NEURODEVELOPMENT

Human-specific *ARHGAP11B* increases size and folding of primate neocortex in the fetal marmoset

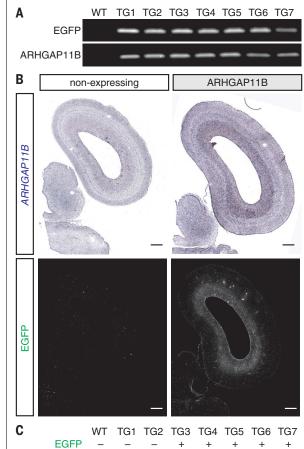
Michael Heide^{1,*}, Christiane Haffner¹, Ayako Murayama^{2,3}, Yoko Kurotaki⁴, Haruka Shinohara⁴, Hideyuki Okano^{2,3}, Erika Sasaki⁴, Wieland B. Huttner^{1,*}

The neocortex has expanded during mammalian evolution. Overexpression studies in developing mouse and ferret neocortex have implicated the human-specific gene *ARHGAP11B* in neocortical expansion, but the relevance for primate evolution has been unclear. Here, we provide functional evidence that *ARHGAP11B* causes expansion of the primate neocortex. *ARHGAP11B* expressed in fetal neocortex of the common marmoset under control of the gene's own (human) promoter increased the numbers of basal radial glia progenitors in the marmoset outer subventricular zone, increased the numbers of upper-layer neurons, enlarged the neocortex, and induced its folding. Thus, the human-specific ARHGAP11B drives changes in development in the nonhuman primate marmoset that reflect the changes in evolution that characterize human neocortical development.

volutionary expansion of the human neocortex is linked to our cognitive abilities (1-6). The human-specific gene ARHGAP11B (7, 8) is implicated in this neocortical expansion because it is expressed in the human progenitor cells giving rise to neocortical neurons, and when overexpressed in developing mouse and ferret neocortex, two evolutionarily distant mammals, can induce features associated with neocortical expansion (9, 10). ARHGAP11B arose ≈5 million years ago by partial duplication of ubiquitous ARHGAP11A, which encodes a Rho-GAP exhibiting nuclear localization (7-9, 11). However, because of a point mutation that presumably occurred after the partial gene duplication event and leads to a human-specific change in protein sequence, ARHGAP11B lacks Rho-GAP activity in vivo and is localized in mitochondria. This promotes the proliferation of basal progenitors, which are implicated in neocortical expansion through glutaminolysis (11, 12). Here, we tested ARHGAP11B's relevance for neocortical expansion in a nonhuman primate by expressing ARHGAP11B under the control of its own (human) promoter in transgenic fetal marmosets.

To express human-specific *ARHGAP11B* (7, 8) (fig. S1A) in the common marmoset, we constructed a lentiviral vector. In this functionally verified vector (fig. S1, B and C), an \approx 2.7-kb human genomic segment containing the *ARHGAP11B* promoter drives expression of an enhanced green fluorescent protein (EGFP) reporter, followed by the complete ARHGAP11B proteincoding sequence. The two proteins become separate polypeptides after translation because of the presence of a T2A self-cleaving sequence (fig. S1B). This expression vector was used to generate pregnant marmosets carrying *ARHGAP11B*-transgenic fetuses by following a previously established protocol (*13*). This protocol involves microinjection into fertilized marmoset oocytes and transfer of in vitrodeveloped embryos into foster mothers 3 to 5 days after ovulation (with the day of transfer being defined as day 0 of pregnancy; fig. S1D and table S1).

We confined our analyses to marmoset fetuses because we anticipated that expression of this human-specific gene would affect neocortex development in this animal. In light of potential unforeseeable consequences with regard to postnatal brain function, we considered it a prerequisite-and mandatory from an ethical point of view-to first determine the effects of ARHGAP11B expression on the development of fetal marmoset neocortex. To this end, we collected fetuses after Caesarian section at day 101 of the \approx 150-day gestation (fig. S1D). a stage when neocortical development shows both progenitor cell division and production of neurons (destined mostly to the upper layers) and which corresponds to fetal human neocortical development at ≈ 16 weeks after conception. Of the seven EGFP- plus ARHGAP11B-transgenic marmoset fetuses obtained (table S1), five expressed both EGFP and ARHGAP11B in fetal neocortex, whereas two expressed neither (Fig. 1). In the five transgenic fetuses exhibiting EGFP and ARHGAP11B expression in neocortex, we found three or four lentivirus integration events at random genomic positions



ARHGAP11B

Fig. 1. ARHGAP11B and EGFP expression in ARHGAP11B-transgenic marmoset 101-day fetuses.

Shown are the results of genomic PCR for EGFP and ARHGAP11B using somatic cells (A) and the absence (-) or presence (+) of EGFP protein and ARHGAP11B mRNA expression in neocortex (B and C) of one WT and seven ARHGAP11B-transgenic marmoset fetuses. (B) ARHGAP11B mRNA in situ hybridization (top) and EGFP immunohistochemistry (bottom) of ARHGAP11B-nonexpressing (TG2) and ARHGAP11Bexpressing (TG6) neocortex of marmoset fetuses. Scale bars, 500 µm.

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per animal (table S2). *ARHGAP11B* mRNA expression in the marmoset neocortical wall resembled that in fetal human neocortex, with similar intensity and occurring preferentially in the germinal zones [i.e., the ventricular zone (VZ), inner subventricular zone (iSVZ), and outer subventricular zone (oSVZ) (*14*)] (*9*, *15*), like EGFP, as revealed by in situ hybridization (fig. S1E) and reverse transcription quantitative polymerase chain reaction (PCR) (fig. S1F).

The ARHGAP11B-expressing marmoset neocortex was larger and its cortical plate (CP) thicker than that in normal marmoset neocortex (Figs. 1B and 2A and fig. S1E) and, in contrast to the smooth surface of the normal marmoset brain, exhibited surface folds (Fig. 2A). Quantification of fetal marmoset neocortex as a whole indicated no statistically significant difference in width but a significant increase in length of ARHGAP11B-expressing neocortex compared with wild-type (WT) and ARHGAP11B-non-expressing neocortex (Fig. 2B). To quantify cortical folding, we analyzed coronal sections of fetal marmoset neocortex along the rostrocaudal axis (Fig. 2C) to obtain the gyrification index (GI) (fig. S2A),

which is the ratio of tracing the de facto length of the (unfolded or folded) cortical surface (Fig. 2E, green) over a hypothetical minimal length, i.e., smooth, tracing of the cortical surface (Fig. 2E, magenta) (16, 17). Applying this tracing to the entire dorsoventral dimension of the coronal sections analyzed, WT and ARHGAP11B-non-expressing neocortex exhibited a GI of nearly 1.0 (Fig. 2C), consistent with the essentially unfolded, near-lissencephalic nature of the marmoset neocortex (18, 19). The GI of ARHGAP11B-expressing neocortex increased rostrally (Fig. 2C) and reached nearly 1.1 when the tracing was confined to the portion of the cortical surface where gyrus-like structures emerged (Fig. 2D and fig. S2B). These structures did not arise by folding of a CP of equal thickness, but rather reflected local CP thickening (fig. S2, C to E), which in turn reflected a specific increase in upperlayer neurons as revealed by immunostaining for markers of specific neuron populations (fig. S2, D and F).

We then quantified CP thickness in WT, *ARHGAP11B*-non-expressing, and *ARHGAP11B*expressing marmoset neocortex, taking into consideration only regions where no gyruslike structures emerged in the *ARHGAP11B*expressing neocortex. This revealed increased CP thickness for *ARHGAP11B*-expressing neocortex compared with WT and *ARHGAP11B*non-expressing neocortex (Fig. 3, A and B, and figs. S3 and S4A).

To understand the basis of this increase in CP thickness, we quantified CP nuclei that were positive for Tbr1 and Ctip2, two markers of deep-layer neurons, and CP nuclei that were positive for Satb2 and Brn2, which are expressed by upper-layer neurons (20, 21) (Fig. 3A and fig. S4B). We observed a nearly 40 and 50% increase in Satb2⁺ neurons and Brn2⁺ neurons, respectively, but not in Tbr1⁺ and Ctip2⁺ neurons, in the CP of *ARHGAP11B*-expressing marmoset neocortex compared with WT and *ARHGAP11B*-non-expressing neocortex (Fig. 3C and fig. S4, C and D).

Consistent with the developmental stage of our analyses (fig. S1D), we noted that a substantial proportion of the Satb2⁺ and Brn2⁺ neurons observed in the cortical wall were found in the subplate (fig. S5, A and B), consistent with these neurons migrating to the CP (22, 23). Accordingly, the numbers specifically of Satb2⁺ and Brn2⁺ neurons in the subplate

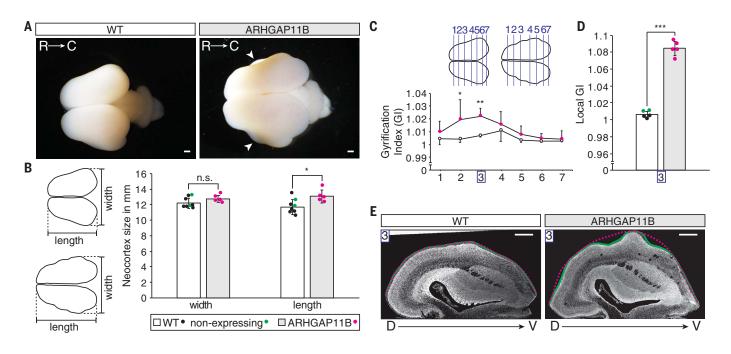


Fig. 2. Size and GI of WT and *ARHGAP11B***-non-expressing versus** *ARHGAP11B***-expressing 101-day fetal marmoset neocortex.** (**A**) WT brain and brain expressing *ARHGAP11B* in neocortex (TG3). Arrowheads indicate cortical folds. R, rostral; C, caudal. Scale bars, 1 mm. (**B**) Width and length (see diagrams) of six WT (black dots, white columns) plus two *ARHGAP11B***-**non-expressing neocortices (green dots, white columns) versus five *ARHGAP11B*-expressing neocortices (magenta dots, gray columns). Data are shown as mean ± SD; n.s., not significant; **P* < 0.05 (two-tailed *t* test). (**C**) GI [see (E) and fig. S2A] of three WT plus two *ARHGAP11B*-non-expressing neocortices (white circles) versus five *ARHGAP11B*-expressing neocortices (magenta circles) at

seven positions along the rostrocaudal axis (see diagrams). Data are shown as mean ± SD; **P* < 0.05; ***P* < 0.01 (one-tailed *t* test). (**D**) Local GI (see fig. S2B) of three WT neocortices (black dots, white column) plus two *ARHGAP11B*-non-expressing neocortices (green dots, white column) versus five *ARHGAP11B*-expressing neocortices (magenta dots, gray column). Data are shown as mean ± SD; ****P* < 0.001 (two-tailed *t* test). (**E**) 4',6-diamidino-2-phenylindole (DAPI)-stained coronal section of WT and *ARHGAP11B*-expressing (TG4) neocortex at position 3 [see (C)]. D, dorsal; V, ventral. Green line indicates the de facto length of the cortical surface; magenta line indicates the hypothetical minimal length of the cortical surface. Scale bars, 500 µm.

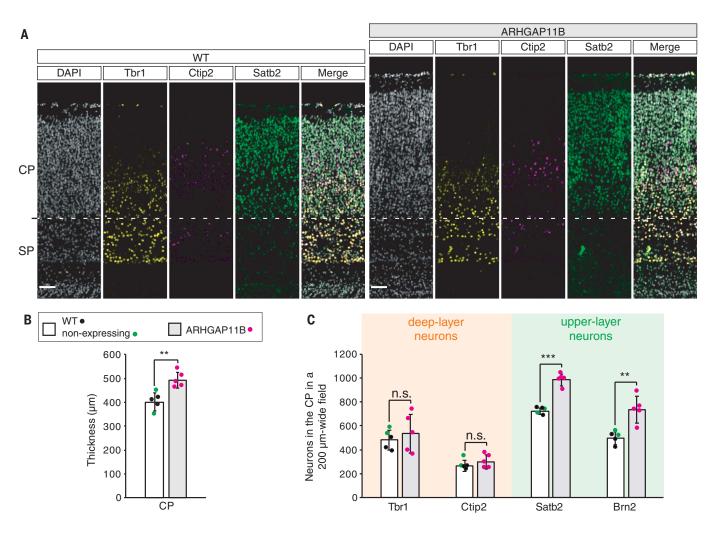


Fig. 3. *ARHGAP11B*-expressing **101**-day fetal marmoset neocortex shows increased CP thickness and elevated numbers specifically of upperlayer neurons. (A) Triple immunofluorescence for Tbr1 (yellow), Ctip2 (magenta), and Satb2 (green) combined with DAPI staining (white), of WT (left) and an *ARHGAP11B*-expressing (TG3, right) neocortex (occipital lobe). Scale bars, 50 μm. (**B** and **C**) CP thickness (B) and Tbr1⁺, Ctip2⁺ Satb2⁺, and

Brn2⁺ neuron number in CP in a 200-μm-wide field (C) of three WT neocortices (black dots, white columns) plus two *ARHGAP11B*-non-expressing neocortices (green dots, white columns) versus five *ARHGAP11B*-expressing neocortices (magenta dots, gray columns). For *ARHGAP11B*-expressing neocortex, quantification excluded gyrus. Data are shown as mean ± SD; ***P* < 0.01; ****P* < 0.001 (two-tailed *t* test).

were greater, but the subplate thickness was equal, for *ARHGAP11B*-expressing marmoset neocortex compared with WT and *ARHGAP11B*-nonexpressing neocortex (fig. S5, C to F).

These data were consistent with an ongoing production of cortical neurons, mostly upperlayer neurons, at the developmental stage of our analyses (fig. S1D). We examined the germinal zones (VZ, iSVZ, and oSVZ) and progenitors therein for WT, *ARHGAP11B*-non-expressing, and *ARHGAP11B*-expressing marmoset neocortex (Fig. 4A). Analysis of the germinal zones showed increased oSVZ thickness for *ARHGAP11B*-expressing neocortex compared with WT and *ARHGAP11B*-non-expressing neocortex (Fig. 4B and fig. S7A). We observed an increase in mitotic basal progenitors that overall was \approx 2-fold in the iSVZ and \approx 3-fold in the oSVZ, but observed no difference in mitotic apical progenitors in the VZ (Fig. 4C and figs. S6 and S7, B and C).

At least half of the mitotic basal progenitors in the oSVZ of ARHGAP11B-expressing neocortex exhibited a basal process and thus were basal (or outer) radial glia (24-27), whereas this proportion was less (≤40%) for WT and ARHGAP11B-non-expressing neocortex (Fig. 4D and figs. S8, A to D), which is consistent with previous data (28, 29). ARHGAP11B expression increased mitotic basal radial glia \approx 3-fold (Fig. 4E and fig. S8E). A significant increase in basal radial glia caused by ARHGAP11B expression was also observed when these cells were quantified in interphase using the marker Hopx (6)(fig. S9). More than 99% of the mitotic basal radial glia in oSVZ were Sox2⁺ (fig. S8F) and about half lacked expression of Tbr2 (Fig. 4, D and E, and fig. S8G). Therefore, the cells amplified upon *ARHGAP11B* expression in fetal marmoset neocortex exhibited a marker signature consistent with the identity of basal radial glia (5, 6, 9).

In this study, we examined physiologically relevant expression of human-specific *ARHGAP11B* (7, 8) in the fetal neocortex of a nonhuman primate, the common marmoset, by using the human *ARHGAP11B* promoter, in contrast to previous studies using a strong constitutive promoter (9, 10). This expression increased fetal neocortex size, CP thickness, upper-layer neurons, oSVZ size, and basal progenitors including basal radial glia, the progenitor type that is thought to drive development of the mammalian neocortex (2–6, 14, 30). Our results suggest that the human-specific *ARHGAP11B* gene may have caused neocortex expansion in the course of human evolution.

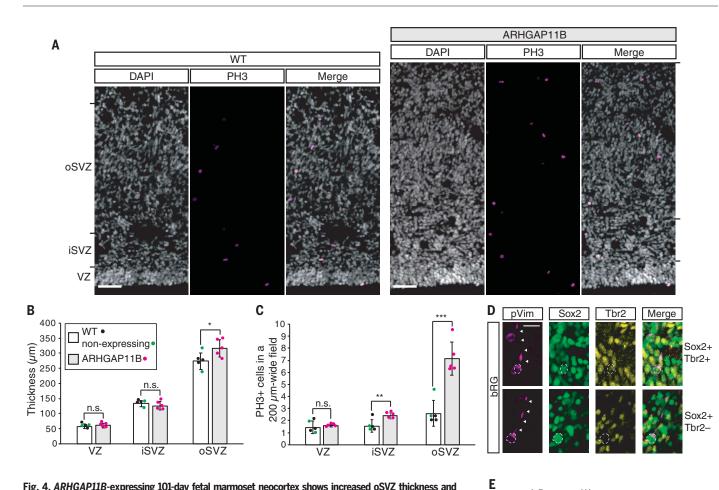


Fig. 4. ARHGAP11B-expressing 101-day fetal marmoset neocortex shows increased oSVZ thickness and elevated numbers of basal progenitors, notably basal radial glia. (A) Immunofluorescence for phosphohistone H3 (PH3, magenta), combined with DAPI staining (white), of WT (left) and ARHGAP11B-expressing (TG6, right) neocortex (occipital lobe). Scale bars, 50 µm. (B and C) Germinal zone thickness (B) and PH3+ cell numbers in germinal zones in a 200-µm-wide field (C) of three WT neocortices (black dots, white columns) plus two ARHGAP11Bnon-expressing neocortices (green dots, white columns) versus five ARHGAP11B-expressing neocortices (magenta dots, gray columns). Data are shown as mean \pm SD; *P < 0.05; **P < 0.01; ***P < 0.001 (two-tailed t test). (D) Triple immunofluorescence for phospho-vimentin (pVim, magenta), Sox2 (green), and Tbr2 (yellow) showing mitotic bRG in oSVZ of ARHGAP11B-expressing neocortex. Arrowheads indicate the basal processes. Top bRG shown is Sox2⁺ Tbr2⁺; bottom bRG is Sox2⁺ Tbr2⁻. Scale bars, 20 μm. (E) Numbers of total (left) and Sox2⁺ Tbr2⁻ (right) basal process-bearing pVim⁺ cells in oSVZ in a 200-µm-wide field of four WT neocortices (black dots, white columns) plus one ARHGAP11B-non-expressing neocortex (green dot, white columns) versus three ARHGAP11B-expressing neocortices (magenta dots, gray columns). Data are shown as mean \pm SD; ***P < 0.001 (two-tailed t test).

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total

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Sox+

Tbr2-

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Basal process-bearing pVim+ cells in the oSVZ in a 200 μm-wide field

200 µm-wide

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SUPPLEMENTARY MATERIALS

science.sciencemag.org/content/369/6503/546/suppl/DC1 Materials and Methods Figs. S1 to S9 Tables S1 to S4 Data S1 References (*31*–33) MDAR Reproducibility Checklist

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Science

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Neocortex in the fetal brain

Along the path of human evolution, gene duplication and divergence produced a protein, ARHGAP11B, that is found in humans but not nonhuman primates or other mammals. Heide *et al.* analyzed the effects of *ARHGAP11B* gene expression, under control of its own human-specific promoter, in the fetal marmoset (see the Perspective by Dehay and Kennedy). In the early weeks of fetal growth, the gene drove greater elaboration of neural progenitors and neocortex than is evident in the normal fetal marmoset. ARHGAP11B expression may be one cause of the more robust neocortex that characterizes the human brain.

Science, this issue p. 546; see also p. 506

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