Hybridization and its impact on the ontogenetic allometry of skulls in macaques

Subtitle: Hybridization's impact on ontogenetic allometry

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Author Contributions

TI, RK, YH, and YK conceived the research. TI, HW, and YK performed basic molecular experiments. AT and AJN conducted ddRAD library preparation. YK contributed samples and data. TI and MT assessed the dental age of skeletal specimens. TI analyzed the data and drafted the manuscript. All authors approved the final version of this manuscript.

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Data Accessibility Statement

Sequence reads will be available in the Sequence Read Archive (SRA) of the National Center for Biotechnology Information (NCBI) upon acceptance of this article in a peer reviewed journal. The other data underlying this article are available in the Dryad Digital Repository upon acceptance of this article in a peer reviewed journal.

Conflicts of interest

The authors declare no conflicts of interest.

Abstract

The importance of hybridization in morphological diversification is a fundamental topic in evolutionary biology. However, despite accumulated knowledge concerning adult hybrid variations, how hybridization affects ontogenetic allometry is less well understood. Herein, we assessed the effects of hybridization on the postnatal ontogenetic allometry in skulls of a putative hybrid population of introduced Taiwanese macaques (*Macaca cyclopis*) and native Japanese macaques (*M. fuscata*). Genomic analyses indicated that the population consisted of individuals with various degrees of admixture, formed by male migration of Japanese to Taiwanese macaques. Hybridization parallelly shifted the ontogenetic trajectories of the overall skull shape in an almost additive manner. Transgressive variations in the overall skull shape were observed mainly in non-allometric components. Hybridization lifted the restriction found in Japanese macaques on the growth rate of the maxillary sinus (the hollow space in the face), producing hybrids with a mosaic pattern, i.e., the maxillary sinus is as large as that in Taiwanese macaques, although the overall skull shape is intermediate. Our findings suggest that the transgressive variations can be caused by prenatal shape modifications and the lifting of the genetic restriction on the regional growth rate, highlighting the complex genetic and ontogenetic bases underlying hybridization-induced morphological diversification.

Keywords: allometry, hybridization, geometric morphometrics, paranasal sinus, ontogeny, population genomics

1. Introduction

Growing understanding indicates that interspecific hybridization is not rare, even in animals (Mallet 2005; Taylor and Larson 2019). Furthermore, hybridization is not always maladaptive and

can facilitate evolutionary novelty and diversity by generating gene combinations not achieved in parental lineages (Seehausen 2004; Arnold and Kunte 2017; Kagawa and Takimoto 2018). Thus, hybridization must have played a critical role in the evolution of various taxa and has consequently been of significant interest to evolutionary biologists.

Primate hybridization is of particular interest as this improves comprehension of the effects of archaic human gene introgression on the modern human lineage. Molecular studies show that hybridization is pervasive in primates, with relics of ancient hybridization or the existence of a natural hybrid zone identified in various taxa of primates, e.g., macaques, baboons, vervet monkeys, marmosets, colobine monkeys, and howler monkeys (Roos et al. 2011; Malukiewicz et al. 2014; Cortés-Ortiz et al. 2015; Svardal et al. 2017; Rogers et al. 2019; Osada et al. 2021). Furthermore, several studies have assessed the morphological effects of hybridization in nonhuman primates (Ackermann et al. 2019). In baboons and gorillas, hybrids exhibit anomalies such as supplementary rotated teeth or atypical sutures of the cranium at higher frequencies than are present in their parental lineages (Ackermann and Bishop 2010; Ackermann et al. 2014). In various taxa of primates, hybrids often show heterotic/transgressive phenotypes or increased variation in cranial and postcranial morphologies (Cheverud et al. 1993; Ackermann et al. 2014; Fuzessy et al. 2014; Ito et al. 2015; Eichel and Ackermann 2016; Boel et al. 2019). Such hybridization-driven genetic perturbations may contribute to the morphological diversity in primate evolution.

Any morphological evolution is achieved by the dissociations of the ancient ontogenetic trajectory. For example, a distinct adult human craniofacial morphology is formed by the divergence from the hominid common ontogenetic trajectory in the early postnatal period (Mitteroecker et al. 2004). The difference in brain (endocast) shape between modern humans and Neanderthals was also

formed by the early divergence (Gunz et al. 2010); however, the overall craniofacial difference between the two species was formed by a more or less parallel (but not identical) ontogenetic trajectory originating from the established difference at birth (Ponce de León and Zollikofer 2001; Bastir et al. 2007). As the ontogenetic trajectory reflects the expression of genes that control morphology during development, hybridization-induced genomic admixture potentially alters an ontogenetic trajectory. Hybrid Sulawesi macaques are reported to show acceleration (slope increase) and postdisplacement (intercept decrease) in the ontogenetic trajectory of several craniofacial traits, although this dissociation does not account for adult heterosis (Schillaci et al. 2005). Predisplacement (intercept increase) occurs in the ontogenetic trajectory of body weight of inter-subspecies male hybrids of rhesus macaques but is lacking in female hybrids (Smith and Scott 1989; Taylor and Schillaci 2008). In non-primate taxa, several studies detected various types of ontogenetic modifications, e.g., pure heterochrony, direction dissociations, or intermediate but maternally biased trajectory, in the head or body shape of fish hybrids (Holtmeier 2001; Corse et al. 2012; Sinama et al. 2013; Santos-Santos et al. 2021). However, with the exception of these studies, there remains limited knowledge concerning the effects of interspecific hybridization on an ontogenetic trajectory, especially in mammals.

Anthropogenic hybridization provides opportunities to examine the consequences of hybridization, although it is controversial in the context of conservation. In the Oike area of Wakayama Prefecture, Japan, introduced *Macaca cyclopis* (Taiwanese macaques) that escaped from a zoo in the 1950s hybridized with native *M. fuscata* (Japanese macaques) (Ohsawa et al. 2005). Although only a few individuals escaped, the population grew to approximately 300 with four troops by 2004 (Ohsawa et al. 2005). Genetic analyses suggested that the Oike hybrid population was formed by male immigration from the neighboring native population of *M. fuscata* into *M.*

cyclopis (Kawamoto et al. 2001, 2008a). The government began the elimination of introduced and hybrid individuals from the Oike area to prevent genetic introgression and its impacts on ecosystems in 2002 and finally declared eradication in 2017, with 366 individuals eradicated from the Oike area in total (Shirai et al. 2018). The Oike hybrids show several intriguing morphological variations. For example, unlike the previous studies targeting hybrids of other primate taxa, the Oike hybrids lacked a marked increase in dental anomalies or craniofacial variability compared with their parental species (Boel et al. 2019). The relative tail length variations followed additive model expectations (Hamada et al. 2012). The overall craniofacial shape in adults also follows the additive model expectation or was somewhat closer to that of *M. fuscata* than expected; by contrast, the maxillary sinus size (hollow space in the face) was much closer to that of *M. cyclopis* than the additive model expectation (Ito et al. 2015; Boel et al. 2019). However, it remains unclear how these adult variations manifested during development.

This study sought to elucidate the effects of hybridization on the ontogenetic trajectory of craniofacial morphology using the samples of the Oike hybrid population. First, we estimated the population structure of the Oike population as well as the hybrid index and class (generation) of individuals based on the genome-wide single nucleotide polymorphisms (SNPs). Second, we compared the morphological variations and ontogenetic trajectories of the cranium, mandible, and maxillary sinus with the hybrid index and among the hybrid classes. Comparing the ontogenetic trajectories among hybrids and parental lines will increase our understanding of genetic and ontogenetic bases of hybridization-induced morphological diversification.

2. Materials and methods

2.1. Samples

Almost all available samples of the Oike hybrid population were used, including 245 skeletal specimens and 287 DNA samples (Table S1; Fig. 1). The 215 skeletal specimens could be linked to DNA samples, where we linked them as far as IDs on records were uniquely identified even if they did not show exact matching. These samples were provided from collections obtained under the government eradication program between 2003 to 2006; no animals were sacrificed for research purposes. Skeletal specimens are stored at the Primate Research Institute (now the Center for the Evolutionary Origins of Human Behavior), Kyoto University (Inuyama, Japan). Note, any individuals judged as pure Japanese macaques in the Oike area had been released (Hamada et al. 2008).

Additionally, to check whether pure parental individuals remained in the Oike population, we examined the DNA from pure captive *M. cyclopis* (N = 4) and *M. fuscata* (N = 4) housed at the Primate Research Institute. *M. fuscata* individuals were descendants of those transferred from Arashiyama, Kyoto, approximately 100 km north-northeast of the Oike area. The *M. cyclopis* individuals have no record of their exact origin. Sample collection from these captive individuals was performed according to recommendations in the Guidelines for Care and Use of Nonhuman Primates Version 2 and 3 of the Primate Research Institute, Kyoto University (2002, 2010). DNA was extracted from blood using the phenol–chloroform method.

Skeletal specimens of *M. cyclopis* (N = 54) and *M. fuscata* (N = 88) stored at the Primate Research Institute and the Japan Monkey Centre (Inuyama, Japan) were assessed as a surrogate for parental individuals for morphological analyses (because actual parental populations are unknown).

Captive and unknown-origin specimens were initially included; however, preliminary analyses detected wild-captive morphological differences (see below). Thus, only wild specimens (N = 18 for *M. cyclopis*, N = 86 for *M. fuscata*) were used for the main analyses. Wild *M. cyclopis* specimens were obtained from the introduced population in Izu-Oshima Island, Tokyo, Japan, where *M. fuscata* is not distributed. Wild *M. fuscata* specimens were obtained from localities around the Oike area, and are therefore likely to be genetically close to a parental population (Suzuki-Hashido et al. 2015; Ito et al. 2021).

2.2. Double-digest restriction site-associated DNA library preparation and sequencing

Double-digest restriction site-associated DNA sequencing was performed based on Peterson's protocol (Peterson et al. 2012) with modifications (Sakaguchi et al. 2015, 2017). Genomic DNA (10 ng) was digested with EcoRI and BglII (New England Biolabs, Ipswich, MA, USA), and adapters were ligated at 37 °C overnight in a 10-μL volume containing 1 μL of ×10 NEB buffer 2, 0.1 μL of ×100 bovine serum albumin (New England Biolabs), 0.4 μL of 5 μM EcoRI adapter and BglII adapter, 0.1 μL of 100 mM ATP and 0.5 μL of T4 DNA Ligase (Enzymatics, Beverly, MA, USA). The reaction solution was purified with AMPure XP (Beckman Coulter). Next, 3 μL of purified DNA was used in the PCR amplification in a 10-μL volume containing 1 μL of each 10 μM index and TruSeq universal primer, 0.3 μL of KOD-Plus-Neo enzyme, and 1 μL of ×10 PCR buffer (Toyobo, Osaka, Japan), 0.6 μL of 25 mM MgSO4 and 1 μL of 10 mM dNTP. Thermal cycling was initiated with a 94 °C step for 2 min, followed by 20 cycles of 98 °C for 10 s, 65 °C for 30 s, and 68 °C for 30 s. PCR products were pooled and purified again with AMPure XP. Purified DNA was loaded onto a 2.0% agarose gel, and fragments of around 360 base pairs (bp) were retrieved using E-Gel SizeSelect (Life Technologies, Carlsbad, CA, USA). After quality assessment using an Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA), the

library was sequenced with 51-bp single-end reads in six lanes of an Illumina HiSeq2000 (Illumina, San Diego, CA, USA) by Macrogen Inc. (Seoul, South Korea). Primer sequences used in this study are available in Sakaguchi et al. (2015).

2.3. Variant calling and filtering

Raw reads were filtered for overall sequence quality using TRIMMOMATIC 0.39 (Bolger et al. 2014) with the following parameters: ILLUMINACLIP:TruSeq3-SE.fa:2:30:10, LEADING:19, TRAILING:19, SLIDINGWINDOW:30:20, and AVGQUAL:20 MINLEN:51. Filtered reads were mapped to the RefSeq of *M. mulatta* (rhesus macaque) (Mmul_10; GCF_003339765.1) using BOWTIE2 2.4.4 (Langmead and Salzberg 2012) with –very-sensitive option. The sex of each individual was assessed based on the ratio of the number of reads mapped onto the Y-chromosome versus those mapped to the X-chromosome, using sam_sexing.py (https://github.com/itots/sam_sexing.git). Genotypes were called using STACKS 2.59 (Rochette and Catchen 2017), wherein the Marukilow model in the gstacks function was applied to search variant sites with relatively stricter criteria than the default setting: –var-alpha 0.01 (a significant level for calling variant sites), –gt-alpha 0.01 (a significant level for calling genotype), and –min-mapq 20 (minimum PHRED-scaled mapping quality to consider a read). Next, the populations function was used for calling SNPs with the following parameters: –write-single-snp (extract only the first SNP per locus) and –ordered-export. Since STACKS provides diploid genotypes, those on the sex chromosomes of males were converted to be haploid using diploid2haploid.py (https://github.com/itots/diploid2haploid.git), where heterogeneous genotypes (1.2% for X-chromosome and 0.8% for Y-chromosome) were omitted.

The SNPs dataset was filtered using PLINK 1.90b6.21 (Purcell et al. 2007; https://www.cog-genomics.org/plink2/) to retain individuals with missing rate <0.2 and sites with missing rate <0.2 and minor allele frequency >0.01 (–geno 0.2 –mind 0.2 –maf 0.01). Autosomal and X-chromosome SNPs were further filtered to remove sites in strong linkage disequilibrium (–indep-pairwise 10 3 0.5). These filtrations yielded 6461 variant sites in 289 individuals for autosome (total genotyping rate = 0.96), 171 sites in 289 individuals for X-chromosome (0.96), and 12 sites in 152 individuals for Y-chromosome (0.95) DNA.

2.4. Global ancestry inference and data screening

Global ancestry was inferred based on the SNPs separately for autosomes and X-chromosomes, using ADMIXTURE (Alexander and Novembre 2009); the X-chromosome of males were treated as haploid using the –haploid flag. Principal component analysis (PCA) was performed using the "adegenet" package (Jombart 2008) in R (R Developmental Core Team 2021). For Y-chromosome, the *K*-means cluster analysis ($K = 2$) was performed based on the first principal component (PC).

Data were also examined from Kawamoto et al. (2008a), including sex, and a nine-step hybrid index calculated from four autosomal markers (blood proteins of transferrin, adenosine deaminase, diaphorase, and SNP of natural resistance-associated macrophage protein 1), and ancestry types of the mitochondrial DNA (mtDNA) and the testis-specific protein Y (TSPY). Some missing data on the Y-chromosome ($N = 52$) and mtDNA ancestries ($N = 9$) were supplemented in this study; the method applied was identical to that in Kawamoto et al. (2008a), but if the results of the TSPY marker were unclear, two STR markers (DYS472 and DYS569) were additionally examined following Kawamoto et al. (2008b).

To screen the data, data from Kawamoto et al. (2008a) and this study were compared. Sex identification was inconsistent in five samples. The ADMIXTURE Q score (K = 2) was highly correlated with the nine-step hybrid index (R^2 = 0.79, $F_{1, 275}$ = 1005.7, P < 0.001), but two samples were detected as outliers in their residual component (Bonferroni-adjusted P < 0.05). These six samples (one sample showed inconsistency in both tests) were removed from the analyses. The Y-chromosome ancestry was identical between the two datasets, except for three samples with missing values in Kawamoto et al. (2008a).

2.5. Hybrid index and class

Individuals in the Oike population were classified into 23 *M. cyclopis* (Q < 0.001), 11 *M. fuscata* (Q > 0.999), and 242 putatively admixed individuals (0.001 ≤ Q ≤ 0.999) based on the ADMIXTURE Q score (K = 2) of autosomal SNPs. Diagnostic markers were detected as differentially fixed sites (allele frequency difference between the two parental populations [δ] = 1), wherein loci with missing genotype rates within any of the two parental populations > 0.1 were omitted. Hybrid index, the proportion of the ancestry belonging to *M. fuscata*, and interspecific heterozygosity, the proportion of loci with alleles from both parental populations, were calculated based on the 196 autosomal diagnostic markers using a custom R script.

The hybrid class was estimated for individuals of the Oike population using NewHybrids 1.1 (Anderson and Thompson 2002). The SNP dataset of 196 autosomal diagnostic markers was converted to a NewHybrid format using PGDSpider 2.1.1.5 (Lischer and Excoffier 2012). The “z” option was applied to instruct NewHybrid that the individuals with a hybrid index = 0 or 1 were pure parental individuals. Ten replicates were run with randomly differentiating seeds using the “parallelnewhybrid” R package (Wringe et al. 2017) with minor modifications. Each run started

with Jeffery's prior and default six genotype frequency classes and consisted of 10,000 Markov Chain Monte Carlo (MCMC) sweeps after 10,000 burn-in iterations. We confirmed MCMC convergence by visual inspection. Based on the mean posterior probabilities, each individual was assigned to one of six genealogical classes: *M. cyclopis* (P0), *M. fuscata* (P1), F1, F2 hybrids, and backcrosses of *M. cyclopis* (BC0) and *M. fuscata* (BC1). We discarded assignments with mean posterior probability <0.99, P0 with hybrid index >0, P1 with hybrid index <1, and F1 with interspecific heterozygosity <0.95; these were removed from the analyses that evaluate hybrid class differences (represented as NA in figures).

2.6. Morphological data collection and screening

The 10-step dental stage was determined based on the dental eruption pattern and spheno-occipital synchondrosis, according to Mouri (1994), with minor modifications (Table S2). Developmental stages were determined as infants (dental stage <3), juveniles (<8), and adults (≥8).

Craniums and mandibles were assessed with computed tomography (CT), the Asteion Premium 4 helical scanner (Toshiba Medical Systems, Otawara, Japan), with a 0.5-mm thick slice at the Primate Research Institute. Serial CT images were reconstructed from original volumetric data, with a pixel size between 0.093 to 0.314 mm and an inter-slice interval between 0.1 to 0.3 mm, depending on the specimen size. CT images were segmented based on edge detection and watershed methods (Ito 2019), and three-dimensional (3D) surface models were created using create_mesh.py (https://github.com/itots/dicom2stl.git).

Image stacks and the 3D models were loaded into 3D Slicer (https://www.slicer.org/) (Kikinis et al. 2014), and 3D landmarks were digitized on the cranium (the number of landmarks = 50), the mandible (28), and maxillary sinus (10) (Table S3; Fig. S1). All landmarks on the maxillary sinus

were Type III and were used only to evaluate the size, not shape. Digitization was performed twice for all the specimens by a single observer to evaluate and minimize measurement errors. Samples with a missing landmark ratio > 0.2 (three samples for the cranium and one for the mandible) were removed. For the remaining samples, missing landmarks (1–10 in 53 samples for the cranium, 1–4 in 10 samples for the mandible, and 1–2 in 30 samples for the maxillary sinus) were imputed based on the Bayesian PCA method, using the "LOST" R package (Arbour and Brown 2014, 2020).

The generalized Procrustes analysis and Procrustes analysis of variance were performed to evaluate measurement errors using the "geomorph" R package (Collyer and Adams 2018, 2021; Adams et al. 2021; Baken et al. 2021). For the cranium and mandible, measurement errors of shape were negligible compared with inter-individual variations (Table S4), and a symmetric component was used in the following analyses. Measurement errors were negligible in the centroid size of the cranium, mandible, and maxillary sinus (Table S5), and the mean of replicates (mean of replicates and sides for maxillary sinus) was used in the following analyses.

Only wild specimens were analyzed because significant morphological differences were detected between captive and wild samples (Tables S6 and S7).

2.7. Statistical analyses of morphological data

Ontogenetic allometry was evaluated by a multivariate regression using the "geomorph" R package. The response variable was the shape component, and the explanatory variables were lnCS, hybrid class, and their interaction. Each sex was separately analyzed. To consider nonlinear allometric trajectory, PCA was conducted for the shape components, quadratic regression was performed on the first five PCs on lnCS, and terms were selected by stepwise

AIC. This approach was repeated for the relative size of the maxillary sinus. Each sex and hybrid class were separately analyzed but omitted if the sample size was ≤10.

Variations in adults were evaluated in relation to the hybrid index. The degrees of transgression (*T*) and closeness (*C*) were calculated, modifying the formulas of Renaud et al. (2012) to decompose the deviations into two orthogonal components:

$$T = \frac{d_{\mathrm{h}} \sin \theta}{d_{\mathrm{p}}},$$

$$C = \frac{d_{\mathrm{h}} \cos \theta}{d_{\mathrm{p}}},$$

where θ is the angle between the vector passing through the means of pure *M. cyclopis* and a hybrid class and that of pure *M. cyclopis* and *M. fuscata*; d_{h} and d_{p} are the magnitudes of the two vectors, respectively. For the shape of the cranium and mandible, distances were calculated as the Procrustes distance using the "shapes" R package (Dryden 2021). For the relative maxillary sinus size, only the closeness was calculated, as this is univariate. Females and males were separately analyzed. $T > 0$ indicates transgression standardized by the inter-parental species distance. Any deviations of C from the hybrid index denote dominance, and particularly $C < 0$ and $C > 1$ indicate over-dominance.

3. Results

3.1. Population structure

PCA and ADMIXTURE showed that the Oike population consisted of individuals with various degrees of admixture, probably including pure *M. cyclopis* and *M. fuscata* (Figs. S2 and S3). The *M. cyclopis* individuals housed at the Primate Research Institute appeared to have a small portion

of *M. fuscata*-derived ancestry (Fig. S3), but this did not affect the following analyses that included only the Oike population samples. The NewHybrids analysis indicated that the Oike population consists of the six predefined hybrid classes (P0, P1, F1, F2, BC0, and BC1; Fig. 2). In the Oike population, the mean admixture proportion of *M. fuscata*-derived ancestry is 0.45 for autosomal, 0.46 for X-chromosomal in both sex, and 0.50 for Y-chromosomal DNA. Note that the mean admixture proportion for autosomes was slightly biased toward *M. cyclopis* in BC0 and F2 than expected by random mating starting from the same number of parental lines (Table S8). The *M. fuscata*-type mtDNA ancestry was observed only in the P0, namely pure *M. fuscata*. The P0 individuals were all males, while males were significantly less abundant than females in the F1 ($\chi^2 = 5.76, Df = 1, P = 0.016$) (Table S9; Fig. 2). In the other hybrid classes, the sex ratios lacked any significant bias. The age structure was biased toward adults in F1 but was biased toward earlier dental stages in F2 (Table S10; Fig. 2).

3.2. Ontogenetic allometry

The multivariate regression indicated that larger (more developed) individuals had more elongated faces, relatively smaller neuro-craniums, and narrower and longer mandibles (Figs. 3 and S4). The allometric slope heterogeneity was small but marginally significant in the female cranium and male mandible (Tables 1 and S11). The allometric elevations were significantly different among the hybrid classes, where the hybrids were positioned between the parental species. The allometric elevations were slightly biased toward *M. fuscata* in males than expected in the additive model, although the mean admixture proportion of autosomes was rather biased toward *M. cyclopis* in BC0 and F2 (Table S8). PCA supported the finding that the ontogenetic trajectories were almost parallel among the hybrid classes, although the trajectories lacked stability because of the small sample size (Figs. 4, S5–S8). Several trajectories produced parallel curves with detouring in

juveniles and returning to an infant-like shape in adults. Among the first five PCs explaining >80% of the total variance (Table S12), PC2 represented the interspecific differences throughout the development (Tables S13 and S14; Figs. 4, S9, and S10). *M. fuscata* had larger cranium and mandible sizes and, represented by PC2, showed a relatively longer face with an inferiorly-inclined anterior maxilla and a mandible with a deeper ramus and shorter corpus than those of *M. cyclopis*; the hybrids were positioned between them almost in an additive manner.

The allometric slope of the maxillary sinus size significantly differed among the hybrid classes (Table S15; Figs. 5 and S11). Small, but significant, differences were present in the absolute and relative sizes of the maxillary sinus, even at the early dental stages (Table S16; Fig. S12). *M. fuscata* exhibited a gentler allometric slope than that in the other hybrid classes, including *M. cyclops*, and the difference between *M. fuscata* and the others, therefore, increased at later dental stages. The results were similar between the reduced major axis and ordinary least squares regressions (Figs. 5 and S11).

3.3. Adult morphology

The admixed adult individuals of the Oike populations followed additive model expectations or were sometimes slightly biased toward *M. fuscata* in the size and the shape component representing interspecific differences (PC2) (Tables 2 and S17, S18; Fig. 6). The major allometric components (the regression score and PC1) did not markedly differ among the hybrid classes except for the mandible shape of BC0, which was somewhat neotenistic compared with that of the others (Tables S13 and S14; Figs. 6, S13, and S14). In contrast, the maxillary sinuses of the hybrids were as large as those of *M. cyclopis* regardless of the hybrid index and significantly deviated from the additive model expectations (Table S19; Figs. 6 and S15). Marked transgressive

segregations were observed in the shape of cranium and mandible (Table 2), particularly in the non-allometric shape space represented by PC2 and PC3 (Fig. S5). Some hybrids were also transgressive in the morpho-space of cranium shape (PC2) and the relative size of the maxillary sinus (Fig. S16).

4. Discussion

4.1. Population structure

This study examined 281 samples (after filtering) captured between 2003 to 2006 in the Oike area. Considering that the estimated population size was approximately 200–300 in the early 2000s (Ohsawa et al. 2005) and that the total number of captured individuals was 366, the samples used in this study were sufficient to evaluate the population structure of the Oike area.

Our results suggested that the Oike population consisted of pure *M. cyclopis*, pure *M. fuscata* (only males), the first- and subsequent-generation hybrids, and the backcross hybrids of both parental species. The first generation mainly consisted of adults, whereas few adults were observed in the subsequent generations. This implies successful interbreeding between pure *M. cyclopis* and *M. fuscata* was likely sporadic and rare, at least in the years before eradication. In contrast, backcrossing and inter-hybrid breeding were probably pervasive. As indicated in previous studies (Kawamoto et al. 2001, 2008a), no *M. fuscata*-type mtDNA was observed in the admixed individuals, indicating that only male *M. fuscata* individuals migrated into the Oike population. Considering the philopatric nature of female macaques, this is a reasonable scenario. Given male migration and assuming random breeding, the proportion of the Y-chromosome ancestry was expected to be twice that of autosomes, but this was much lower than expected. Therefore, a mechanism that prevents random breeding, such as Haldane’s rule, population subdivision, or

assortative mating, may have existed in this population. Fewer males than females in the F1 generation imply a lower survival rate or emigration of males, although this is inconclusive because of the small sample size. The population subdivision scenario is also plausible, as four troops were observed in the Oike area (Ohsawa et al. 2005); heterogeneity in the migration rate from neighboring *M. fuscata* among troops may underlie the relatively low frequency of *M. fuscat*a-type Y chromosome in the Oike population.

4.2. Effects of hybridization on the ontogenetic trajectory and adult morphology

In the multivariate shape space, the ontogenetic trajectories of the cranium and mandible were parallelly differentiated between the parental species. Hybridization almost parallelly shifts the ontogenetic trajectories by the proportion of ancestry, although this is in some cases slightly biased toward *M. fuscata* from that in the additive model expectations. No marked evidence of ontogenetic direction change was observed. In other words, the hybridization-induced shape differentiations were already manifested at birth; the differences are parallelly maintained during postnatal ontogeny. This result is consistent with those from a study of Sulawesi macaques that showed no marked differentiation in the ontogenetic trajectory of the cranium between hybrids and their parental species in multivariate allometric space (Schillaci et al. 2005). Schillaci et al. (2005) reported hybridization-induced heterochrony in several cranial traits in bivariate allometric trajectories; this is pure heterochrony (*sensu* Mitteroecker et al. 2004), which cannot be evaluated when trajectories do not overlap in multivariate space. Thus, hybridization did not alter the ontogenetic direction in the shapes of the cranium or mandible of the macaques but parallelly shifted the trajectory or caused pure heterochrony. The parallel shifts in the major allometric component did not influence the variations in adult shape among the hybrids and their parental

species. Instead, the hybridization-induced adult shape variations, including transgressive ones, were likely caused by prenatal shape alternations.

The maxillary sinus of *M. cyclopis* is already larger than that of *M. fuscata* at birth; furthermore, the postnatal growth rate is much faster in *M. cyclopis* than in *M. fuscata*. Hybridization shifted the maxillary sinus size at birth by the proportion of ancestry, whereas the growth rate of hybrids was as fast as that of *M. cyclopis*, regardless of the proportion of ancestry. Although the genetic mechanisms that underlie the non-additive inheritance in the postnatal growth rate of the maxillary sinus are unknown, two hypotheses can be proposed. The first is that *M. fuscata*-type cytoplasmic (e.g., mitochondrial) genes restrict the growth of the sinus, which were not introduced in the hybrids because of male-biased migration, and thus all hybrids exhibited a growth rate as fast as that of *M. cyclopis*. Maternal inheritance associated with nuclear genes, e.g., genomic imprinting, cannot explain the deviations in the second and subsequent-generation hybrids. The second is that the epistatic interaction of *M. fuscata*-type alleles restricted the growth of the sinus, which was collapsed by hybridization. Given that backcrossed individuals did not retrieve the *M. fuscata*-like slow growth rate, the epistatic interaction, if any, was controlled by not a few genes. In either case, hybridization likely lifted the restriction in *M. fuscata* on the growth rate of the maxillary sinus. Consequently, the adult hybrids show a mosaic pattern, i.e., the maxillary sinus is as large as that in *M. cyclopis*, although the cranium shape is almost intermediate between the two parental species.

How hybridization affects the ontogenetic trajectory probably depends on the evolutionary processes that formed the difference in genetic architecture between parental lines. This idea originates with the finding that genetic architecture sets limits on transgressive segregations (Albertson and Kocher 2005). Unlike the cranium and mandible of macaques, the fish's whole body exhibits differences in ontogenetic direction between parental lines and between these and

their hybrids in multivariate allometric space (Sinama et al. 2013; Santos-Santos et al. 2021). It can be hypothesized that the fish body might be less integrated among modules and have experienced selective pressures that act differently on each module, producing changes in ontogenetic direction. In contrast, the evolutionary forces forming the interspecific differences in macaque skulls may not have been sufficiently significant to affect ontogenetic directions without the necessary genetic architecture to cause differentiation of ontogenetic direction in hybrids. The maxillary sinus in macaques is peculiar as the growth rate shows cytoplasmic or epistatic inheritance. If epistatic interaction restricts the growth rate of the maxillary sinus in *M. fuscata*, then the genetic architecture could have been formed via natural selection, i.e., a co-adapted gene complex. Given that, the maxillary sinus growth rate may be controlled by a genetic factor that pleiotropically affects an unknown functional trait because it is questionable whether the maxillary sinus itself has a functional role (Rae and Koppe 2004; Márquez 2008). A somewhat independent trait that is under different selective pressure from the surrounding structure, such as the maxillary sinus, may result in specific ontogenetic trajectory differentiations in hybrids, whereas highly integrated traits may not.

4.3. Conclusions

This study showed that: (1) Hybridization almost parallelly shifts the ontogenetic trajectories of the cranium and mandible shapes in macaques. (2) The transgressive phenotypes observed in the cranium and mandible shapes were not ascribed to the dissociations of postnatal ontogenetic directions in multivariate shape space but were likely formed by prenatal shape modifications. (3) Hybridization lifted the restriction in one parental species on the growth rate of the maxillary sinus, producing hybrids with a mosaic pattern, i.e., the maxillary sinus was as large as that of the opposite parental species, although the cranium shape was intermediate. This study has some

limitations. First, the skeletal specimens used as surrogates for parental populations may differ in morphology from the actual parental populations because of regional intraspecific variations, although the surrogates were selected from localities as close to the hybrid population locality as possible; this may distort the evaluation of transgression and closeness. Second, the ontogenetic trajectories lack stability because of the small sample size, and the present findings should be validated based on a larger sample size. Despite these limitations, this study highlights the complex genetic and ontogenetic bases underlying hybridization-induced differentiations in ontogenetic trajectory and the resultant morphological diversifications.

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Tables

Table 1. Multivariate regression of the shape on the lnCS, hybrid class, and their interactions. Each sex was separately analyzed.

Response	Source	*Df*	*SS*	*MS*	R^2	*F*	*Z*	*P*
Female								
cranium	lnCS	1	0.474	0.474	0.522	290.1	3.8	0.001
	hybrid class	5	0.084	0.017	0.092	10.3	7.0	0.001
	lnCS:hybrid class	5	0.010	0.002	0.011	1.2	1.4	0.074
	residuals	134	0.219	0.002	0.241			
	total	145	0.909					
mandible	lnCS	1	0.433	0.433	0.494	263.8	4.0	0.001
	hybrid class	5	0.097	0.019	0.110	11.8	7.6	0.001
	lnCS:hybrid class	5	0.012	0.002	0.013	1.4	2.2	0.015
	residuals	133	0.218	0.002	0.249			
	total	144	0.877					
Male								
cranium	lnCS	1	0.691	0.691	0.659	414.9	3.4	0.001
	hybrid class	5	0.059	0.012	0.056	7.1	7.6	0.001
	lnCS:hybrid class	5	0.012	0.002	0.011	1.4	2.5	0.011
	residuals	126	0.21	0.002	0.200			
	total	137	1.05					
mandible	lnCS	1	0.582	0.582	0.614	319.9	3.7	0.001
	hybrid class	5	0.067	0.013	0.070	7.3	8.0	0.001
	lnCS:hybrid class	5	0.012	0.002	0.012	1.3	1.6	0.053
	residuals	124	0.226	0.002	0.238			
	total	135	0.947					

Type II sum of squares is used.

Table 2. Closeness and transgression.

	BC0		F1		BC1	
	Female	Male	Female	Male	Female	Male
hybrid index	0.21	0.29	0.50	0.49	0.77	0.78
Closeness						
cranium	0.30	0.36	0.74	0.72	0.77	1.01
mandible	0.18	0.33	0.51	0.30	0.77	0.81
maxillary sinus	−0.05	0.16	−0.24	0.07	0.24	0.03
Transgression						
cranium	0.56	0.48	0.82	0.60	0.53	0.55
mandible	0.34	0.62	0.58	0.49	0.53	0.51

Figures

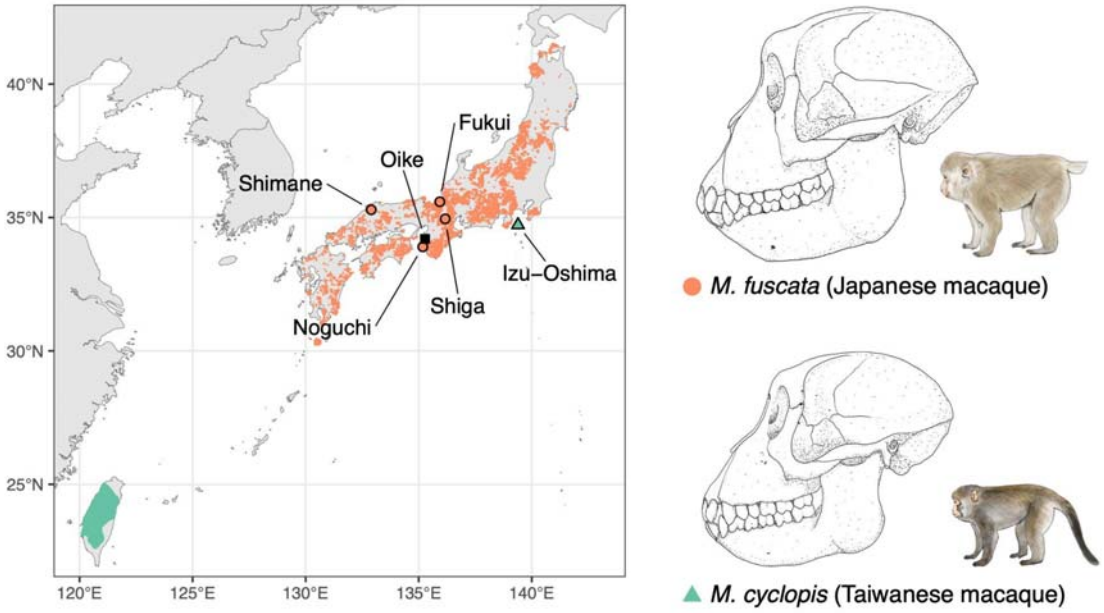

Figure 1: Natural distributions of *Macaca cyclopis* (Taiwanese macaques; blue) and *M. fuscata* (Japanese macaques; magenta) and the sampling localities. Oike is the location of the hybrid population. *M. fuscata* skeletal specimens are from Fukui (N = 15), Shimane (N = 21), Shiga (N = 49), and Noguchi (N = 1). *M. cyclopis* skeletal specimens are from Izu-Oshima Island (N = 20), where introduced *M. cyclopis* is distributed. This map was created by the authors using the IUCN Red List Data (version 3, May 2017) and the distribution surveys of Japanese animals (mammals) by the Biodiversity Center of Japan, Nature Conservation Bureau, Ministry of the Environment.

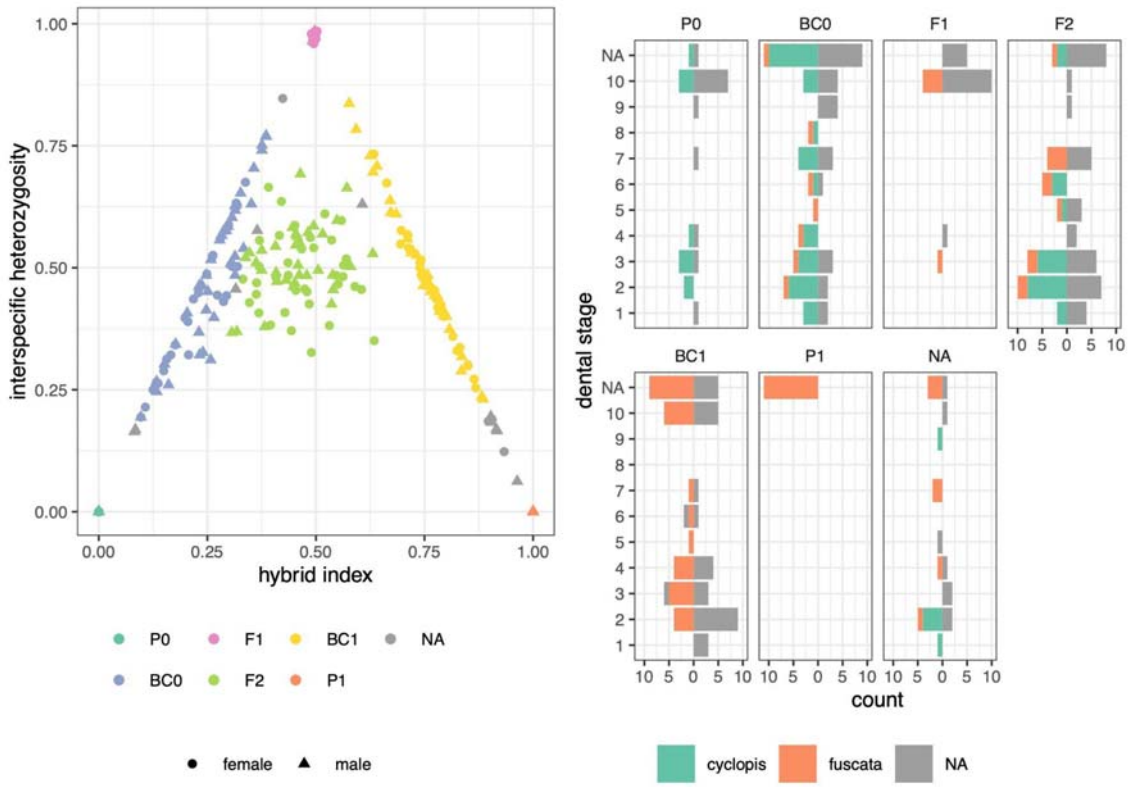

Figure 2: Population structure of the Oike population. Left panel indicates the relationship between the hybrid index and interspecific heterozygosity, where each individual is colored by the hybrid class. Right panel indicates the population pyramid, where the right side is the number of females and the left-side the number of males; males are colored by Y-chromosome ancestry.

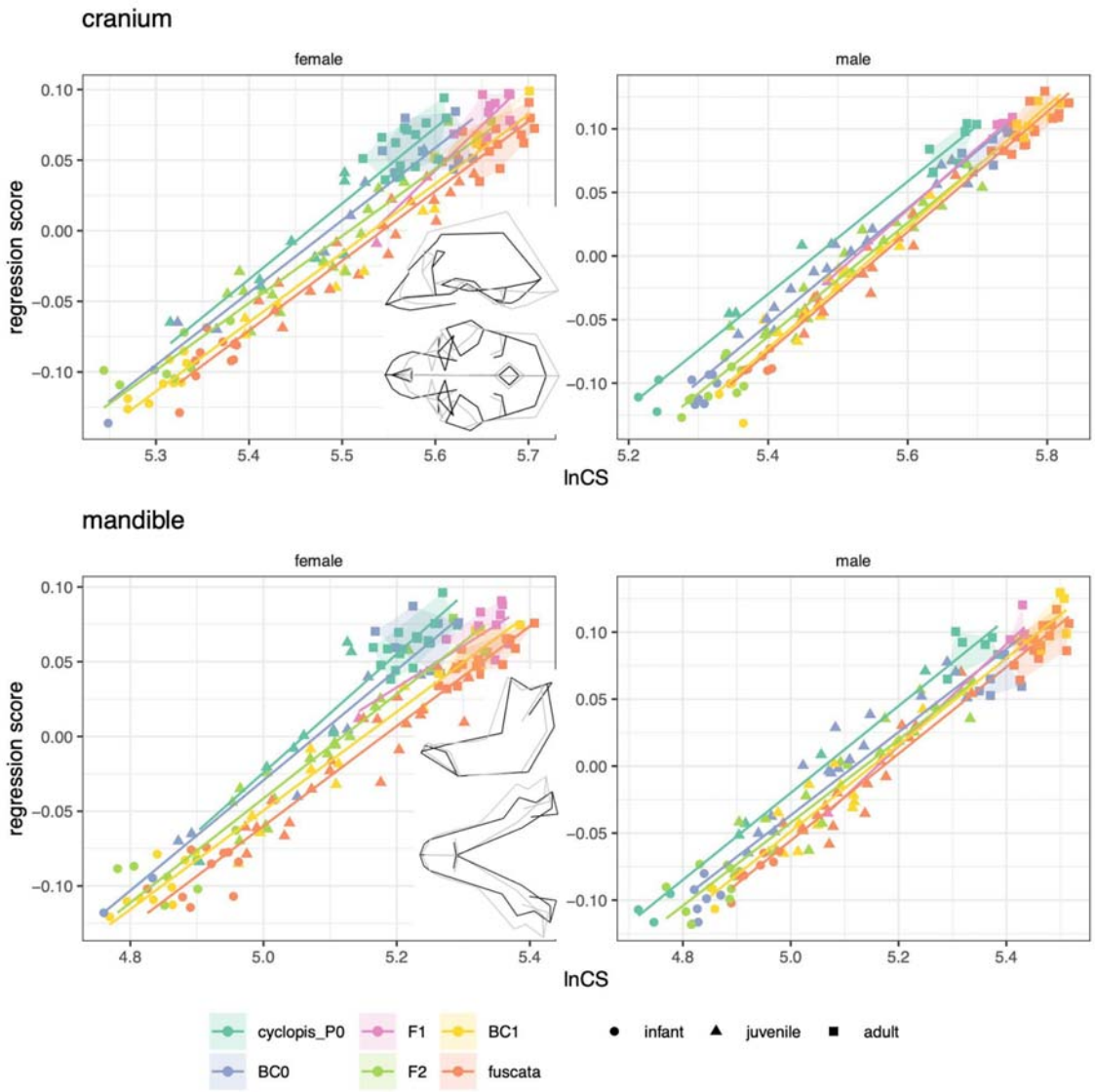

Figure 3: Ontogenetic allometry of cranium and mandible shape represented by the multivariate regression of the shape against the lnCS, hybrid class, and their interactions. Each sex was separately analyzed. A regression score is a projection of data on the normalized vector that expresses the covariation between shape and the regression coefficients for size, conditioned on other model effects (Adams et al. 2021). Lines

denote ordinary least square regressions. Convex hulls indicate adult samples. Shape changes along the regression score are represented by wireframes (black, positive extreme; gray, negative one); male shape visualizations were omitted because these were almost identical to females.

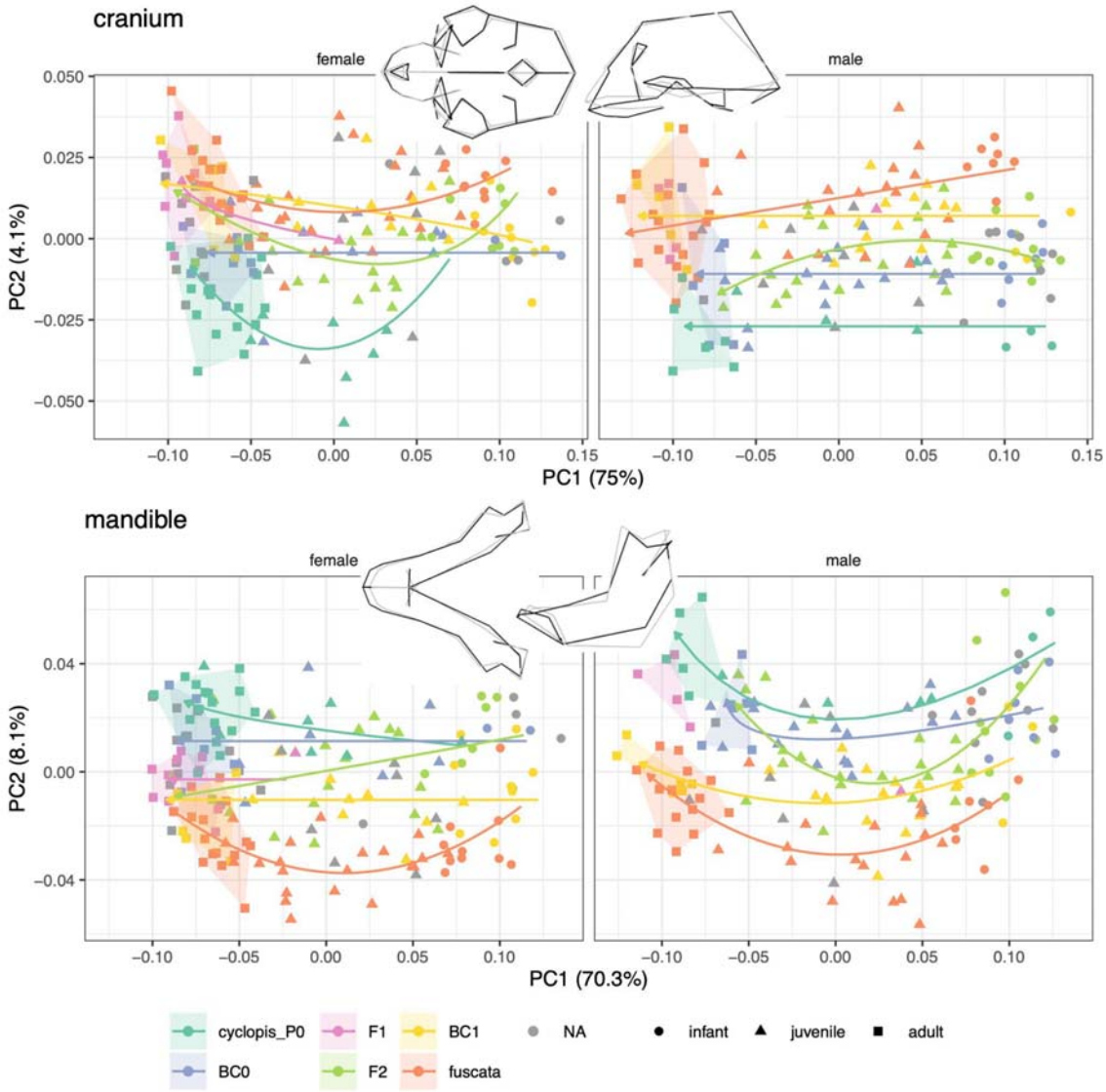

Figure 4: Ontogenetic allometry of cranium and mandible shape represented by the first two principal components (PCs). The arrows denote the regressions of PC scores on lnCS, where quadratic regression is considered, and terms are selected based on step AIC. Convex hulls indicate adult samples. The shape changes along PC2 are represented by wireframes (black, positive extreme; gray, negative one); the PC1 shape visualizations were omitted because these were almost identical to those of the multivariate regression.

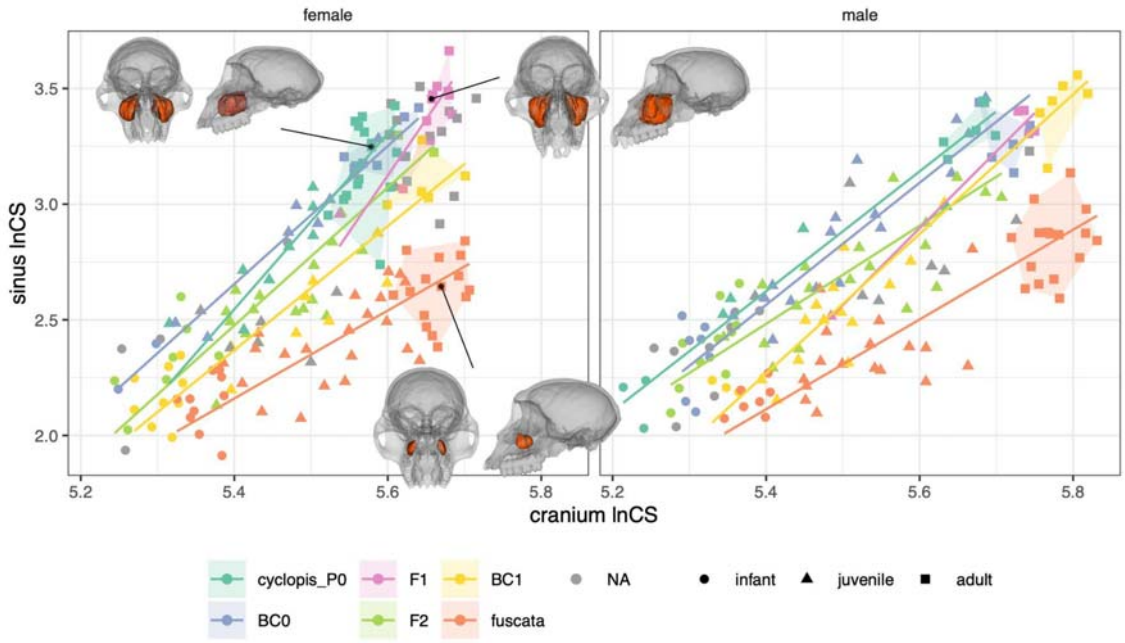

Figure 5: Ontogenetic allometry of the maxillary sinus size against the cranial size. Lines denote the reduced major axis regression. Convex hulls indicate adult samples.

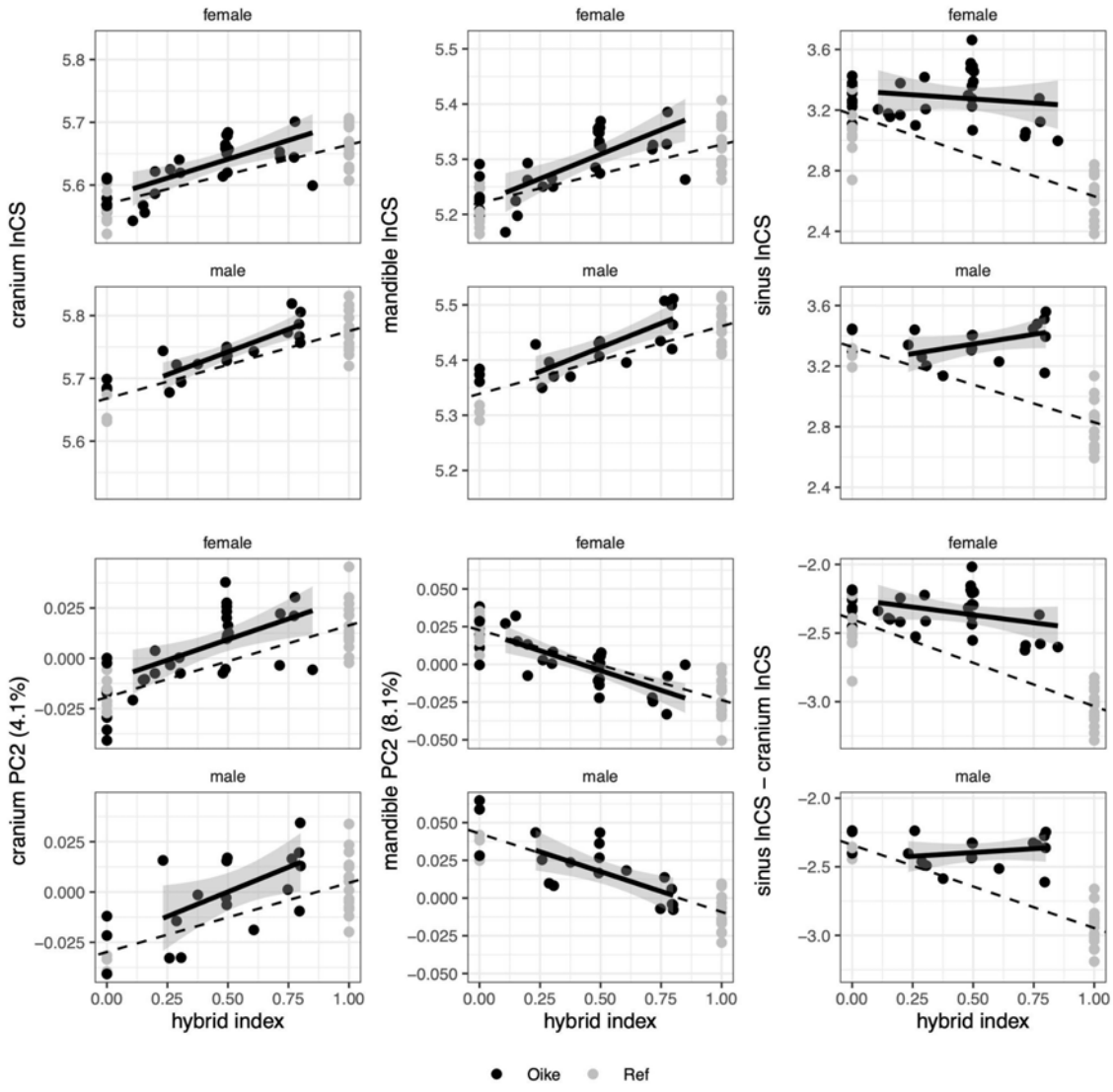

Figure 6: Relationship between morphological variations and the hybrid index in adult samples. Individuals of the Oike population are colored black. *M. cyclopis* and *M. fuscata* from the other populations are placed as 0, and 1 on the hybrid index, respectively, and are colored gray. Dashed lines denote the expectations of the additive model, which pass through the mean value of the *M. cyclopis* (P0 and the other *M. cyclopis*) and the *M.*

fuscata populations. Solid lines denote ordinary least square regression for the admixed individuals of the Oike population.