

1 **The heritability of chimpanzee and human brain asymmetry**

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16

17 **ABSTRACT**

18 Human brains are markedly asymmetric in structure and lateralized in function, which suggests a
19 relationship between these two properties. The brains of other closely related primates, such as
20 chimpanzees, show similar patterns of asymmetry, but to a lesser degree, indicating an increase
21 in anatomical and functional asymmetry during hominin evolution. We analyzed the heritability
22 of cerebral asymmetry in chimpanzees and humans using classic morphometrics, geometric
23 morphometrics and quantitative genetic techniques. In our analyses, we separated directional

24 asymmetry and fluctuating asymmetry, which is indicative of environmental influences during
25 development. We show that directional patterns of asymmetry, those that are consistently present
26 in most individuals in a population, do not have significant heritability when measured through
27 simple linear metrics, but they have marginally significant heritability in humans when assessed
28 through three-dimensional configurations of landmarks that reflect variation in the size, position
29 and orientation of different cortical regions. Furthermore, genetic correlations between left and
30 right hemispheres are substantially lower in humans than in chimpanzees, which points to a
31 relatively stronger environmental influence on left-right differences in humans. We also show
32 that the level of fluctuating asymmetry has significant heritability in both species in some regions
33 of the cerebral cortex. This suggests that brain responsiveness to environmental influences,
34 which may reflect plasticity, has genetic bases in both species. These results have implications
35 for the evolvability of brain asymmetry and plasticity among humans and our close relatives.

36

37 **Keywords:** Brain evolution, primates, environment, geometric morphometrics, fluctuating
38 asymmetry, quantitative genetics

39

40 **INTRODUCTION**

41 For more than a century, anatomical observations and functional studies have demonstrated that
42 human brains are markedly asymmetric. This asymmetry is especially noticeable in areas of the
43 brain that are involved in higher-order cognition and language, such as the inferior frontal,
44 superior temporal, and inferior parietal regions [1–4]. For example, functional studies have
45 shown a high density of unilateral activation peaks for language-related tasks in these frontal and
46 parietal perisylvian areas, particularly in the left hemisphere [5]. These findings suggest that

47 anatomical asymmetry is linked to functional lateralization [6,7], which is thought to optimize
48 processing speed and synchronization through minimized wiring in large brains [8].

49

50 Subsequent studies have demonstrated that chimpanzees, one of the closest living relatives of
51 humans, also show similar anatomical asymmetries, although to a lesser degree [9–12]. Other
52 studies have further demonstrated that behavioral lateralization, especially handedness for
53 different tasks, is common in chimpanzees and other great apes, although population-level
54 handedness is not as pronounced as in humans [13–15]. Additionally, neuroimaging studies of
55 chimpanzees have shown functional lateralization in Broca’s area homolog related to
56 communicative behavior [16] and in the hand knob, the motor-hand region of the precentral
57 gyrus, in relation to reach-and-grasping responses [17]. These observations, together with
58 endocranial changes evident in the hominin fossil record [18–20], indicate that cerebral
59 asymmetry was present in the last common ancestor of chimpanzees and humans by 6-8 million
60 years ago and in early hominins, but that it has increased during hominin evolution, probably in
61 parallel with the evolution of greater functional lateralization [21].

62

63 Most previous studies have focused on directional patterns of cerebral asymmetry. Directional
64 asymmetries are defined as those that are consistently identified in most individuals in a given
65 population and are considered to have a genetic origin. We have recently shown, however, that
66 the human brain is characterized not only by a strong degree of directional asymmetry as
67 compared with chimpanzees, but also by a high degree of fluctuating asymmetry [12].

68 Fluctuating asymmetry corresponds to random departures from the population-specific mean
69 directional asymmetry, and it is usually considered to result from the impact of environmental

70 influences on developmental processes [22]. The most classic account for fluctuating asymmetry
71 is that it is the outcome of developmental instability, that is the inability of individuals to buffer
72 the effects of various perturbations during development [23]. We have proposed, however, that
73 the high degree of fluctuating asymmetry observed in healthy human brains is more likely
74 indicative of a high level of developmental plasticity, a hypothesis that is further supported by
75 the low heritability for cortical anatomy observed in human brains compared to chimpanzees
76 [24].

77

78 The available evidence, therefore, indicates that certain aspects of brain asymmetry are
79 genetically determined, whereas other features of anatomical lateralization might be the result of
80 environmental influences during development. In order to tease apart the causal factors
81 underlying the phenotypic expression of brain asymmetry and their evolution, in the current
82 study we evaluate the heritability of different forms of brain asymmetry and the genetic
83 correlations between variables measured in the left and the right side in humans and
84 chimpanzees. Based on the observation that human brains are structurally and functionally more
85 asymmetric than chimpanzee brains, as well as more plastic, we have three major hypotheses.
86 First, we hypothesize that heritability for directional cerebral asymmetry will be higher in human
87 than in chimpanzee brains. Second, we hypothesize that environmental influences on brain
88 asymmetry will be stronger in humans. Third, we hypothesize that fluctuating asymmetry will be
89 genetically heritable, reflecting the capacity for plasticity to evolve.

90

91 **MATERIALS AND METHODS**

92 **Samples and MRI scans.**

93 A sample of 206 chimpanzee (79 males, 127 females, age range: 8-53 years) and 218 human (87
94 males, 131 females, age range: 22-30 years) MRI scans was used. Chimpanzees used in this
95 study were housed at the Yerkes National Primate Research Center (YNPRC) in Atlanta, GA,
96 and at the National Center for Chimpanzee Care (NCCC) at The University of Texas MD
97 Anderson Cancer Center (UTMDACC) in Bastrop, TX. Chimpanzees were scanned using a 3T
98 scanner (Siemens Trio, Siemens Medical Solutions, Malvern, USA) or a 1.5T scanner (Phillips,
99 Model 51, Philips Medical Systems, N.A., Bothell, Washington, USA). Technical details
100 regarding scanning procedures and processing can be found in ref. [25]. Scanning procedures in
101 chimpanzees were approved by the Institutional Animal Care and Use Committees at YNPRC
102 and UTMDACC, and also followed the guidelines of the Institute of Medicine on the use of
103 chimpanzees in research. No paternity tests were conducted for the purposes of this study, but a
104 well-documented pedigree is available for these chimpanzees, which includes information on
105 mother, father and offspring identity for many individuals.

106
107 Human MRI scans were obtained from the Human Connectome Project (HCP) database [26].
108 Individuals were scanned with a Siemens Skyra 3T scanner. Technical details regarding scanning
109 procedures and processing in human subjects can be found in refs. [26,27]. Consent from human
110 participants was obtained in the context of the Human Connectome Project, and data-use terms
111 for open and restricted data were accepted and observed as per HCP requirement [28]. The HCP
112 database includes monozygotic twins, non-monozygotic twins and non-twin siblings. In order to
113 maximize sample size and minimize inter-population variability due to genetic ancestry, which
114 might correlate with general brain anatomy [29], only individuals with the same ancestry (as
115 self-reported) were selected.

116

117 **3D reconstructions and landmarks**

118 Three-dimensional models of the cerebral cortical surface were reconstructed from MRI scans
119 using BrainVisa software [30] for chimpanzees and FreeSurfer software [31] for humans (3D
120 models were directly obtained from the HCP database for the human sample). Thirty-two
121 anatomically homologous landmarks (16 bilateral landmarks) were placed on the intersections
122 and extreme points of the most constant sulci on the chimpanzee and human cortical surface
123 [12,24] (Figure S1, Table S1). Because of the anatomical complexity of the human cortical
124 surface, which makes it difficult to identify some sulci, landmark placement was aided by a
125 comparison with automatically parcellated models. These parcellated models, obtained with
126 FreeSurfer software version 5.3.0 according to the Desikan surface atlas [32], are provided in the
127 HCP database. These or similar configurations of landmarks have been previously used in our
128 other studies of brain variation in chimpanzees and humans [12,24,33].

129

130 **Linear metrics and asymmetry quotients**

131 Linear distances were calculated between several pairs of landmarks as a measure of the general
132 proportions of the major lobes of the brain and of the length of the most prominent sulci (Table
133 S2). These distances are linear approximations and they do not include variation along the course
134 of a given sulcus. Linear distances were measured separately for the right and the left side in
135 order to measure heritabilities for each side and genetic correlations between correspondent
136 variables in each hemisphere (see below). Additionally, linear distances were used to measure
137 asymmetry quotients (AQs) for all the variables, the heritability of which was estimated as well.
138 AQs were calculated as the value of a variable in the right hemisphere minus the value of that

139 variable in the left hemisphere, divided by the mean of that variable in both hemispheres (R-
140 L)*100/((R+L)*0.5). Linear metrics were measured in Procrustes-superimposed configurations
141 of landmarks (see below) because original distances are highly influenced by brain size, even if
142 brain size has a quantitatively very small effect on sulcal anatomy [12]. However, some of the
143 studied variables, such as AQs, are independent of total size, so this transformation does not have
144 any effect in this case.

145

146 **Geometric morphometrics**

147 Configurations of landmarks were also studied in a geometric morphometric context. Original
148 configurations of landmarks were Procrustes-superimposed to remove information regarding the
149 location, orientation and size of the original specimens [34]. Each configuration was later mirror-
150 imaged and relabeled following ref. [35]. The mean of the original and mirror-imaged
151 configurations yielded a symmetric consensus configuration for each individual, whereas the
152 difference between both configurations corresponded to the asymmetric component of shape
153 variation [35]. The asymmetric component of variation was analyzed through separate principal
154 components analyses (PCAs) for each species. The first 5 PCs for each species were explored in
155 further detail.

156

157 PCs were tested for their association with the pattern of directional asymmetry (DA) typical of
158 each species, which was calculated by averaging the asymmetric components of shape variation
159 of each individual for each species (in other words, directional asymmetry in shape was
160 calculated simply as the mean shape asymmetry for each species). These comparisons tested if
161 variation associated with each PC is similar to the pattern of directional asymmetry observed in

162 the population or whether variation is not aligned with this population-typical pattern. The
163 association between each PC and directional asymmetry was measured by calculating the angle
164 between each eigenvector and the species-specific DA vector, which was calculated as the
165 arccosine of the inner product of both vectors. An angle of 0 degrees indicates a correlation of 1
166 between two vectors, whereas an angle of 90 degrees indicates a correlation of 0. Significance
167 was tested against a null distribution of 1,000 angles formed between randomly selected vectors.
168 For vectors of the length included in our study, 78.42 degrees is the significance threshold above
169 which vectors are uncorrelated.

170

171 Additionally, fluctuating asymmetry (FA) scores were calculated for each individual as the
172 difference between individual configurations of landmarks and the norm directional asymmetry
173 configuration within the species-specific sample population [36,37]. FA scores are calculated
174 across all landmarks and represent the extent to which each individual departs from the norm DA
175 pattern. A FA score of 0 indicates that a given individual shows exactly the same pattern of
176 asymmetry that is defined as characteristic of the population, whereas a high FA score indicates
177 that individuals depart from this population-specific pattern, regardless of the identity of the
178 particular anatomical variation that is driving this departure.

179

180 **Quantitative genetics**

181 Variance components and heritabilities were estimated using an animal model approach
182 implemented in the R package *MCMCglmm* [38]. In evolutionary biology and quantitative
183 genetics, an ‘animal model’ is a particular type of mixed-effects statistical model that can be
184 used to decompose phenotypic variance into different genetic and environmental sources and to

185 estimate key parameters such as the heritability and the genetic correlation between traits [39].
186 For humans, the classic implementation of *MCMCglimm* was changed as proposed in ref. [40] to
187 use the kinship matrix instead of a pedigree, which was necessary to include the degree of
188 genetic similarity corresponding to monozygotic twins. All data were standardized prior to
189 analysis by subtracting the mean from each individual value and dividing the difference by the
190 standard deviation. Sex, age and the interaction between sex and age were used as fixed effects
191 in both species. Additionally, scanner type was included in chimpanzee analyses to account for
192 the possible effect of using two different scanners. Phenotypic and genetic correlations between
193 corresponding left and right variables were tested using bivariate animal models, which used the
194 same fixed effects. Following other studies [41], we used slightly informative priors of the form
195 ($V = V_p/r, \eta = 1$), where V_p is the phenotypic variance and r the number of random factors,
196 modified as ($V = \text{diag}(n) * V_p/r, \eta = n$), where n is the number of traits, for bivariate analyses.
197 Because all variables were standardized to a variance of 1 and all models included only one
198 random factor, priors had the form ($V=1, \eta = 1$) for univariate models and ($V = \text{diag}(2), \eta = 2$)
199 for bivariate models. Parameter-expanded priors [42,43] yielded similar overall results, but they
200 more often tended to result in null estimates. Models were run for 1,000,000 iterations, during
201 which model parameters were updated. As it is the standard procedure, the first 500,000
202 iterations were discarded as a burn-in period. Posterior distributions were sampled every 100th
203 iteration to a final amount of 5,000 samples.
204
205 Significance of fixed effects was evaluated by assessing if 95% highest posterior density
206 intervals include 0, which is indicative of non-significance. The significance of phenotypic and
207 genetic correlations can be tested in the same way. Variance components from which heritability

208 is estimated, however, are bound to be positive and posterior distributions will not overlap 0,
209 even if their effect is not significant. We tested the significance of heritability estimates by
210 comparing the deviance information criterion (DIC) in models including pedigree/kinship
211 information and in models excluding it, which yielded a DIC differential value (Δ DIC). The
212 significance of heritability was assessed using a simulation approach consisting of measuring the
213 heritability of random variables using the same models [44]. By construction, these variables do
214 not have significant heritability as values are randomly assigned to individuals. P-values were
215 calculated as the proportion of 1,000 simulations yielding higher Δ DIC than each evaluated
216 variable.

217

218 **RESULTS**

219 **Description of asymmetry**

220 Asymmetry quotients based on interlandmark distances are roughly consistent with previous
221 studies of AQs based on detailed sulcal anatomy [25]. In general, chimpanzees and humans show
222 the same direction of AQ patterns, although values are greater in humans (Fig. 1). Distances
223 related to the perisylvian region, such as the inferior parietal length and the lengths of the
224 Sylvian fissure and of the superior temporal sulcus show a clear leftward bias in both species,
225 although it is stronger in humans than in chimpanzees. Variables related to other regions, such as
226 the frontal and occipital lobes, do not show as consistent asymmetry patterns, either between
227 species or across different variables within each region.

228

229 Geometric morphometric analyses show that directional asymmetric variation is concentrated in
230 the inferior parietal area in both species, although those changes are much more marked in

231 humans, where they also involve a strong reorientation of the Sylvian fissure that is not observed
232 in chimpanzees (Fig. 2). The general pattern of directional asymmetry in humans also includes
233 some changes in the inferior frontal and in the occipital regions. The distribution of individuals
234 in PCA plots shows additional evidence of the stronger degree of directional asymmetry in
235 humans, as demonstrated by the off-centered position of more symmetric individuals with
236 respect to the range of variation of the population in humans, but not in chimpanzees (Fig. 2).

237

238 **Heritabilities and genetic correlations**

239 Our results show that both chimpanzees and humans have significant heritability in most lobe
240 proportions, with the exception of frontal dimensions in the left hemisphere in humans (Tables
241 S3 and S4). Although some studies have evaluated the evolution of lateralization through
242 differential heritability in the left and the right sides [45,46], as well as through different
243 evolutionary trends of variables measured in the left and the right hemisphere [47], our study
244 does not show consistently higher heritabilities for one hemisphere or the other, barring the two
245 non-significant values in humans, which correspond to the left hemisphere. Genetic correlations
246 between corresponding left and right lobe proportions are high in chimpanzees (Fig. 1, Table
247 S5). Genetic correlations are also high in humans, although they are slightly lower than in
248 chimpanzees (Fig. 1, Table S5).

249

250 Heritability for sulcal lengths is substantially higher in chimpanzees than in humans, as has been
251 demonstrated previously [24]. As with lobe proportions, no consistent pattern of higher
252 heritabilities in the left or right hemisphere is observed in either species (Table S6 and S7).
253 Genetic correlations between matching left and right sulcal lengths are in general significant and

254 relatively high for chimpanzees, although there are some exceptions (Fig. 1, Table S8). In
255 humans, most genetic correlations between sulcal lengths in the left and the right hemispheres
256 are not significant, with the exception of the correlation between the left and right central sulci,
257 and the left and right Sylvian fissures (Fig. 1, Table S8). These results indicate that covariation
258 between the left and the right hemispheres is more strongly genetically determined in
259 chimpanzees, whereas it is exposed to higher environmental influence in humans.

260

261 **Heritability of asymmetry**

262 The analysis of the heritability of asymmetry quotients for lobe proportions and sulcal lengths
263 results in generally non-significant values and in marginally significant values only for a few
264 AQs (Tables S9 and S10). This result is initially surprising, because some of these patterns of
265 asymmetry are known to represent very consistent directional asymmetry patterns, which are
266 expected to be genetically determined. However, it is possible that asymmetry quotients based on
267 linear metrics do not have sufficient resolution to detect the genetic origin of brain asymmetries.
268 We further explored this by measuring the heritability of particular aspects of asymmetric shape
269 variation summarized by PC1-PC5 (Tables S11 and S12). These principal components of shape
270 are based on 3D configurations of landmarks, and include all aspects of shape variation, such as
271 the size, position and orientation of the cortical regions included in those configurations. In
272 humans, PC1 and PC2 are the only principal components of asymmetric shape variation that
273 have marginally significant heritability as inferred from our simulation-based significance
274 threshold (PC1: $h^2=0.25$, $\Delta\text{DIC}=16.15$, $P=0.096$; PC2: $h^2=0.29$, $\Delta\text{DIC}=17.86$, $P=0.081$; Fig. 2,
275 Table S12). Interestingly, PC1 is the principal component of shape variation that shows the
276 closest correspondence with directional asymmetry in humans ($\alpha=36.4^\circ$; $P<0.0001$; Table S12).

277 In chimpanzees, no single PC is strongly associated with the directional asymmetry vector,
278 although PC2 shows a slight correlation with DA ($\alpha=64.7^\circ$; $P<0.0001$; Table S11). Principal
279 components of asymmetric shape variation in chimpanzees tend not to show significant or
280 marginally significant heritability.

281
282 Individual fluctuating asymmetry scores are substantially higher in humans than in chimpanzees
283 (Fig. 3), which is consistent with our previous report based on Procrustes ANOVAs [12]. When
284 calculating fluctuating asymmetry scores for total cortical anatomy and for the three major lobes
285 of the brain (frontal, temporo-parietal and occipital), we observed that one of these values has
286 significant heritability for each species: occipital FA for humans ($h^2=0.43$, $\Delta\text{DIC}=46.6$, $P=0.005$)
287 and total FA for chimpanzees ($h^2=0.41$, $\Delta\text{DIC}=33.3$, $P=0.028$), with chimpanzees showing also
288 marginally significant heritability for the frontal lobe ($h^2=0.32$, $\Delta\text{DIC}=23.7$, $P=0.074$). This
289 result shows that the general level of fluctuating asymmetry, which is indicative of the
290 propensity to have a brain that departs from species' typical configurations regardless of the
291 particular changes motivating this departure, is in part genetically heritable in both species.

292

293 **DISCUSSION**

294 Comparisons of heritability values across different populations or species are unavoidably
295 influenced by the different environmental conditions in which different groups live. Indeed,
296 heritability estimates are specific to the groups and conditions in which they were obtained, and
297 they cannot be generalized to other circumstances. This point is particularly important because of
298 the very different environmental conditions corresponding to our chimpanzee and human
299 samples, with chimpanzees living in the more homogenous conditions typical of captive habitats.

300 These differences, however, are much more likely to be reflected in behavioral phenotypes than
301 in anatomical phenotypes. However, differences in the relatedness structure of the chimpanzee
302 and human samples are likely to have a stronger effect on our results. Analyses of brain size have
303 shown that heritability estimates based on twins (as in our human sample) tend to be higher than
304 those based on extended pedigrees (as in our chimpanzee sample) [48]. An implication of this
305 observation is that human heritabilities yielded by our analyses are likely to be overestimated in
306 comparison with chimpanzee heritabilities. With this in mind, we focus our discussion on the
307 comparison of the heritability of different variables within each species.

308

309 Our results shed light on the heritability of directional and fluctuating brain asymmetry in
310 humans and chimpanzees. These two types of asymmetry have different bases in genetics and
311 development, each with distinct implications for the evolutionary origin of neural structure and
312 function. Classic studies of human brain anatomy have focused on directional asymmetries
313 [1,4,45], as they are more consistent and, therefore, easier to identify, and because they have well
314 known functional correlates. Our study, however, highlights the importance of fluctuating
315 asymmetry, which, according to various lines of evidence [12,24], may be interpreted to reflect
316 variation due to plasticity in normal brain development.

317

318 **Directional asymmetry and functional lateralization**

319 Because directional asymmetry of the brain is usually assumed to be genetically determined, our
320 finding that most asymmetry quotients do not show significant heritability in either species does
321 not fit our hypotheses and is initially surprising. Studies of heritability in human neuroanatomy
322 have reported differential heritability for some variables (lobar volume and gray matter

323 distribution) in both hemispheres [45,46]. However, direct evaluations of the heritability of brain
324 asymmetry in humans are not common in the literature [49], which may reflect a publication bias
325 resulting from negative results. In chimpanzees, however, it has been reported that the
326 asymmetry quotient of gray matter volume shows low but significant heritability in the posterior
327 region of the superior temporal gyrus, but not in the inferior frontal gyrus [49]. Because our
328 previous studies have demonstrated that fluctuating asymmetry is preferentially located in the
329 inferior frontal region in chimpanzees [12], we hypothesize that significant heritability for
330 directional asymmetry may be harder to identify in brain regions with strong fluctuating
331 asymmetry. However, our study does not identify significant heritability for the AQ of the
332 superior temporal sulcus, even though this region does not show particularly high fluctuating
333 asymmetry in chimpanzees. This difference may result from the lack of separation between the
334 anterior and posterior segments of the superior temporal sulcus in the present study, or it may
335 indicate that directional asymmetry in gray matter volume is more heritable than landmark-based
336 sulcal lengths.

337

338 When exploring more complex patterns of asymmetric shape variation as described by the 3D
339 configurations of landmarks, chimpanzees and humans show some similarities in their major
340 patterns of directional asymmetry, namely the difference in size and orientation between the left
341 and right superior temporal sulci. In humans, the major pattern of directional asymmetry is
342 strongly associated with the first principal component of shape variation, which is one of the PCs
343 that show marginally significant heritability as determined by our simulation-based significance
344 threshold. These results indicate that complex patterns of asymmetry, which include all
345 parameters of shape variation (size, position and orientation of the different cortical regions with

346 respect to each other), may show moderate but significant heritability in larger samples and,
347 therefore, some level of genetic control.

348

349 Our results are consistent with studies showing low to moderate heritability for neuroanatomical
350 asymmetries in primates [49–51], which contrasts with other studies yielding substantially higher
351 heritability for behavioral lateralization in chimpanzees and humans, usually measured as
352 handedness [52,53]. This apparent paradox highlights the difficulty in drawing direct
353 associations between structural and functional asymmetry. Studies of heritability based on
354 functional neuroimaging in humans, which might serve as an interface between neuroanatomical
355 and behavioral studies, are particularly uncommon [54], which makes it challenging to bridge
356 both types of observations.

357

358 **Fluctuating asymmetry and plasticity**

359 Fluctuating asymmetry was indirectly measured in our study through the analysis of genetic
360 correlations between the left and the right hemispheres. These results show that inter-
361 hemispheric genetic correlations are high for all variables in chimpanzees. In humans, however,
362 general lobe proportions and evolutionary and developmentally primary sulci (such as the central
363 sulcus and the Sylvian fissure) show high genetic correlations between the left and the right side,
364 whereas other sulci show low and not significant correlations. This difference points to a greater
365 environmental influence on left-right differences in humans. Some authors have suggested that
366 “in the absence of differential developmental effects, the correlation between the two sides of the
367 same organ should be 1” (ref. [55], p. 708). This expectation is true for perfectly symmetric
368 organs and for those showing genetically-determined directional asymmetry. Lower inter-

369 hemispheric genetic correlations observed in human brains reflect greater non-genetic
370 developmental effects than in chimpanzees. We interpret this result to reflect a high level of
371 developmental plasticity in human brains, which is consistent with other lines of evidence (see
372 also refs. [12,24]). Our results have been obtained from a healthy human population for which a
373 high level of developmental instability due to stress or illness, which may be another cause of
374 fluctuating asymmetry, would not be expected. In addition, microstructural and gene expression
375 studies show that human evolution has been characterized by increases in the level of cerebral
376 plasticity, as evident by an extended period of environment-dependent myelination [56] and
377 upregulation of genes associated with synaptogenesis [57]. The results of the current study
378 provide further support from an analysis of brain anatomy that elevated plasticity characterizes
379 the human cerebral cortex compared to other primate species. In addition, developmental
380 changes are known to have occurred during hominin evolution that have extended the period of
381 time during which brain maturation is exposed to a complex extra-uterine environment [58].
382 Studies based on endocranial anatomy, furthermore, also show that the level of fluctuating
383 asymmetry observed in modern human endocasts is higher than that observed in great apes,
384 including chimpanzees, bonobos and gorillas [59].

385

386 Even if particular plastic changes are not genetically heritable, the general propensity to have a
387 more plastic brain that will be more responsive to environmental influences can be coded by
388 genes. This is what our results show, at least partially, by revealing significant heritability for
389 fluctuating asymmetry scores in some brain areas in chimpanzees and humans. Indeed, our
390 analyses yield unexpected results because the heritability of some aspects of fluctuating
391 asymmetry is substantially higher than the heritability of asymmetry quotients and principal

392 components of asymmetric shape variation, which are more reflective of directional asymmetry.
393 Although this result should be confirmed in other samples and using additional methods to
394 characterize cortical organization, it seems to indicate that brain anatomy's responsiveness to
395 environmental influences is more strongly genetically controlled than structural asymmetry
396 itself. The finding of non-significant heritability for fluctuating asymmetry in some areas of the
397 brain may reflect more complex patterns of inheritance, or the inability of our relatively small
398 samples to detect heritability levels that are expected to be moderate [60]. In fact, several studies
399 have demonstrated that human-specific variants of certain genes are associated with increases in
400 the level of plasticity in the formation of cortico-basal neural circuits [61] and in the maturation
401 of synaptic spines [62]. The evolution of neural plasticity can be also mediated in part by
402 epigenetic mechanisms that allow for context-dependent changes of synapses and circuits [63].
403 Taken together with the findings from the current analysis, these observations indicate that the
404 level of brain plasticity in the chimpanzee-human clade has a genetic basis and, therefore, is
405 heritable and evolvable.

406

407 **Data accessibility.**

408 The datasets supporting this article are available in Dryad database at
409 <http://dx.doi.org/10.5061/dryad.n04r6>.

410

411 **Authors' contributions**

412 A.G.-R. and C.C.S. conceived of the study; W.D.H. and S.J.S. collected chimpanzee scan data;
413 A.G.-R. collected morphometric data, designed and performed analyses; A.G.-R. and C.C.S.
414 wrote the manuscript, with contributions from W.D.H. and S.J.S.

415

416 **Competing interests**

417 The authors declare that they have no competing interests.

418

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427

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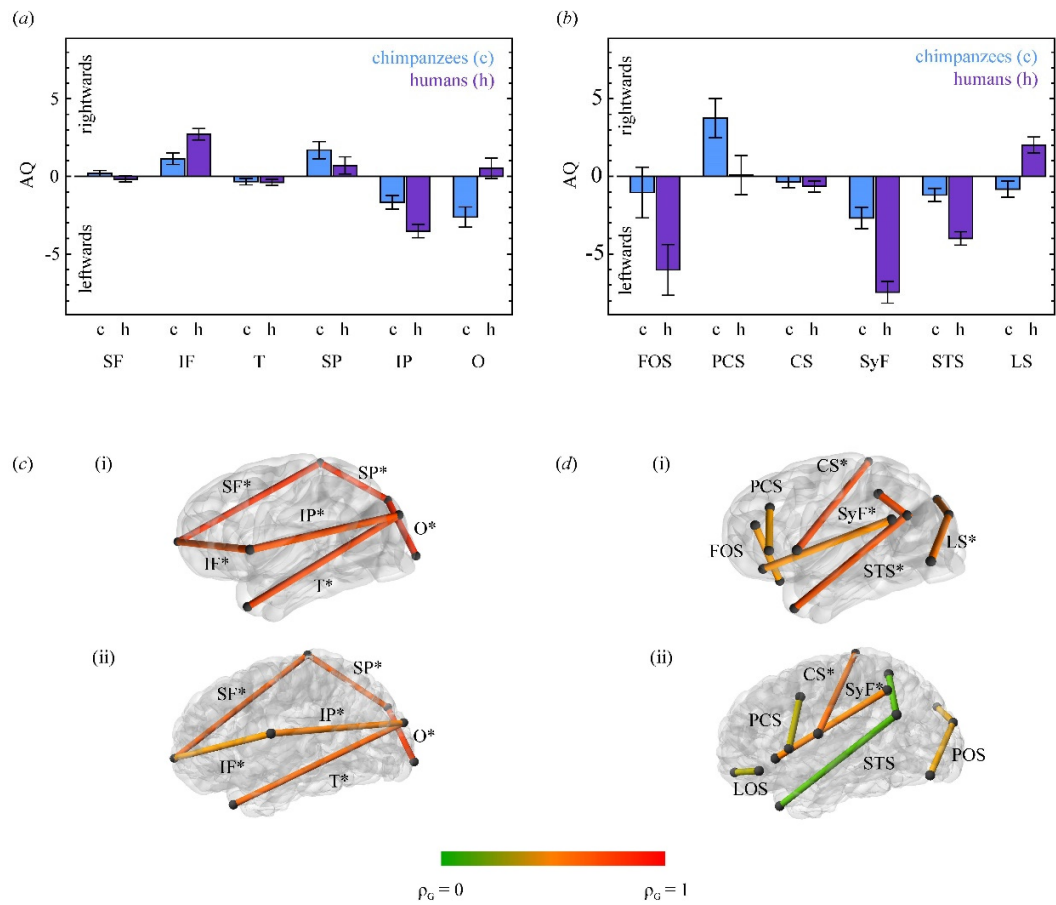
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- 596

597 **Table 1.** Heritability of fluctuating asymmetry scores.

	Chimpanzees				Humans			
	h²	HPDI	ΔDIC	Fixed	h²	HPDI	ΔDIC	Fixed
			(P)				(P)	
Frontal	0.32	0.12-	23.68	—	0.17	0.07-	5.13	—
		0.58	(0.074)			0.39	(0.415)	
Temporo- parietal	0.21	0.08-	9.30	—	0.17	0.08-	2.58	—
		0.47	(0.358)			0.36	(0.546)	
Occipital	0.23	0.10-	9.00	—	0.43	0.17-	42.65	—
		0.45	(0.373)			0.68	(0.005)	
Total	0.41	0.14-	33.28	—	0.19	0.08-	5.56	—
		0.63	(0.028)			0.40	(0.338)	

598 h²: heritability; HPDI: 95% highest posterior density interval (credible intervals indicating that
599 the heritability of each trait has 95% of probability to lie between the lower and the upper
600 bounds); ΔDIC (P): difference in the deviance information criterion between the model with and
601 without pedigree information (P-value); Fixed: significant fixed effects.

602



603

604 **Figure 1. Analysis of asymmetry based on interlandmark linear distances.** (a) Asymmetry

605 quotients for lobe proportions (mean AQs and standard errors). (b) Asymmetry quotients for

606 sulcal lengths. (c) Genetic correlations between left and right lobe proportions in chimpanzees (i)

607 and humans (ii). (d) Genetic correlations between left and right sulcal lengths in chimpanzees (i)

608 and humans (ii). Asterisks mark significant genetic correlations in (c) and (d), but no AQ shows

609 significant heritability in (a). Numerical values for heritabilities and color-coded genetic

610 correlations are provided in Tables S5, S8, S9 and S10. SF: superior frontal length; IF: inferior

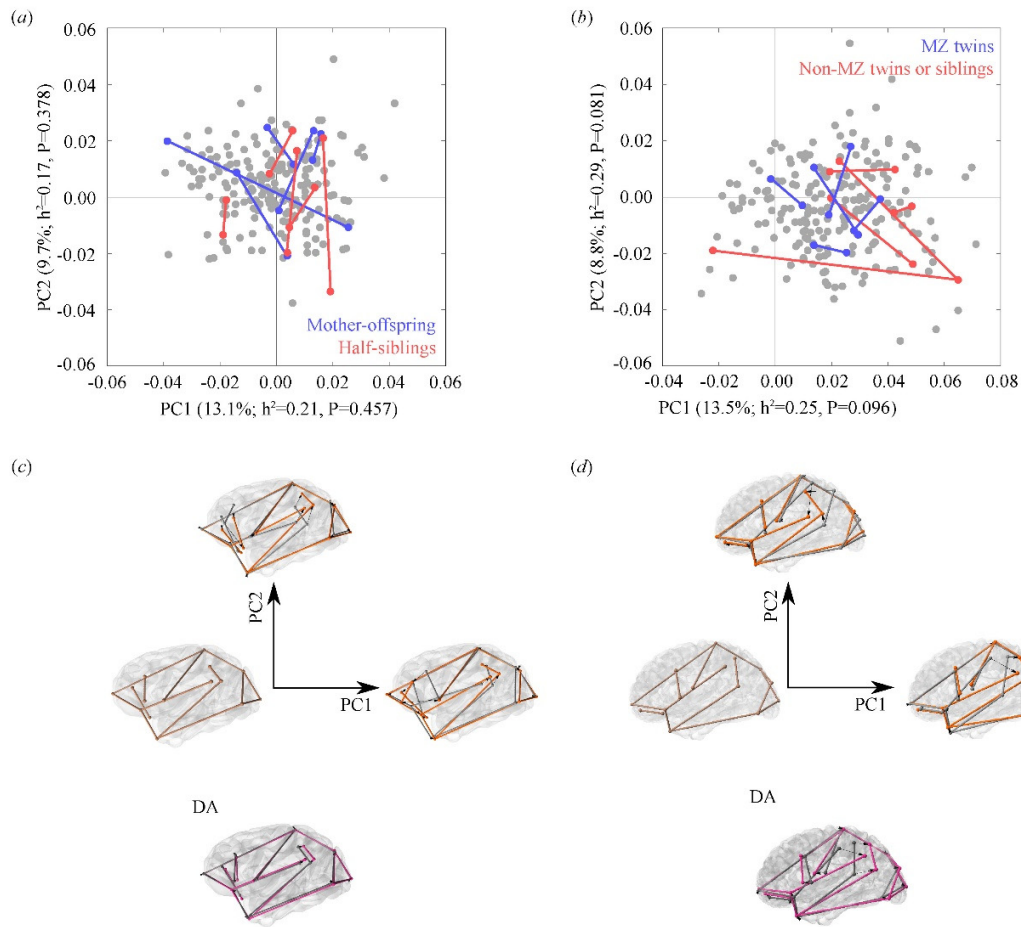
611 frontal length; T: temporal length; SP: superior parietal length; IP: inferior parietal length; O:

612 occipital length; FOS: fronto-orbital sulcus (latero-orbital sulcus —LOS— in humans); PCS:

613 precentral sulcus; CS: central sulcus; SyF: Sylvian fissure; STS: superior temporal sulcus; LS:

614 lunate sulcus (parieto-occipital sulcus —POS— in humans).

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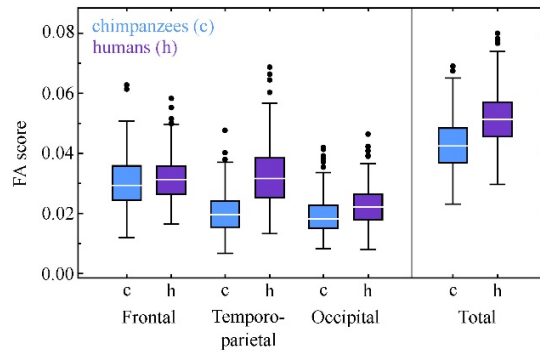
616

617 **Figure 2. Geometric morphometric analysis of asymmetry.** (a) Principal component analysis
 618 of asymmetric shape variation in chimpanzees showing five randomly selected mother-offspring
 619 and half-siblings pairs (50% versus 25% genetic similarity). (b) Principal component analysis of
 620 asymmetric shape variation showing five randomly selected pairs of monozygotic twins and of
 621 non-monozygotic twins or non-twin siblings (100% versus 50% genetic similarity). PCA plots in
 622 (a) and (b) are centered on a hypothetical perfectly symmetric individual. The percentage of
 623 variance explained by each PC and their heritabilities and P-values are provided (see tables S11
 624 and S12 for extended information). (c) Major patterns of shape variation in chimpanzees. (d)

625 Major patterns of shape variation in humans. (c) and (d) show the symmetric consensus for each
626 species and major patterns of variation corresponding to the positive extremes of PC1 and PC2
627 (gray for the right hemisphere and orange for the left). The directional asymmetry (DA) pattern
628 for each species is shown on the bottom panels. For DA, gray corresponds to the right
629 hemisphere and magenta to the left hemisphere. PC1, PC2 and DA shape variation has been
630 exaggerated beyond the range observed in actual data to facilitate visualization.

631

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633

634 **Figure 3. Fluctuating asymmetry scores for chimpanzees and humans.** FA scores have been

635 calculated as the residual variation in each individual after removing the DA pattern typical of

636 each species. Heritabilities of FA scores are provided in Table 1.

637