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APPENDICES

Appendix 1

99

Site 72-86

Burial No. T-338

Sex H, Age 30-40

3/1 14/6 25 75

TEETH

2

Upper teeth

	1	2	3	4	5	6	7	8
BL					8.7			
MD					8.1			
H/W					0.5			
C					3			
					u-6			
C								
H/W								
BL								
MD								

Lower teeth

al?

C - caries: surface o - occlusal, b - buccal, l - lingual, d - distal, m - mesial, n - neck
H - hypoplasia: r - ring, p - pitting
W - wear: degree 0-4
al - ante-mortem loss, u - unerupted
Genetic traits: Carabelli cusps, protostylid, shape (peg, shovel etc).
Anomalies: rotations, taurodontia, hypodontia, hyperodontia, shape of the dental arcade etc.
Others: unusual wear, tartar, colouring, periodontal disease, abscesses, loss of teeth (special reason)
etc l - teeth-loose

Lower right → granulation after loss of H₂ → gangrene pulpae
reduction of the H₃ - left upper, all 3 roots joined; rows of joint
visible, unusual shape of the tooth, small in size if looked at it
no periodontal disease

Appendix 2

1990 RM

(14)

P2-83

al No T-66-5

F Age 22-27

TEETH

Upper Teeth

R

L 1.1 1.3

	8	7	6	5	4	3	2	1	1	2	3	4	5	6	7	8
AB	-	-	-	-	1.0	1.2	-	-	-	-	-	-	-	-	-	-
CD	-	-	-	-	1.2	1.3	2.0	-	2.8	2.6	2.6	0	-	-	-	-
M	1	1?	2	1	1	1	2	3	3	2	2	1	-	2	1	-
S	1	0	2	-	-	-	-	-	-	-	-	-	-	2	1	-
ulus 0-4	-	-	1?	-	-	-	3	0	?	-	-	-	-	0	0	-
tl	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1	-	-	-	-	2.5	2.2	2.9	-	3.0	2.6	1.9	2.8	-	3.4	-	-
2	-	-	-	-	3.0	3.0	5.7	-	3.2	5.1	3.0	-	-	-	-	-
3	-	-	-	-	3.6	3.0	7.4	-	3.9	6.1	3.8	-	-	-	-	-
4	-	-	-	-	-	-	-	-	5.0	-	5.7	-	-	-	-	-
5	-	-	-	-	-	-	-	-	5.8	-	6.8	-	-	-	-	-
plasia 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2	-	-	-	-	-	-	-	-	4.8	4.9	6.3	5.5	-	-	-	-
1	-	-	-	-	4.3	4.3	6.4	5.0	4.3	4.6	4.4	4.3	-	-	-	-
ulus 0-4	-	-	0?	0	0	0	0	0	0	0	0	0	-	0?	0?	-
M	-	1	2?	1	1	1	2	3	3	-	2	-	1	2	1	-
S	-	1	0	-	-	-	-	-	-	-	-	-	-	3	1	-
AB	-	-	-	-	-	-	-	-	0	-	-	-	-	-	-	-
CD	-	-	-	-	-	-	1.4	0.4	0.2	-	0.8	-	1.3	1.3	1.4	-

Lower Teeth

exposure: heights in mm, AB - buccal height, CD - interdental height

wear : M - Molnar's scale (0-7), S - Scott's scale (0-10)

ulus : Dobney and Brothwell (1986) scale (0-4)

lasia : t1 - total crown height, 1-5 rings, distance in mm from the cemento-enamel junction to the line

comments:

enamel "pearl" - 3d.
upper and lower
molars

"big" + "tiny" rings + pit?
big rings well visible

Appendix 3

1990 RH

P2-83

1 No. T-66-5
F Age 22-27

DENTAL TRAITS

R

L

	8	7	6	5	4	3	2	1	1	2	2	3	4	5	6	7	8
Upper teeth									C	C							
ing (Scott, 1973)									2	2+	C-2						
illing + I ₁ + I ₂									2	2+							
ie tubercle									+		-						
ie distal isory ridge									3		2						
of cusps	4	4													4	4	
elli's trait (berg, 1963)			6												6		
cone (DL) son, 1978, Dahlberg)	6	6													6	4	
conule ris, Baillit, 1980)	1	4													5	3	
ular nodule									-		-						
ne distal ssory ridge									1		0?						
ual cusps No. tt, 1983)									2/3A	2/3A	5A	2/3A	3				
ttal furrow ry, 1978)									5A?	+		+	5A				
of cusps	4	5													5	4	
ve pattern 'gensen, 1955)	+	Y													Y	+	
lecting wrinkle ris, 1970)		-													-		
ostylid	0	2?													2	0	

Lower teeth

Appendix 4

Scott's scale of dental wear. Chart designed by R.J. Henneberg.

Burial No. P2-83, T-66-5

Sex. F.....Age. 22-27....

			M ₃	M ₂	M ₁		M ₁	M ₂	M ₃			
Left	Maxilla	Total score			5	7		6	4	4		
		Quadrant	I	II	I	II	I	II	II	I	II	I
					2	2	2	2	2	1	1	1
					1	1	1	2	2	1	1	1
	Quadrant	III	IV	III	IV	III	IV	IV	III	IV	III	
	Mandible	Quadrant	I	II	I	II	I	II	II	I	II	I
				1	1	1	2	2	1			
				1	1	1	2	2	1	1		
Quadrant		III	IV	III	IV	III	IV	IV	III	IV	III	
Total score			4	6		6	5					
			M ₃	M ₂	M ₁		M ₁	M ₂	M ₃			

Burial No. P2-83, T-68-13-5

Sex. F.....Age. 40-50....

			M ₃		M ₂		M ₁			M ₁		M ₂		M ₃ +	
Left	Maxilla	Total score			27										
		Quadrant	I	II	I	II	I	II			II	I	II	I	
					7	8									
					5	7									
Right	Mandible	Quadrant	III	IV	III	IV	III	IV			IV	III	IV	III	IV
		Quadrant	I	II	I	II	I	II			II	I	II	I	
					5	6									
					7	7									
		Quadrant	III	IV	III	IV	III	IV			IV	III	IV	III	
		Total score			25										

Appendix 5

THE CHORA OF METAPONTO

THE NECROPOLES

VOLUME I

By Joseph Coleman Carter

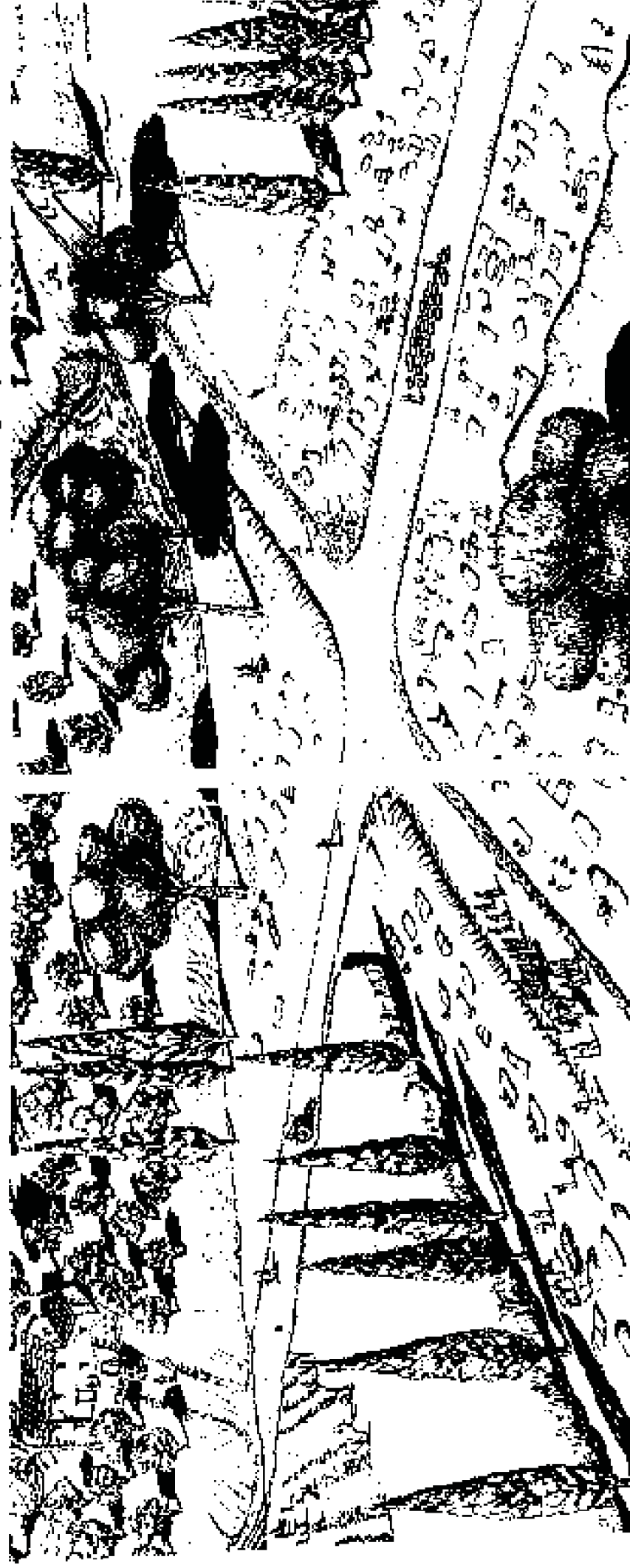
Special studies by: James T. Abbott, Lucilla Burn, Maria Elliott, Bruce Erickson, Jon Hall, Maciej Henneberg, Renate J. Henneberg, Mary Link Malone, Jon Marten, Marianne Prokiszka, Anne Parmenter
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Frontispiece: Reconstruction drawing of the Pantanello Necropolis by Michael Guarino

Appendix 5A.3

Establishing Family Relationships on Grounds of Biological Characteristics of Skeletal Material

by Maciej Henneberg and Renata J. Henneberg

Individuals who are biologically related share parts of the genetic endowment and share living conditions. This is especially true for siblings growing up in the same household. Some biological characteristics are a direct reflection of the genotype (genetic markers). Appearing early in ontogeny (an individual's development), some traits (epigenetic) are predominantly controlled by heredity;⁴¹ other traits (polyfactorial) result from the interaction of many factors, a large portion of which are genetic (polygenetic determination); the rest are determined by living conditions during the period of childhood and adolescence. In the present investigation, we have used examples of all these groups of characteristics that can be obtained in the skeletal material. Genetic markers are represented by blood groups. Epigenetic characteristics include Cambelli's traits (grooves or cusps on the lingual side of molars), meropic sutures (suture dividing frontal bone into right and left halves, persisting beyond 2 years of life), and parietal foramina (openings in the parietal bones for the emissary veins draining blood from the diploe into the scalp veins). Polyfactorial characteristics include tooth size (mesiodistal and bucco-lingual diameters) and body height reconstructed from the length of bones by means of Trotter-Gleser formula.⁴² Both the tooth size and body size are known to be under genetic control and to respond to living conditions.⁴³

The skeletal material from Pannanello, despite careful excavation, was poorly preserved and often fragmentary. This prevented us from applying a uniform set of characteristics to each family group. In some, determination of blood groups was impossible but a number of these individuals had dentitions preserved. It was possible to reconstruct stature of several individuals, but due to poor preservation of skulls, observations of neither metopism nor the presence of parietal foramina were possible.

Fragmentary preservation of the skeletal material produced small sample sizes for tooth dimensions and stature. Tooth di-

mensions differ from tooth type to tooth type and between sexes; statures show obvious sexual dimorphism. Sample sizes decrease further with these as separate statistical analysis for each tooth type and sex group is required.

In order to avoid this partitioning and to allow a maximum number of comparisons of tooth size and stature among individuals irrespective of the state of preservation and sex, we applied the Z-scoring procedure to each tooth dimension and to all statures. The procedure gives the position of an individual dimension $x[i]$ with respect to the arithmetic mean $\bar{x}$ of the group from which it has been derived in units of the standard deviation for this group: $Z[i] = (x[i] - \bar{x})/s$.⁴⁴ Z-scores of various dimensions of males and females become comparable as they are rescaled to the same mean (zero) and standard deviation (one). For example, a Z-score of -0.50 for the bucco-lingual dimension of the first molar tooth of a female means that her tooth is one half of a standard deviation narrower than that of an average woman. A Z-score of -0.50 for a man's stature means that the body height of this individual lies one half of a standard deviation below the mean for males. Although the width of a tooth is just several millimeters while body height of a male exceeds 1.5 m, in both cases the assessment of size is the same: the female and the male are somewhat smaller than average. This allows a general comparison of size irrespective of a particular dimension compared. Since two dimensions (length and width) can be taken from each of 32 teeth of an individual, we used an average Z-score of all tooth dimensions of each individual as a single figure expressing his/her tooth size. Some individuals had complete dentitions; some had only a few teeth preserved. Z-scoring provided a uniform expression of tooth size for each, thus maximizing the number of individuals who could be compared. For 48 individuals we were able to determine both the average Z-score of tooth size and the Z-score of stature. Correlation between the two ($r=0.30$) is

significant despite obvious random statistical errors normally involved in computation of Z-scores and reconstruction of stature by means of regression equations. Existence of this correlation supports the assumption that Z-scores of tooth size and of stature reflect general body size which is itself indicative of both genetic endowment and of living conditions.

We used the biological traits of individuals grouped into nuclei on the basis of the burial ground topography, dating, and material characteristics of tombs and their furnishings to test the hypothesis that individuals buried in the same nucleus were biological relatives. The null hypothesis tested was that the distribution of biological characteristics was the same in each nucleus as it was in the entire skeletal sample (taken to represent the general population). The alternate hypothesis was that biological characteristics of members of a nucleus were clustered due to their genetic and/or socioeconomic similarity. In the case of discrete characteristics (blood groups, epigenetic traits), this meant significantly increased or decreased frequency of a particular variant. In the case of continuous characteristics (Z-scores), a reduction in variance was expected. In addition, it was likely that an average Z-score for a nucleus may differ significantly from zero. Fisher's exact test⁴⁵ was used to test discrete characteristics. Significance of the reduction in Z-score variance in a nucleus was tested by means of the Snedecor's F-test with the variance in the general population assumed to be 1.00 as defined by the Z-scoring procedure. Significance of the deviation of Z-score average from zero expected for the general population was tested by computing the random error of the mean (square root of variance divided by sample size) and by checking whether the nucleus's mean lay more than two standard errors from zero. Throughout, the significance level of 0.05 was applied.

It must be stressed that our analysis can only prove family relationship when the null hypothesis is rejected. When the null hy-

⁴¹ Berry and Berry (1967); Berry (1976).

⁴² Krogman and Iscan (1986).

⁴³ Cambelli-Sforza and Bodmer (1971); Mueller (1976); Townsend and Brown (1978); Guagliardo (1982).

⁴⁴ Snedecor and Cochran (1980).

⁴⁵ Maki (1960).

pothesis is not rejected (no significant relationship found), no judgment on family relationships can be made. This does not mean that individuals in question are unrelated. Simply, due to small sample sizes and scarce or fragmentary data, we cannot tell one way or the other. Clustering of biological characteristics within a family group is weakened by the obvious fact of exogamous marriage (by definition, an individual must be unrelated biologically to his/her spouse) and the possibility of remarriage (following widowhood) producing half-siblings. Thus, it must be stressed that rejection of the null hypothesis (i.e., finding of a statistically significant clustering of biological traits in a nucleus) was *a priori* expected to be rare. This rarity was increased as we dealt with fragmentary material.

The nuclei in which one or several characteristics rejected the null hypothesis are described below in decreasing order of the strength of biological arguments supporting family relationships.

Family group N10.2

Seven individuals had tooth size Z-scores determined. Standard deviation of these was -0.407, significantly smaller than zero ($F=6.03$, $p<0.05$). The average tooth size Z-score was +0.547, significantly greater than zero (standard error=0.154). Thus, assumption of family relationship is supported.

Six individuals had frontal bones preserved. None of these had metopic suture present. Since metopic suture occurs in about one out of each five frontal bones excavated at Pantalanello, the probability that one individual will not have it is 4/5 or 0.80. The probability of coincidence of six individuals without the suture is calculated as a product of individual probabilities: $0.80 \times 0.80 \times 0.80 \times 0.80 \times 0.80 \times 0.80 = 0.262$. This is greater than conventional 0.05 and, thus, in itself does not allow us to reject the null hypothesis. In four individuals it was possible to establish presence/absence of the Carabelli's trait. All four had this trait present as a cusp, a groove, or a trace. Probability of such a coincidence in the Pantalanello material is 0.244. All three individuals whose parietal bones were preserved had no parietal foramina. The probability of this happening by random coincidence is 0.313 on the right and 0.528 on the left. Only two individuals had statures reconstructed. In both cases they were taller than the average. Probability of such a coincidence is 0.250. The combined probability of random events

causing presence in this nucleus of individuals all not having metopic sutures and parietal foramina, all displaying Carabelli's trait, and being taller than the average is 0.005. Thus, it seems that a nonrandom factor—most probably biological relationship—is responsible for the distribution of characteristics observed. Caution, however, must be exercised in drawing this conclusion since the fragmentary nature of the material prevented uniform observation of all characteristics on all skeletons.

Nucleus 3

Nucleus 3 individuals all had tooth size Z-score determined. The standard deviation was 0.171, significantly smaller than zero ($F=34.20$, $p<0.05$). The average Z-score of +0.239 with random error of 0.099 is significantly greater than zero. Thus, the null hypothesis of the random coincidence of tooth sizes can be rejected and assumption of family relationship supported.

Family group N6.5

Four individuals had tooth size Z-scores determined. The standard deviation of 0.263 is significantly smaller than one ($F=14.48$, $p<0.05$); the mean -0.339 is significantly smaller than zero (standard error 0.132). Unfortunately, too few other characteristics could be determined to support the conclusion of biological relatedness. Tooth size supports the assumption that individuals buried in this family group can be relatives.

Family group N18.2

Three individuals had Z-scores of tooth size determined. The standard deviation of 0.211 is significantly smaller than one ($F=22.46$, $p<0.05$) while the mean Z-score of -0.340 is significantly smaller than zero (standard error 0.122). This support for family relationship is further strengthened by the observation that both individuals for whom it was possible to determine the presence/absence of Carabelli's trait had the trait present and by the fact that the two individuals whose statures it was possible to reconstruct were of similar height.

Family group N18.1

We were able to determine Z-scores of tooth size of all four individuals. Their standard deviation of 0.338 is significantly smaller than zero ($F=8.75$, $p<0.05$). The mean of +0.105 does not differ significantly from zero. This, however, can be expected in cases of those groups of relatives whose tooth size

happens to be average. The occurrence of heterodont average tooth size is obviously common. Thus, tooth size supports the assumption of biological relatedness. All four individuals had their body heights reconstructed; however, neither the mean of +0.206 nor the standard deviation of 1.138 allow rejection of the null hypothesis. Here, stature does not support the assumption of relatedness, but it does not reject it either. Too few other traits were observed to discuss relationships.

Family group N10.3

Z-scores of tooth size of five individuals were determined. Neither their mean (+0.052) nor the standard deviation (0.503) allows us to reject the null hypothesis. Thus, they do not support the assumption of family relationship. In five individuals it was possible to determine presence/absence of Carabelli's trait. All of them had the trait expressed either as a cusp or as a trace of a cusp. The probability of such coincidence occurring at random is 0.01. This is small enough to assume biological relatedness even though the trait is common in European populations.

It must be added that all individuals in family group N10.2 also had Carabelli's trait expressed. Moreover, of the three individuals from family group N10.3 whose frontal bones were preserved, all three did not have metopic sutures open, similar to six individuals in N10.2. The two individuals with parietal bones present in N10.3 did not have parietal foramina, similar to the three individuals in N10.2. It is therefore likely that N10.2 and N10.3 contained members of the same family. The only reservation is that both the absence of metopic suture and the absence of parietal foramina were common traits, that it is not unusual to find together several individuals without those traits.

Family groups N3.3 and N3.4

Treated separately, these two groups had too few data to yield meaningful results. Treated jointly, analysis of Z-scores neither for tooth size nor for stature allowed the null hypothesis to be rejected. Thus, no proof of family relationship was obtained. Remains of too few individuals were preserved well enough to allow analysis of epigenetic traits. Determination, however, of blood groups yielded an interesting result. Among nine individuals with blood group determined, five had blood group B; the rest were type O.

This distribution was significantly different from that expected by coincidence (Fisher's exact test, $p=0.038$). Thus, biological relationship is likely. It should be noted that in many other nuclei, many individuals had blood groups determined, but often they were all of the same type (O). Since this was a frequent type, its coincidence could not be distinguished from random. In the two nuclei analyzed here, a high frequency of a rarer type B occurred. This was less likely to happen at random.

Family group N8.5

Neither tooth size nor the presence of epigenetic traits supported the assumption of family relatedness. Distribution of blood groups (only two Os, two As, one B, and one AB) seemed to be suggestive, but Fisher's exact test results did not reach significant levels (comparing O against all others yielded $p=0.175$; comparing A against others gave $p=0.153$, both far in excess of the required 0.05). This nucleus provided a good example of how careful one must be not to draw conclusions before applying proper statistical testing. There was nothing in our statistical analyses that contradicted the assumption of family membership, but there was equally nothing that could soundly support it.

Family group N8.1

Tooth size Z-scores were calculated for five individuals. Three individuals had skulls reconstructed. Too few epigenetic traits were observable for analysis. Calculated for all individuals, average and standard deviation of Z-scored tooth size did not allow the null

hypothesis to be rejected. Neither did calculations for stature Z-scores. There was, however, a problem with making the woman in T 22 a wife of T 211 and a mother of T 210. On the rules of blood group inheritance, it is impossible for an AB woman to have an O daughter with an O husband. When individuals AB and O produce offspring, all their children will be either A or B because O is recessive. Thus, we propose removing the woman in T 22 from the family. When T 22 is removed, the standard deviation of Z-scored tooth size for the remaining 4 individuals, 0.284, becomes significantly smaller than one ($F=12.40$, $p<0.05$) while the mean of -0.752 is significantly smaller than zero (standard error 0.142). Statures of both individuals for whom reconstruction was possible (T 338, T 331) were similar. Thus, family relationship is indicated. One individual (T 331) had metopium while the other two (T 221, T 210) did not, but this does not contradict the assumption of relatedness; it merely does not support it. Similarly, the presence of strong Caribelli's cusp in T 212 and its absence in T 210 merely do not support family relationship.

This nucleus provides a good example how complex the analysis of biological traits can become but also how it can correct placement of an individual in a family.

In all other family groups, as defined on separate sheets, biological data did not provide support for family relationships—chiefly because too few data could be obtained from the fragmentary material or because distributions of Z-scores for tooth size did not deviate from that in a general population.

When, however, the entire Nucleus 6 was analyzed jointly (i.e., family groups 6.1, 6.2, 6.3, 6.4, 6.6), Z-scores of tooth size for 13 individuals were available. Their standard deviation of 0.500 was significantly smaller than one ($F=4.0$, $p<0.05$) while the mean -0.308 was significantly smaller than zero (standard error = 0.139). None of the 6 individuals whose frontal bone was preserved had metopium. At random, this has a probability of as much as 0.262 of occurring, but together with tooth size it is suggestive of a possible relationship. On the other hand, analysis of statures of 10 individuals for whom reconstruction was possible yielded means and standard deviation insignificantly different from those for the entire sample of all individuals buried at Pantanello.

Similarly, Z-scores of tooth size and body size were analyzed for the entire Nucleus 8 comprising family groups 8.1, 8.2, 8.3, 8.4, and 8.5. Z-scores of tooth size were available for 20 individuals. Their standard deviation was 0.684, significantly smaller than one ($F=2.13$, $p<0.05$). The average tooth size Z-score of -0.089 did not differ significantly from zero, but similar to N18.1, this fact does not weaken the argument for family relationship as inherited tooth size may be average. Z-scores of stature were available for five individuals. Their standard deviation of 1.005 obviously did not differ significantly from one, and the average of +0.505 did not differ significantly from zero (standard error=0.449). Overall, there was only weak support for the assumption that this combined nucleus comprised family members.

Joint analysis of all parts of Nucleus 11 did not yield significant results.