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Supplemental Data

A Common Variation in EDAR Is a Genetic

Determinant of Shovel-Shaped Incisors

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Table S1. Summary of dental morphology data.

| Item ^a | Tokyo (n = 102) | | | | Sakishima (n = 100) | | | | Student's t test ^b | | | | | |
|-------------------|-----------------|------|-----------------|------|---------------------|------|-----------------|------|-------------------------------|----------|----------|--------|----------|----------|
| | Male (n = 25) | | Female (n = 77) | | Male (n = 43) | | Female (n = 57) | | M vs F | TM vs TF | SM vs SF | T vs S | TM vs SM | TF vs SF |
| | Mean | SD | Mean | SD | Mean | SD | Mean | SD | | | | | | |
| SH | 2.59 | 1.14 | 3.06 | 1.00 | 2.68 | 0.96 | 2.89 | 0.99 | | | | | | |
| DSH | 1.45 | 0.74 | 1.77 | 1.16 | 1.31 | 0.92 | 2.15 | 1.28 | * | | ** | | | |
| UI1 BL | 7.05 | 0.69 | 6.86 | 0.60 | 7.23 | 0.68 | 7.11 | 0.69 | | | | | | |
| UI1 MD | 8.74 | 0.65 | 8.43 | 0.48 | 8.70 | 0.49 | 8.65 | 0.46 | | | | | | * |
| UI2 BL | 6.56 | 0.64 | 6.25 | 0.58 | 6.69 | 0.44 | 6.43 | 0.60 | ** | | | | | |
| UI2 MD | 7.35 | 0.64 | 7.13 | 0.54 | 7.27 | 0.52 | 7.22 | 0.45 | | | | | | |
| UC BL | 8.44 | 0.72 | 7.83 | 0.75 | 8.15 | 0.61 | 7.93 | 0.49 | ** | * | | | | |
| UC MD | 8.13 | 0.49 | 7.74 | 0.42 | 8.26 | 0.42 | 8.03 | 0.33 | *** | ** | * | *** | | *** |
| UP1 BL | 9.78 | 0.55 | 9.59 | 0.53 | 9.92 | 0.52 | 9.70 | 0.47 | * | | | | | |
| UP1 MD | 7.65 | 0.52 | 7.51 | 0.54 | 7.55 | 0.42 | 7.59 | 0.42 | | | | | | |
| UP2 BL | 9.70 | 0.56 | 9.32 | 0.62 | 9.66 | 0.56 | 9.47 | 0.58 | * | | | | | |
| UP2 MD | 7.22 | 0.61 | 6.96 | 0.44 | 7.11 | 0.45 | 7.11 | 0.42 | | | | | | |
| UM1 BL | 11.45 | 0.72 | 11.26 | 0.70 | 11.68 | 0.62 | 11.41 | 0.45 | * | | | | | |
| UM1 MD | 10.70 | 0.75 | 10.31 | 0.63 | 10.61 | 0.66 | 10.52 | 0.48 | * | | | | | |
| UM2 BL | 11.75 | 0.71 | 11.07 | 0.68 | 11.56 | 0.92 | 11.36 | 0.56 | ** | ** | | | | |
| UM2 MD | 10.12 | 0.92 | 9.58 | 0.59 | 10.22 | 0.65 | 10.18 | 0.61 | * | * | | *** | | *** |
| LI1 BL | 5.95 | 0.40 | 5.77 | 0.41 | 5.94 | 0.49 | 5.87 | 0.66 | | | | | | |
| LI1 MD | 5.76 | 0.34 | 5.43 | 0.36 | 5.57 | 0.30 | 5.56 | 0.35 | * | ** | | | | |
| LI2 BL | 6.40 | 0.48 | 6.13 | 0.46 | 6.46 | 0.48 | 6.26 | 0.48 | ** | | | | | |
| LI2 MD | 6.35 | 0.48 | 5.95 | 0.38 | 6.13 | 0.29 | 6.12 | 0.36 | * | *** | | | | |
| LC BL | 7.93 | 0.51 | 7.33 | 0.51 | 7.54 | 0.55 | 7.11 | 0.56 | *** | *** | ** | | * | |
| LC MD | 7.10 | 0.37 | 6.58 | 0.43 | 7.18 | 0.35 | 6.82 | 0.26 | *** | *** | *** | *** | | ** |
| LP1 BL | 8.28 | 0.46 | 7.95 | 0.50 | 8.37 | 0.55 | 8.03 | 0.46 | *** | * | ** | | | |
| LP1 MD | 7.60 | 0.51 | 7.37 | 0.42 | 7.44 | 0.43 | 7.28 | 0.38 | | | | | | |
| LP2 BL | 8.66 | 0.54 | 8.32 | 0.54 | 8.79 | 0.64 | 8.67 | 0.48 | * | | | ** | | ** |
| LP2 MD | 7.56 | 0.60 | 7.32 | 0.45 | 7.46 | 0.55 | 7.36 | 0.41 | | | | | | |
| LM1 BL | 10.88 | 0.74 | 10.53 | 0.68 | 11.17 | 0.68 | 11.02 | 0.41 | ** | | | *** | | *** |
| LM1 MD | 11.85 | 0.59 | 11.29 | 0.55 | 11.53 | 0.66 | 11.41 | 0.51 | ** | *** | | | | |
| LM2 BL | 10.57 | 0.68 | 10.25 | 0.64 | 10.62 | 0.74 | 10.74 | 0.56 | | | | * | | ** |
| LM2 MD | 11.37 | 0.83 | 10.74 | 0.62 | 10.61 | 0.64 | 10.51 | 0.55 | | * | | * | * | |

^aAbbreviations: SH, shoveling grade; DSH, double-shovelling grade; U, upper; L, lower; I, incisor; C, canine; P, premolar; M, molar; BL, buccolingual diameter (mm); MD, mesiodistal diameter (mm). ^bAbbreviations: M, male; F, female; T, Tokyo; S, Sakishima. *P < 0.01; **P < 0.001; ***P < 0.0001.

Table S2. Eigenvalues in PCA.

| PC | Eigenvalue | Proportion | Cumulative |
|------|------------|------------|------------|
| PC1 | 12.86 | 45.94% | 45.94% |
| PC2 | 2.21 | 7.90% | 53.84% |
| PC3 | 1.76 | 6.28% | 60.12% |
| PC4 | 1.29 | 4.62% | 64.75% |
| PC5 | 0.92 | 3.28% | 68.03% |
| PC6 | 0.81 | 2.88% | 70.91% |
| PC7 | 0.76 | 2.72% | 73.63% |
| PC8 | 0.69 | 2.45% | 76.08% |
| PC9 | 0.61 | 2.16% | 78.24% |
| PC10 | 0.55 | 1.96% | 80.20% |
| PC11 | 0.50 | 1.78% | 81.98% |
| PC12 | 0.49 | 1.75% | 83.73% |
| PC13 | 0.43 | 1.53% | 85.26% |
| PC14 | 0.41 | 1.48% | 86.74% |
| PC15 | 0.38 | 1.37% | 88.11% |
| PC16 | 0.35 | 1.26% | 89.37% |
| PC17 | 0.33 | 1.17% | 90.55% |
| PC18 | 0.30 | 1.06% | 91.61% |
| PC19 | 0.29 | 1.05% | 92.66% |
| PC20 | 0.28 | 1.01% | 93.67% |
| PC21 | 0.27 | 0.97% | 94.65% |
| PC22 | 0.27 | 0.95% | 95.60% |
| PC23 | 0.26 | 0.93% | 96.53% |
| PC24 | 0.24 | 0.85% | 97.37% |
| PC25 | 0.21 | 0.76% | 98.13% |
| PC26 | 0.20 | 0.71% | 98.84% |
| PC27 | 0.18 | 0.65% | 99.49% |
| PC28 | 0.14 | 0.51% | 100.00% |

Table S3. Comparison of principal component scores between regions.

| PC | Male (n = 68) | | | | Female (n = 134) | | | |
|-----|----------------|-------|--------------------|-------|---------------------|-------|--------------------|-------|
| | Tokyo (n = 25) | | Sakishima (n = 43) | | Tokyo (n = 77) | | Sakishima (n = 57) | |
| | Mean | SD | Mean | SD | Mean | SD | Mean | SD |
| PC1 | 0.311 | 3.890 | -0.067 | 3.721 | -0.690 ^a | 3.404 | 0.846 ^a | 2.708 |
| PC2 | -0.326 | 1.575 | 0.172 | 1.460 | 0.068 | 1.467 | -0.138 | 1.603 |
| PC3 | 0.168 | 1.282 | -0.065 | 1.236 | -0.122 | 1.146 | -0.025 | 1.484 |
| PC4 | 0.001 | 1.028 | -0.267 | 1.022 | -0.209 | 1.125 | 0.088 | 0.940 |

^aSignificantly different between regions ($P < 0.01$).

Table S4. Genotype and allele frequencies.

| SNP rs | Chr: position | Allele | Tokyo | | | | Sakishima | | | | P | | | | |
|------------|---------------|---------|-------|-----------------|-----------------|-----------------|----------------|----------------|-----|-----------------|----|-----------------|-----------------|----------------|----------------|
| | | | n | n ₀₀ | n ₀₁ | n ₁₁ | p ₀ | p ₁ | n | n ₀₀ | | n ₀₁ | n ₁₁ | p ₀ | p ₁ |
| rs3827760 | 2: 108880033 | 0:T 1:C | 102 | 7 | 36 | 59 | 0.245 | 0.755 | 100 | 7 | 43 | 50 | 0.285 | 0.715 | 0.36 |
| rs12623957 | 2: 108880086 | 0:C 1:T | 102 | 2 | 32 | 68 | 0.176 | 0.823 | 100 | 2 | 40 | 58 | 0.220 | 0.780 | 0.27 |
| rs10495392 | 1: 235489612 | 0:C 1:T | 102 | 0 | 15 | 87 | 0.074 | 0.926 | 99 | 3 | 28 | 68 | 0.172 | 0.828 | 2.6E-03 |
| rs17265387 | 2: 199957247 | 0:T 1:C | 102 | 1 | 10 | 91 | 0.059 | 0.941 | 100 | 2 | 14 | 84 | 0.090 | 0.910 | 0.23 |
| rs17075469 | 4: 185363004 | 0:C 1:G | 99 | 0 | 14 | 85 | 0.071 | 0.929 | 98 | 6 | 39 | 53 | 0.260 | 0.740 | 4.0E-07 |
| rs2071652 | 6: 29743296 | 0:T 1:C | 102 | 2 | 32 | 68 | 0.176 | 0.824 | 100 | 0 | 5 | 95 | 0.025 | 0.975 | 4.6E-07 |
| rs555766 | 10: 78685945 | 0:T 1:C | 101 | 1 | 10 | 90 | 0.059 | 0.941 | 100 | 4 | 29 | 67 | 0.185 | 0.815 | 1.2E-04 |

rs3827760 and rs12623957 correspond to *EDAR* T1540C and C1487T, respectively. Chromosome positions are according to NCBI Build 36.3. Abbreviations: n, number of genotyped individuals; n₀₀, n₀₁ and n₁₁, number of individuals with each genotype; p₀ and p₁, allele frequency; P, P value of the chi-square test for comparison in the allele frequency between populations.

Table S5. Correlations between SNPs.

| | rs3827760 | rs10495392 | rs17265387 | rs17075469 | rs2071652 | rs555766 |
|------------|-----------|------------|------------|------------|-----------|----------|
| rs3827760 | | 0.137 | 0.143 | 0.083 | -0.069 | 0.069 |
| rs10495392 | 0.053 | | -0.063 | 0.058 | -0.101 | 0.050 |
| rs17265387 | 0.042 | 0.376 | | 0.002 | -0.032 | -0.034 |
| rs17075469 | 0.247 | 0.418 | 0.973 | | -0.116 | -0.058 |
| rs2071652 | 0.327 | 0.155 | 0.651 | 0.103 | | -0.048 |
| rs555766 | 0.333 | 0.481 | 0.631 | 0.422 | 0.498 | |

rs3827760 corresponds to *EDAR* T1540C. The correlation coefficients are shown in the upper-right of the matrix, and P values are in the lower-left.