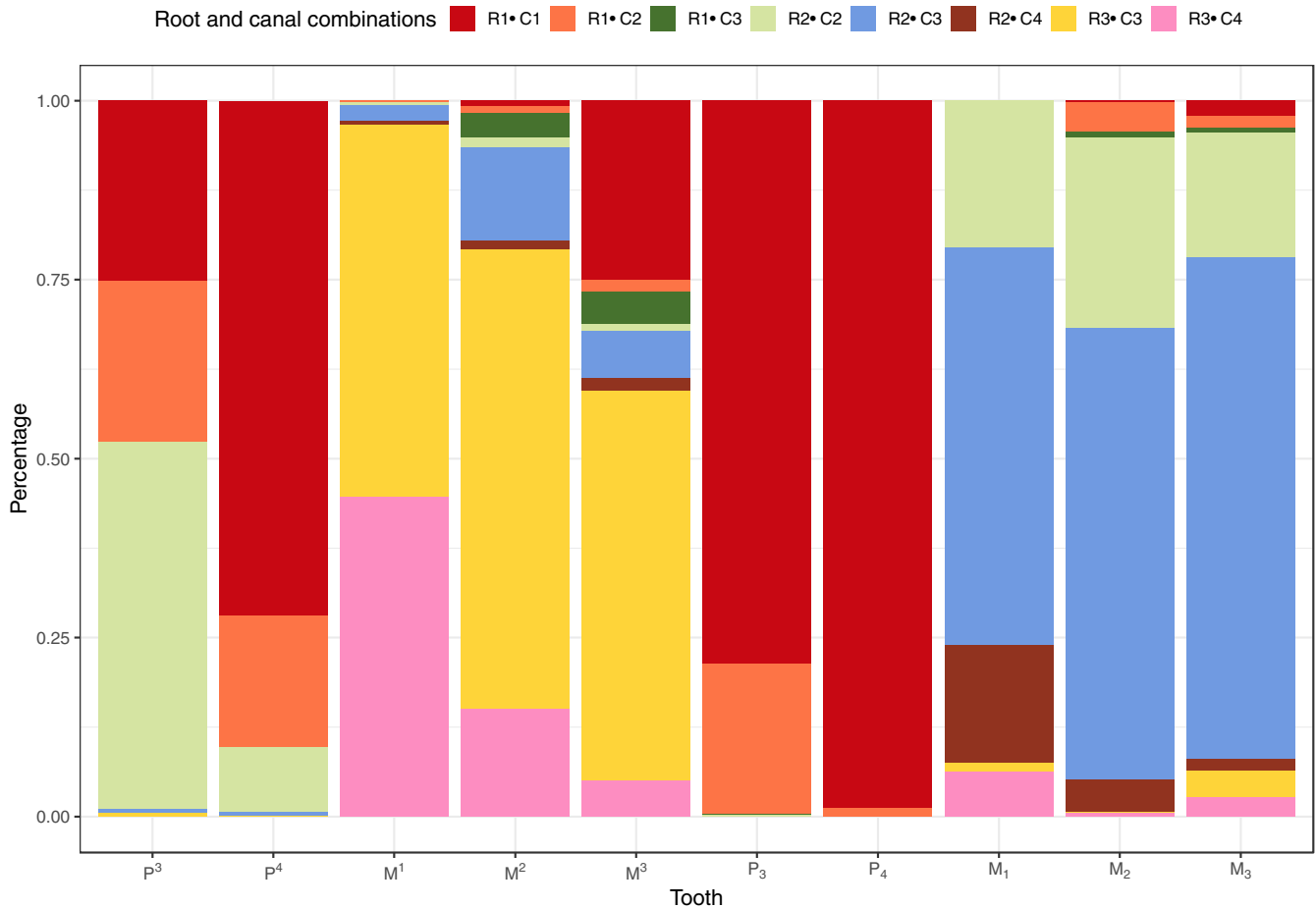
FIGURE 9 Proportion of canal and root number phenotype permutations for individual teeth. R = root number and C = canal number (Gellis & Foley, 2021). For example, R1-C2 indicates a single-rooted tooth with two canals. R1-C4 = 9, R3-C5 = 6, R3-C6 = 1 and R4-C4 = 8, are not visualized on this plot due to small sample size. Counts for imputed values used in analyses are provided in Supplementary Materials Tables C–L.

of tooth roots in M^{1}s (Kupczik et al., 2018). The authors (ibid) concluded that it was increasing in root splay that accommodated higher masticatory loadings, but that the mesio-distal expansion of the root bases in robust hominins might be an adaptive response to different jaw kinematics for chewing different food types—horizontally directed repetitive chewing in *P. boisei* (Demes & Creel, 1988; Wood & Constantino, 2007), versus multi-directional loading of *P. robustus* (Macho, 2015). However, the extant and fossil species from this study are already characterized by multi-rooted molars and premolars (Kupczik et al., 2005; Shields, 2005; Sperber, 1974; Wood & Engleman, 1988); so it is difficult to discern if mesio-distal expansion of the roots is an adaptive response to biomechanical pressures, a bi-product of additional roots, or both. If root splay is in fact the primary adaptive response to increased masticatory loading, the selective pressures underlying what point single root surface area/size stops increasing and root differentiation begins have yet to be elucidated.

Alternatively, variation may arise from space required for growing teeth in the developing jaws. Consider that maxillary and mandibular 1st molars are the first adult teeth to erupt (at 6–7 years)

followed by the anterior teeth (7–10 years), premolars (10–12 years), followed by second (12–13 years) and third molars (17–21 years). In this spatial scenario, maxillary and mandibular first molars have the greatest number of roots and canals, while late-forming and erupting premolars have the least as they are sandwiched between 1st molars and the already erupted anterior teeth. Constrained variation, especially in the premolars may be explained by limited space for growth and development, while maxillary and mandibular molars have spatial restrictions on their growth and development limited by dimensions of the palate and by the ascending ramus of the mandible.

Biomechanical and spatial explanations need not be mutually exclusive. It may be the case that canal and root variation found in modern humans is a product of reduction in space as a consequence of reduced selection for intensive biomechanical chewing pressures in early human evolutionary history. Premolar root number has been documented as more variable than in all other tooth types (Kupczik et al., 2005; Shields, 2005; Sperber, 1974; Wood & Engleman, 1988). Contrary to the molarization of the robust paranthropines, the reduction of premolar root number is present in South-African gracile hominins. Robinson (1956) and Sperber (1974)
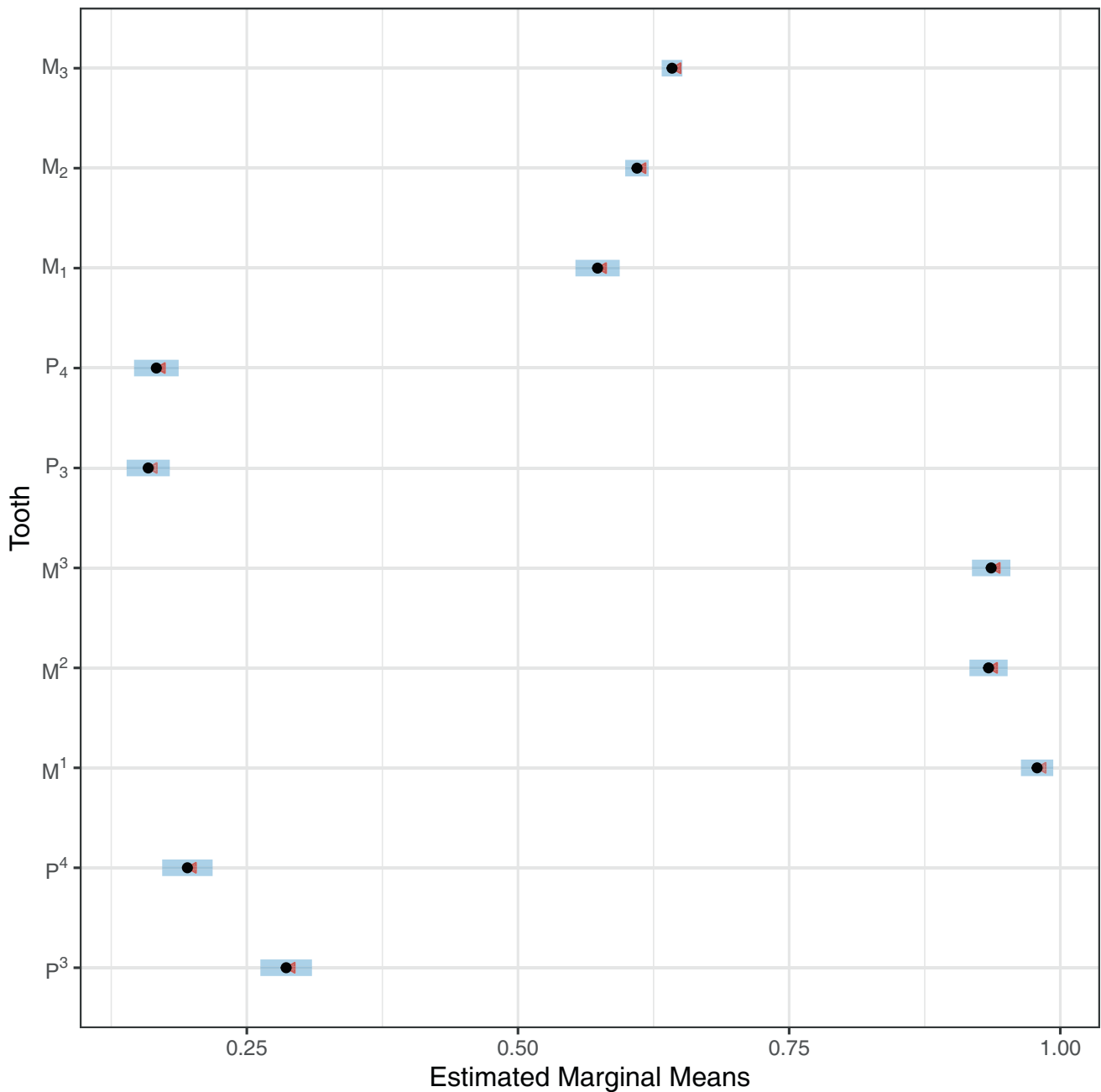
FIGURE 10 Tukey pair-wise comparisons of estimated marginal means (means extracted from the PGLM analysis) of canal to root number by tooth. Black dot = mean value; Blue bar = confidence intervals. The degree to which red comparison arrows overlap reflects the significance ($p = 0.05$) of the comparison of the two estimates. Counts for imputed values used in analyses are provided in Supplementary Materials Table B. Full statistical output is presented in Supplementary Materials Table M.

report predominantly (84%) double-rooted maxillary premolars in a sample of *Australopithecus africanus*, though single (8%) and triple-rooted (8%) variants do occur. *A. africanus* mandibular premolars are reported as having single C-shaped (also referred to as Tomes' root) and double-rooted mandibular molars (Moore et al., 2016; Robinson, 1956; Sperber, 1974). Thus, this trend for reduction in premolar root number appears early in human evolutionary history (3.4–2.4 Ma) and coincides with dietary shifts towards meat and/

or softer cooked foods (Luca et al., 2010), and reduction of hominin tooth crowns, jaws and face. At 1.8 Ma, *Homo erectus* has fewer tooth roots, especially M_3s, than earlier members of our genus, and *H. erectus* premolars are frequently single rooted (Anton, 2003). This trend in root number reduction continues through more recent members of Genus *Homo* including some specimens allocated to *H. heidelbergensis* and *H. neanderthalensis* (Benazzi et al., 2011; FitzGerald, 1998; Zanolli & Mazurier, 2013).

TABLE 6 Regression parameters for the PGLM testing the association between canal and root number by tooth in major human geographical groups, ranked by odds ratio from greatest to least[a]

Groups	Estimate	Odds ratio	Std. error	Wald	*p*-value
Canal number	0.329	1.389	0.002	29139.9	<0.0001
Sub-Saharan Africa	−0.211	0.810	0.007	816.8	<0.0001
Sino-Americas	−0.235	0.790	0.006	1749.3	<0.0001
Sunda-Pacific	−0.250	0.779	0.010	658.8	<0.0001
West Eurasia	−0.238	0.789	0.007	1065.3	<0.0001
Sahul-Pacific	−0.258	0.773	0.007	1206.2	<0.0001

[a]Model fitted without intercept. Counts for imputed values used in analyses are provided in Supplementary Materials Tables C–L.
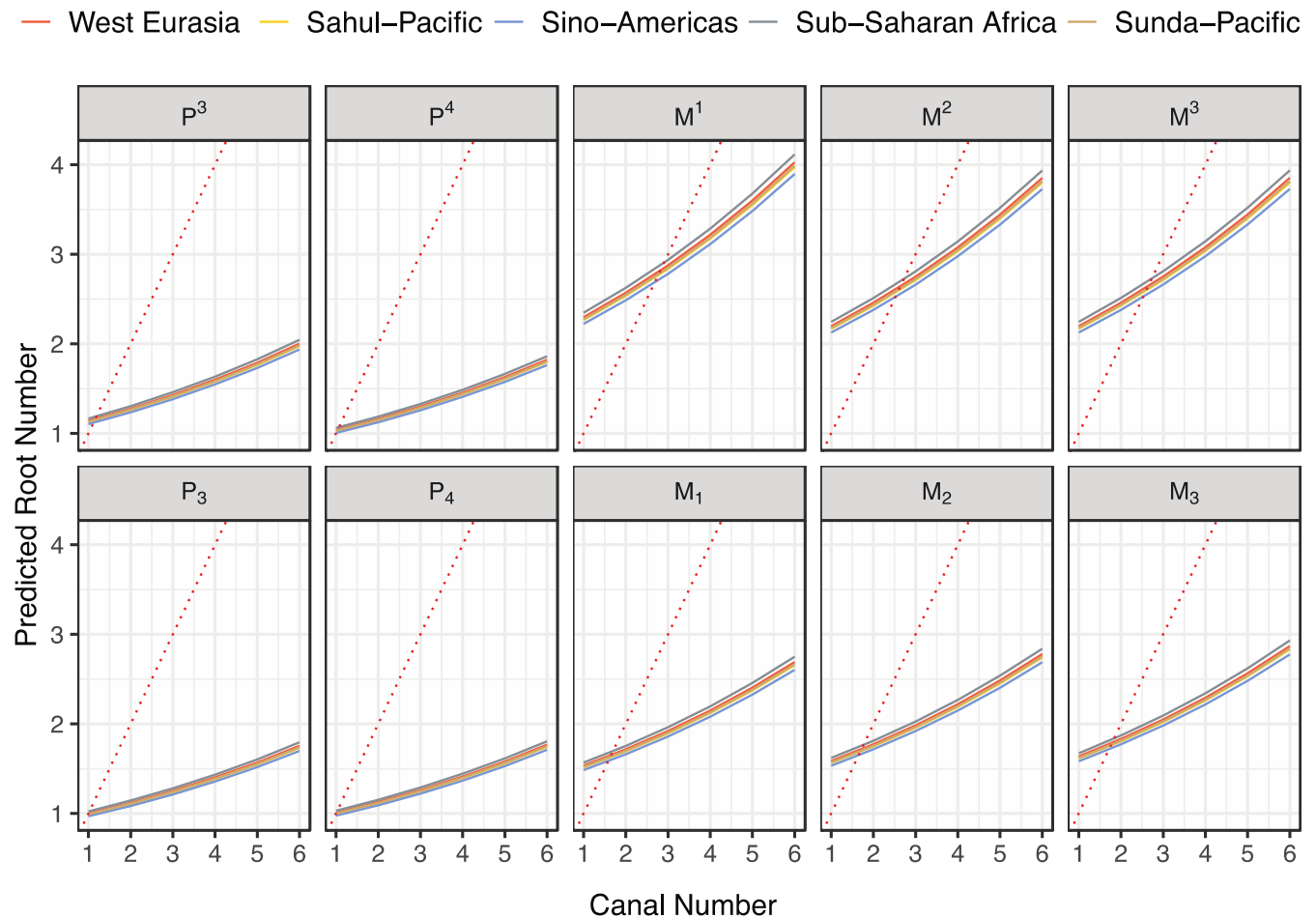
FIGURE 11 PGLM prediction curve for root to canal number by major human geographical groups. Dotted red line represents 1:1 root to canal relationship. Over prediction in the number of roots for single canaled M^1/M_1s–M^3/M_3s is owing to very small sample of individuals with one root to one canal (see Table 3 for counts). Counts for imputed values used in analyses are provided in Supplementary Materials Tables C–L.

4.3 | Differences in geographical major human geographical groups

Our results show significant differences in root and canal proportions (Figures 13 and 14) between Sino-American and Sahul-Pacific groups, and that Sub-Saharan Africans are significantly different from all other groups (Figure 14), Supplementary Materials

(Tables C–L). Several clear patterns are evident: (1) Within major geographical groups, combinations of root and canal numbers vary, and are inconsistent. For example, while P_3s of Sub-Saharan Africans are primarily R1-C2, the dominant phenotypic permutation for the rest of the major geographic groups is R1-C1. In contrast, the dominant phenotypic permutation of Sino-American P^3s is R1-C1, while the dominant phenotypic permutation for P^3 in the
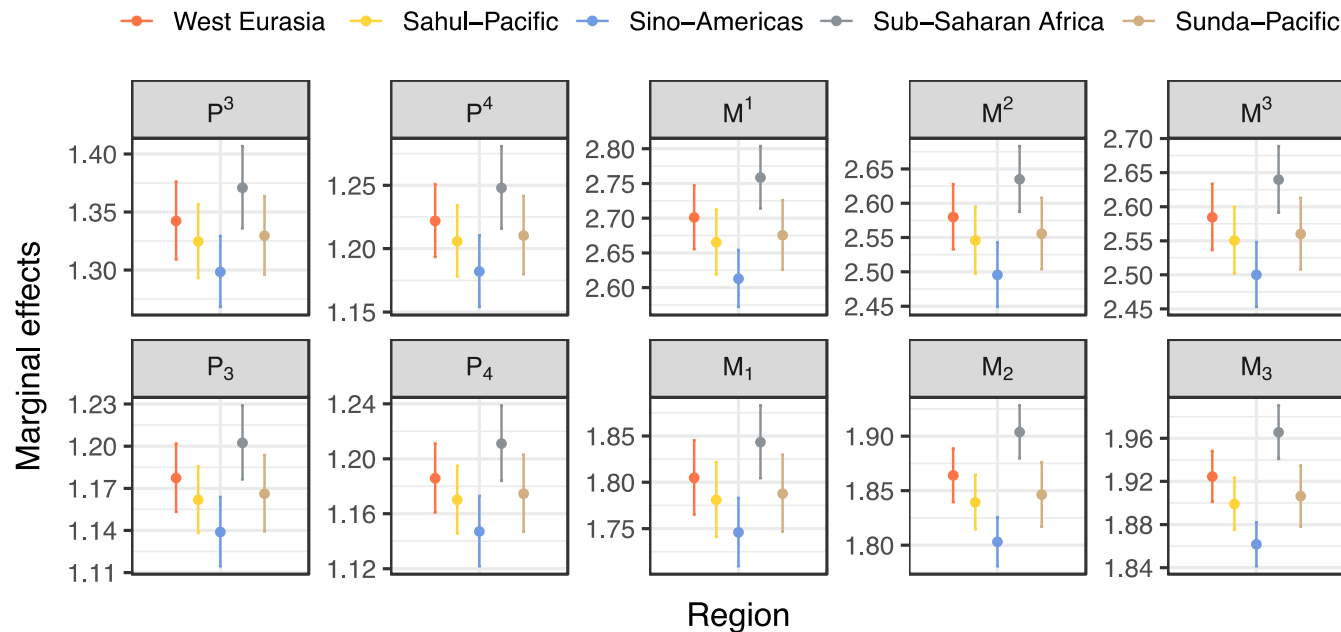
FIGURE 12 Marginal effects of canal to root count in individual teeth by geographical region. Counts for imputed values used in analyses are provided in Supplementary Materials Tables C–L.
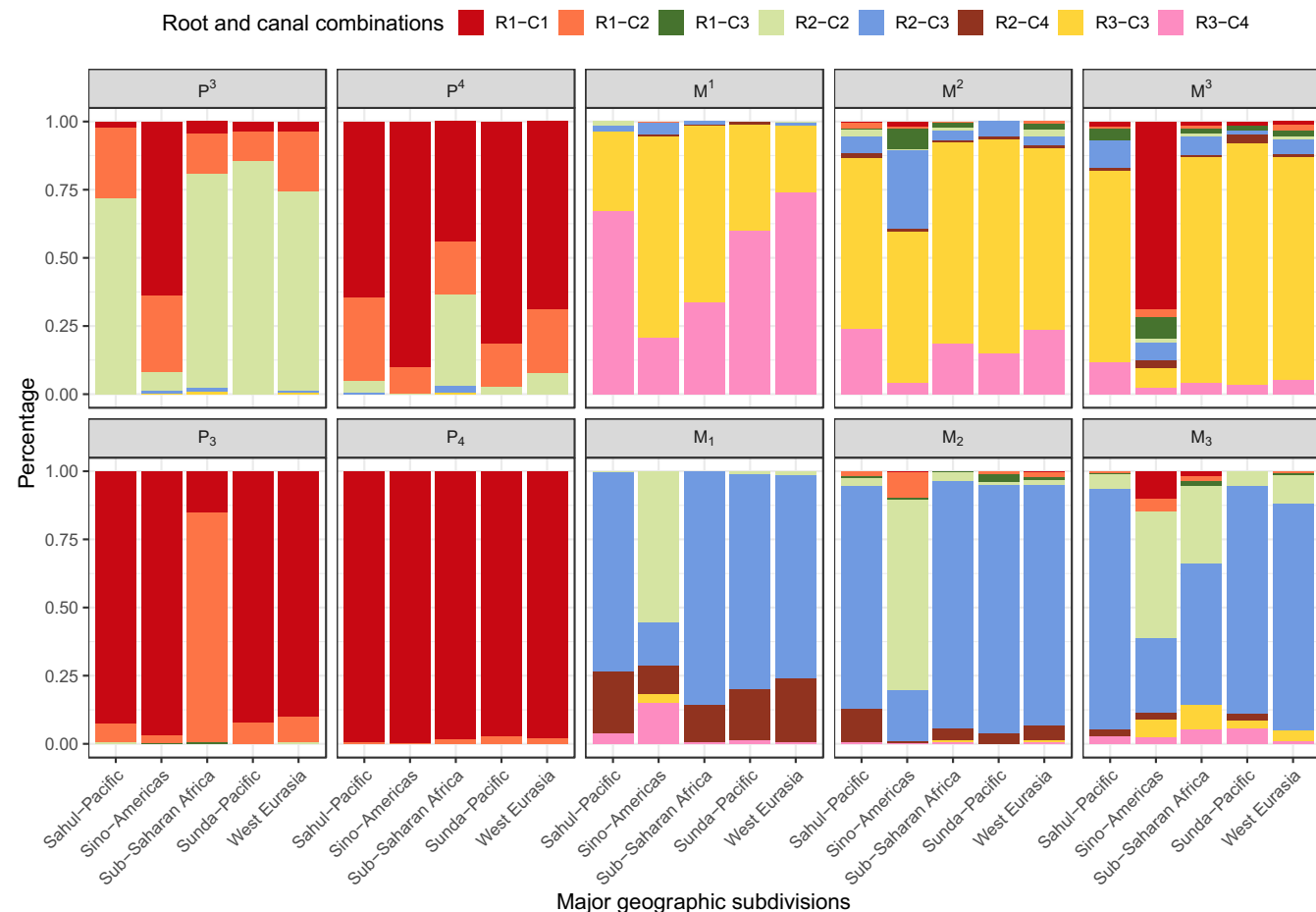

FIGURE 13 Proportions of canal and root number phenotype permutations for individual teeth across major geographical groups. R stands for root number and C for canal number (Gellis & Foley, 2021). For example, R1-C2 indicates a single-rooted tooth with two canals. R1-C4 = 9, R3-C5 = 6, R3-C6 = 1 and R4-C4 = 8, are not visualized on this plot due to small sample size. Counts for imputed values used in analyses are provided in Supplementary Materials Tables C–L.
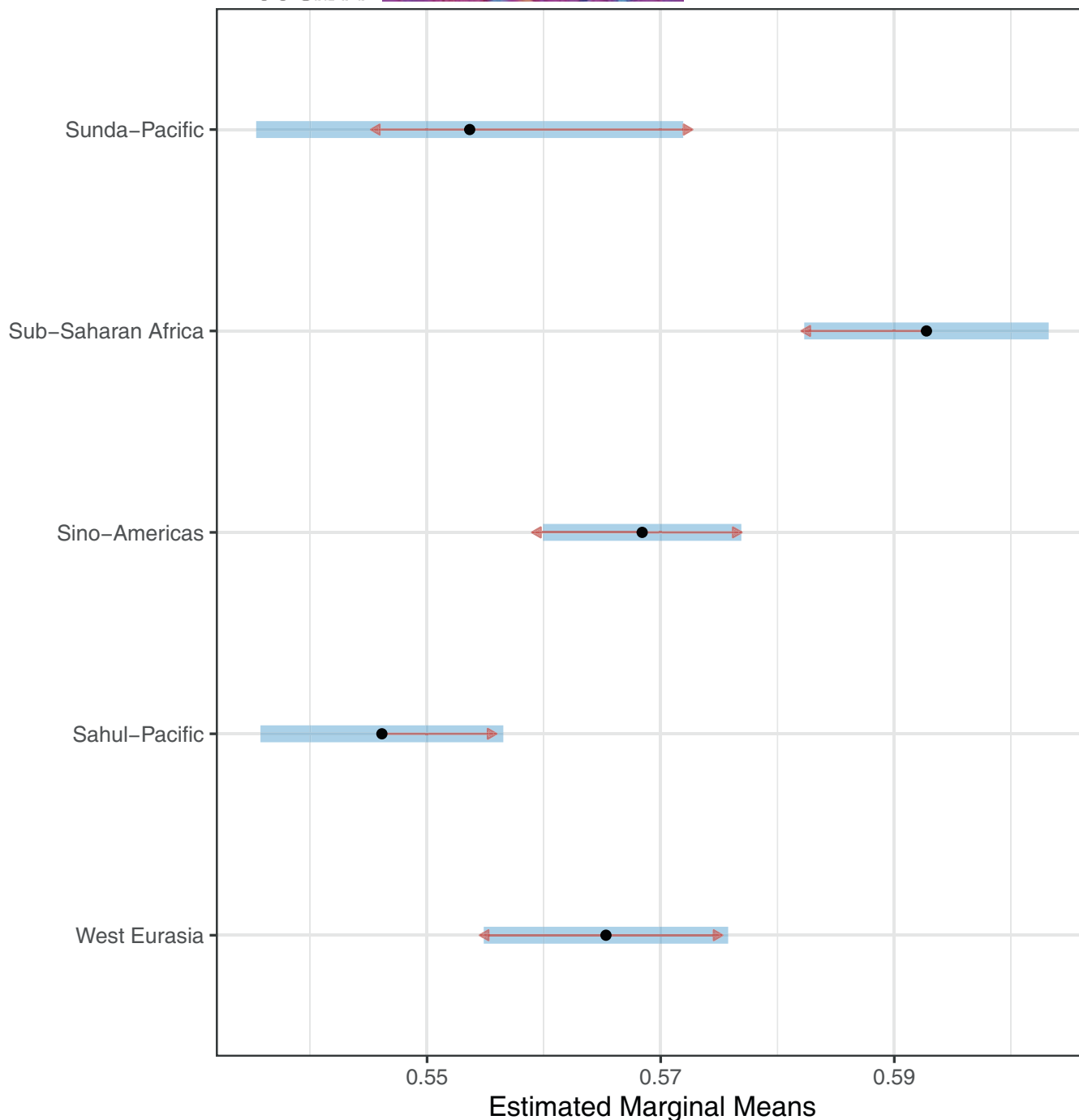
FIGURE 14 Tukey pair-wise comparisons of estimated marginal means (means extracted from the PGLM analysis) of canal to root number by geographical region. Black dot = mean value; Blue bar = confidence intervals. The degree to which red comparison arrows overlap reflects the significance ($p = 0.05$) of the comparison of the two estimates. Counts for imputed values used in analyses are provided in Supplementary Materials Tables C–L. Full statistical output is presented in Supplementary Materials Table N.

remainder of individuals is R2-C2. (2) With the exception of mandibular premolars, Sino-American phenotypic permutations are different from all other groups. The overall trend for this group can be characterized as a reduction in root and canal numbers across teeth, and/or a 1:1 root canal ratio. For example, in addition to the aforementioned R1-C1 P^{3}s, Sino-American M^{1}s are predominantly R3-C3 compared to other groups, and M^{3}s are overwhelmingly R1-C1. Sino-American mandibular teeth also show a trend towards

reduction in canals and a 1:1 canal-to-root ratio. Mandibular molars are primarily R2-C2 compared to the majority R2-C3 phenotypic permutation for other groups. (3) The number of phenotypic permutations increases in M^{2}s/M$_2$s and M^{3}s/M$_3$s. This is due, in part, to the presence of accessory roots such as Entomolaris (Table 3). This form represents a relatively rare polymorphism and appears with frequencies around 30%–50% in East Asian, Inuit and Aleut populations; 5%–15% in Southeast Asian and Pacific populations;

compared to 1% in European and Sub-Saharan African populations (Scott et al., 2018).

As with individual teeth, there is no clear explanation for changes in canal to root number between major geographical groups. The reasons may be biomechanical in nature and relate to different diets between populations. However, the effect of different diets on tooth root and canal morphologies is poorly understood, with only a few studies centred on non-human primates, and gracile and robust Australopiths (see Kupczik et al., 2018 for an overview).

The study of dental traits has an extensive history and utility for characterizing and assessing the biological relationships within and populations (see Scott et al., 2018 for a comprehensive review). Dental morphology has been shown to be under strong genetic control and minimally affected by environmental factors (Corruccini et al., 1986; Dempsey & Townsend, 2001). The evolutionary trend of teeth has also been described as towards reduction in size and simplification in morphology (Scott & Turner, 1988). While the authors of these studies were describing tooth crowns, it is unclear if tooth roots are operating under the same genetic and environmental constraints, and evolutionary trends.

PGLM predictions (Table 6) and marginal effects (Figure 12) support evidence of simplification in terms of reduction. Sub-Saharan Africans and Sino-Americans are furthest in distance from one another in time and space, and the former group shows the greatest variation in root and canal number, while the latter shows a reduction. For example, Sino-Americans have a higher proportion of single rooted, double-canaled M_2s and M_3s than all other groups. Additionally, congenitally absent M_3s are common (>25%) in Sino-Americans (Daito et al., 1992; Rakhshan, 2015; Scott et al., 2018; Turner II et al., 1991). Compared to Sub-Saharan Africa, Western Eurasia, Sahul- and Sunda-Pacific groups have reduced variability, though not as much as Sino-Americans. These three groups share similar linear relationships (Figure 11) and canal-to-root proportions (Figure 13), though marginal means of West Eurasian and Sunda-Pacific groups reveal their canal-to-root relationships are more similar to Sub-Sharan Africans, while Sahul-Pacific is closer to Sino-America.

Recent works have highlighted the decrease of genetic and phenotypic diversity in human populations with increasing distance from Sub-Saharan Africa (Handley et al., 2007; Pickrell & Reich, 2014). This decrease in diversity has been interpreted as evidence of an African origin for anatomically modern humans (Hublin et al., 2017). Reduced intra-population diversity has been ascribed to an "Out of Africa" migration, and sequence of founder events due to rapid expansions and colonization of the world (Li et al., 2008; Liu et al., 2006; Prugnolle et al., 2005). This reduction in diversity has been recorded in human dental (Hanihara, 2008; Hanihara & Ishida, 2005), craniofacial (Betti et al., 2009; Hanihara & Ishida, 2009), and morphometric traits (Manica et al., 2007), further supporting genetic hypotheses of this single African origin and subsequent expansions. However, some exceptions to this exist. For example, three rooted M_1s, sometime referred to as Radix entomolaris (see Calberson et al., 2007 for a review), increase in Sino-American populations while appearing in

low frequency in other populations; especially Sub-Saharan Africa (Scott et al., 2018). This trait has been most commonly attributed to genetic drift (Scott et al., 2018), though a recent study has suggested archaic introgression (Bailey et al., 2019); however, see Scott et al. (2020) for a rebuttal.

5 | CONCLUSION

This paper presents a novel investigation into the relationship between canal and root number in human post-canine teeth. In all cases, canal number is either equal to or exceeds root number, supporting our hypothesis that canal number precedes and is, in part, responsible for root number in all post-canine teeth. These canal-to-root relationships are significantly different between tooth types (i.e. molars and premolars), within and between the maxilla and mandible. When working with multiple teeth from the same individual there is an increased risk of violating statistical assumptions of independence. Future studies should consider how this might affect their choice of statistical model. Results indicate that Sub-Sharan African and Sino-American groups are significantly different in their canal to root numbers, and this difference represents an overall reduction in root number with distance from Africa, but not necessarily canal number. Canal to root relationships differ across all populations studied, however, the reasons for these differences are not ultimately clear. To test group affinities and differences, future studies should include morphological distance-based analysis to test divergence, as well as consider additional biological, historical, linguistic and cultural data. Results also show that tooth types within and between the jaws have different linear relationships and that these relationships are significantly different. Future studies of biomechanical and spatial hypotheses related to tooth crown size in hominin evolution may benefit from inclusion of root *and* canal count in their analysis.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are openly available from the Open Science Foundation *Tooth Root Phenotypic Set Data - internal_external_root_data.txt*; at https://doi.org/10.17605/OSF.IO/9YNUR

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