



The nucleus accumbens and ventral pallidum exhibit greater dopaminergic innervation in humans compared to other primates

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Received: 22 October 2020 / Accepted: 10 May 2021 / Published online: 25 May 2021
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Abstract

Recent evidence suggests that increased dopaminergic signaling within the dorsal striatum played a central role in the evolution of the human brain. This increase has been linked to human prosociality and language in what has been described as a dopamine-dominated striatum personality style. Increased striatal dopamine is associated with an increase in ventral striatal activity and promotes externally driven behaviors, including cooperation and social conformity. In contrast, decreased striatal dopamine is associated with increased dorsal striatal activity and favors internally driven and goal-oriented behaviors. Previous comparative studies have focused on the dorsal striatum, measuring dopaminergic innervation in the dorsal and medial caudate nucleus and putamen. Here, we add to this knowledge by examining regions of the ventral striatum. We quantified the density of tyrosine hydroxylase-immunoreactive axons, as a measure of dopaminergic innervation, in the nucleus accumbens and ventral pallidum of humans, great apes, platyrrhine and cercopithecoid monkeys. Our data show that humans have a significantly greater dopaminergic innervation in both structures, supporting the hypothesis that selection for a prosocial neurochemistry in the human basal ganglia may have contributed to the evolution of our uniquely social behavior profile.

Keywords Nucleus accumbens · Ventral pallidum · Tyrosine hydroxylase · Human evolution

Introduction

The striatum is a component of the nigrostriatal and mesolimbic dopaminergic pathways that facilitate motor production and reward regulation, respectively (Arias-Carrión et al. 2010; Haber 2003). The nigrostriatal pathway connects the substantia nigra pars compacta with the dorsal striatum (caudate nucleus and putamen), while the mesolimbic pathway connects the ventral tegmental area (VTA) to the ventral striatum, mediating pleasurable experiences (Báez-Mendoza et al. 2013; Haber 2003). The mesolimbic dopaminergic reward pathway is part of the brain's primary mechanism for encoding reward, and has been the subject of numerous clinical studies, as it can be targeted by addictive drugs (Kalivas and Volkow 2005; Volkow and Morales 2015). From an evolutionary standpoint, the reward system can perpetuate behaviors that enhance fitness by linking successful ones to elevated dopamine (DA) (Haber 2003; O'Connell and Hofmann 2011).

The striatum thus plays a major role in modulating social behaviors, particularly those involved in reward. It is, therefore, of interest that dorsal and ventral regions are

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functionally distinct (Báez-Mendoza et al. 2013; Báez-Mendoza and Schultz 2013; van den Bos 2015). The dorsal region is involved in internally motivated, goal-directed behavior, whereas the ventral region regulates behaviors that are externally guided and is associated with various limbic structures of the brain (van den Bos 2015). Moreover, the ventral striatum is thought to facilitate behavioral flexibility by promoting greater sensitivity to social and environmental cues, thus contributing to cooperation and social conformity in humans (Klucharev et al. 2009; Stallen and Sanfey 2015; van den Bercken and Cools 1982; Zaki et al. 2011). Neurotransmitter concentrations largely regulate differential activity in the striatum with high levels of acetylcholine favoring activity in the dorsal region and its associated internally motivated behaviors, and increased DA promoting externally guided behaviors that are regulated by the ventral region (Cools et al. 1990; Cools et al. 1975; van den Bercken and Cools 1982; van den Bos 2015). These results suggest that individual striatal neurochemical profiles predict individual-specific behaviors and personality style. Inter-individual differences in this system may provide a target for selection by favoring particular behaviors in different environments, and may, therefore, underlie species-specific social and behavioral adaptations.

Recently, Raghanti et al. (2016, 2018) reported that humans, compared to other primates, exhibit a unique striatal neurochemical signature that includes greater DA, serotonin, and neuropeptide Y but decreased acetylcholine in specific regions of the dorsal striatum. The present study builds on these earlier findings by directly quantifying DAergic innervation in the ventral striatum (i.e., nucleus accumbens, NAcc) and ventral pallidum (VP) with the goal of determining if greater DAergic transmission also extends to these regions as well. The NAcc is the ventromedial portion of the ventral striatum with afferent connections with the amygdala and regions of the prefrontal cortex (Haber and McFarland 1999; Haber et al. 1995, 2006). The VP, located ventral and adjacent to the anterior commissure, receives GABAergic projections from the ventral striatum and projects to additional brain regions that regulate motivation (e.g., Haber and Knutson 2010). The NAcc and VP are part of the reward system, with the NAcc playing a role in motivational and emotional responses to environmental stimuli and the VP involved in encoding the value of reward as well as the motor actions required to attain reward (e.g., Haber and McFarland 1999; Tachibana and Hikosaka 2012). Elevated DA in the NAcc has been linked to social conformity, compassion, and altruism (Filkowski et al. 2016; Klimecki et al. 2014; Klucharev et al. 2009; Stallen and Sanfey 2015). Higher levels of DA in the ventral striatum have also been linked to monogamy in some rodents (Aragona et al. 2006) and increased glucose uptake in both the NAcc and VP has been reported for pair-bonded versus lone male titi monkeys

(Bales et al. 2007). Monogamy in these species includes biparental care, aggression towards unfamiliar conspecifics, and pair bonding (i.e., partner preference, but not sexual fidelity) (e.g., Young et al. 1998; Young and Wang 2004).

Humans are among the few species that are characterized by social monogamy, a behavioral complex hypothesized to consist of elevated intragroup cooperation, habitual upright walking, and virtual elimination of the canine crown's capacity to either serve as a weapon or signal of aggressive intent (Lovejoy 1981, 2009, 2014). We anticipated that monogamous, or semi-monogamous, species within our sample (humans, tamarins, marmosets, and owl monkeys) would possess significantly higher DA within the VP compared to non-monogamous species. We further anticipated that humans would possess higher DA within the NAcc which could account for our uniquely high levels of social conformity and capacity for compassion and altruistic acts.

Materials and methods

Specimens

We processed postmortem brain samples from 50 individuals across nine primate genera. Subjects included platyrrhines (cotton-top tamarins, common marmosets, owl monkeys, and tufted capuchins), cercopithecids (pig-tailed and rhesus macaques), African great apes (chimpanzees and bonobos), and humans (see Table 1 for details). Sexes were balanced as much as possible. All individuals were adult, free of gross neuropathology. Nonhuman primates had been housed in accordance with their home institution's animal care and use standards. We obtained the human brain specimens from the Northwestern University Alzheimer's Disease Center Brain Bank and the NIH NeuroBioBank. All individuals were non-geriatric and free of neuropathological disease. We received whole brains or sections for nonhuman primates from the National Chimpanzee Brain Resource, The Great Ape Neuroscience Project, the Oregon National Primate Research Center, the Washington National Primate Research Center, the New England Regional Primate Research Center (Harvard University), Alpha Genesis, and various zoos. Brain samples were fixed by immersion in 10% buffered formalin for 7–10 days, then transferred to a solution of 0.1 M phosphate-buffered saline (PBS, pH 7.4) containing 0.1% sodium azide and stored at 4 °C until further processing.

Sample processing

All samples were cryoprotected in a graded series of sucrose solutions (10, 20, and 30%) prior to sectioning. The brain samples were rapidly frozen with dry ice and then sectioned at 40 µm using a freezing sliding microtome (SM2000R,

Table 1 Subjects included in analyses

Species	Common name	Sex	Age (years)	PMI	Sexual maturity	Longevity (years)
<i>Callithrix jacchus</i>	Common marmoset	M	4.5	–	11–24 months	22.8
<i>Callithrix jacchus</i>	Common marmoset	M	2.75	–	11–24 months	22.8
<i>Callithrix jacchus</i>	Common marmoset	M	6	–	11–24 months	22.8
<i>Callithrix geoffroyi</i>	Geoffroy's marmoset	M	5.7	–	11–24 months	17.6
<i>Callithrix geoffroyi</i> ^b	Geoffroy's marmoset	M	8.5	–	11–24 months	17.6
<i>Callithrix pygmaeus</i>	Pygmy marmoset	F	11.25	–	18–24 months	18.6
<i>Saguinus oedipus</i>	Cotton-top tamarin	M	10.9	–	18–24 months	26.2
<i>Saguinus oedipus</i>	Cotton-top tamarin	M	8.4	–	18–24 months	26.2
<i>Saguinus oedipus</i>	Cotton-top tamarin	M	9.5	–	18–24 months	26.2
<i>Saguinus oedipus</i>	Cotton-top tamarin	F	10	–	18–24 months	26.2
<i>Saguinus oedipus</i>	Cotton-top tamarin	F	10	–	18–24 months	26.2
<i>Saguinus oedipus</i>	Cotton-top tamarin	F	10	–	18–24 months	26.2
<i>Aotus trivirgatus</i> ^a	Northern owl monkey	M	>18	–	2 years	30.1
<i>Aotus</i> spp.	Owl monkey	M	18	–	2 years	27
<i>Aotus</i> spp.	Owl monkey	F	3	–	2 years	27
<i>Aotus vociferans</i>	Spix's night monkey	F	5	–	2 years	22.1
<i>Cebus apella</i>	Tufted capuchin	M	2.9	–	4–8 years	46
<i>Cebus apella</i>	Tufted capuchin	M	16.6	–	4–8 years	46
<i>Cebus apella</i>	Tufted capuchin	M	15.9	–	4–8 years	46
<i>Cebus apella</i>	Tufted capuchin	F	12.6	–	4–8 years	46
<i>Cebus apella</i>	Tufted capuchin	F	17.5	–	4–8 years	46
<i>Cebus apella</i>	Tufted capuchin	F	18.3	–	4–8 years	46
<i>Macaca mulatta</i>	Rhesus macaque	M	8	–	2.5–8 years	40
<i>Macaca mulatta</i>	Rhesus macaque	M	13	–	2.5–8 years	40
<i>Macaca mulatta</i>	Rhesus macaque	M	13	–	2.5–8 years	40
<i>Macaca mulatta</i>	Rhesus macaque	F	14	–	2.5–8 years	40
<i>Macaca mulatta</i>	Rhesus macaque	F	11	–	2.5–8 years	40
<i>Macaca mulatta</i>	Rhesus macaque	F	12.5	–	2.5–8 years	40
<i>Macaca nemestrina</i>	Pigtailed macaque	M	15.73	–	2.5–8 years	37.6
<i>Macaca nemestrina</i>	Pigtailed macaque	M	4.28	–	2.5–8 years	37.6
<i>Macaca nemestrina</i>	Pigtailed macaque	M	2.5	–	2.5–8 years	37.6
<i>Macaca nemestrina</i>	Pigtailed macaque	F	15.1	–	2.5–8 years	37.6
<i>Macaca nemestrina</i>	Pigtailed macaque	F	14	–	2.5–8 years	37.6
<i>Macaca nemestrina</i>	Pigtailed macaque	F	5.95	–	2.5–8 years	37.6
<i>Pan troglodytes</i>	Chimpanzee	M	19.8	–	7–9 years	59.4
<i>Pan troglodytes</i>	Chimpanzee	M	19.5	–	7–9 years	59.4
<i>Pan troglodytes</i>	Chimpanzee	F	30.8	–	7–9 years	59.4
<i>Pan troglodytes</i>	Chimpanzee	F	18.5	–	7–9 years	59.4
<i>Pan troglodytes</i> ^a	Chimpanzee	F	17.8	–	7–9 years	59.4
<i>Pan paniscus</i>	Bonobo	M	34	–	7–9 years	55
<i>Pan paniscus</i>	Bonobo	M	5	–	7–9 years	55
<i>Pan paniscus</i>	Bonobo	M	25	–	7–9 years	55
<i>Pan paniscus</i>	Bonobo	F	52	–	7–9 years	55
<i>Pan paniscus</i> ^a	Bonobo	F	25	–	7–9 years	55
<i>Homo sapiens</i>	Human	M	44	19		
<i>Homo sapiens</i>	Human	M	56	15		
<i>Homo sapiens</i>	Human	M	44	24		
<i>Homo sapiens</i>	Human	F	39	19		
<i>Homo sapiens</i>	Human	F	25	12		
<i>Homo sapiens</i>	Human	F	53	17		

Postmortem interval (PMI) is provided for humans. Specific PMI for nonhuman specimens was not available, but < 24 h. Average age for sexual maturity and lifespan are provided for nonhuman primates (Nowak 1999; AnAge Database, <https://genomics.senescence.info/species/index.html>)

^aOnly included in among-species analysis for NAcc

^bOnly included in among-species analysis for VP

Leica, Chicago, IL, USA). Each section was placed into an individual centrifuge tube containing freezer storage solution (30% each distilled water, ethylene glycol, and glycerol and 10% 0.244 M PBS), numbered sequentially, and then stored at -20°C until histological or immunohistochemical processing. Every tenth section was Nissl-stained to visualize the regions of interest for immunohistochemical staining and stereological quantification of neuron cell density.

Figures 1 and 2 show the two areas of interest for the present study: the NAcc, which comprises most of the ventral striatum and in this study we conservatively defined as the portion of the ventromedial striatum that is ventral and medial to the inferior border of the internal capsule in sections rostral to the appearance of the anterior commissure; the VP, which was traced in sections ventral and adjacent to the anterior commissure with readily discernable borders (Paxinos et al. 2000, 2012; Haber and McFarland 1999). We did not differentiate between the shell and core region of the NAcc in this study as TH does not provide clear boundaries between these regions (e.g., McCollum et al. 2016).

Immunohistochemistry

Sections that spanned the NAcc and VP for each subject were stained for tyrosine hydroxylase (TH), the rate-limiting enzyme for catecholamine synthesis, using the avidin–biotin–peroxidase method as described previously (Raganti et al. 2008, 2009, 2016). Briefly, sections were pretreated for antigen retrieval by incubating in 0.05% citraconic acid (pH 7.4) at 86°C in a water bath for 30 min. Sections were

then rinsed, and endogenous peroxidase was quenched using a solution of 75% methanol, 2.5% hydrogen peroxide (30%), and 22.5% distilled water for 20 min at room temperature. Sections were pre-blocked in a solution of 4% normal goat serum, 0.6% Triton X-100 detergent, 90.4% PBS, and 5% bovine serum albumin. Following this, sections were incubated in a rabbit anti-TH polyclonal antibody (Millipore, Bedford, MA, AB152, RRID 390204) diluted to 1:1000 for 24 h at room temperature followed by 24 h at 4°C . Sections were then incubated in a biotinylated secondary antibody (1:200) followed by the avidin–peroxidase complex (PK-6100, Vector Laboratories, Burlingame, CA) for 1 h at room temperature. A 3,3'-diaminobenzidine–peroxidase (DAB) substrate with nickel solution enhancement was used as the chromogen (SK-4100, Vector Laboratories).

Data acquisition

Quantitative analyses were performed using computer-assisted stereology on an Olympus BX-51 photomicroscope system equipped with a digital camera and StereoInvestigator software version 10 (MBF Bioscience, Williston, VT, USA). Subsampling techniques were performed for each species to determine appropriate sampling parameters. TH-immunoreactive (ir) axons were quantified using the SpaceBalls probe at 100x (N.A. 1.4) magnification under Koehler illumination using a hemisphere set at $7\text{ }\mu\text{m}$ with a 2% guard zone. Section thickness was measured at every fifth sampling site with an average mounted section thickness for immunostained sections being $23.9 \pm 8.2\text{ }\mu\text{m}$.

Fig. 1 Nissl-stained coronal sections showing the nucleus accumbens in capuchin (A, D), macaque (B, E), and chimpanzee (C, F). The regions outlined in A, B, and C are shown at higher resolution in D, E, and F, respectively. The NAcc sampled was conservatively estimated to avoid sampling within the ventral striatum, as the border between these regions is indistinct. *ac* anterior commissure, *C* caudate nucleus, *cc* corpus callosum, *ic* internal capsule, *P* putamen, *NAcc* nucleus accumbens. Scale bar = 1 cm for panels A, B, and C

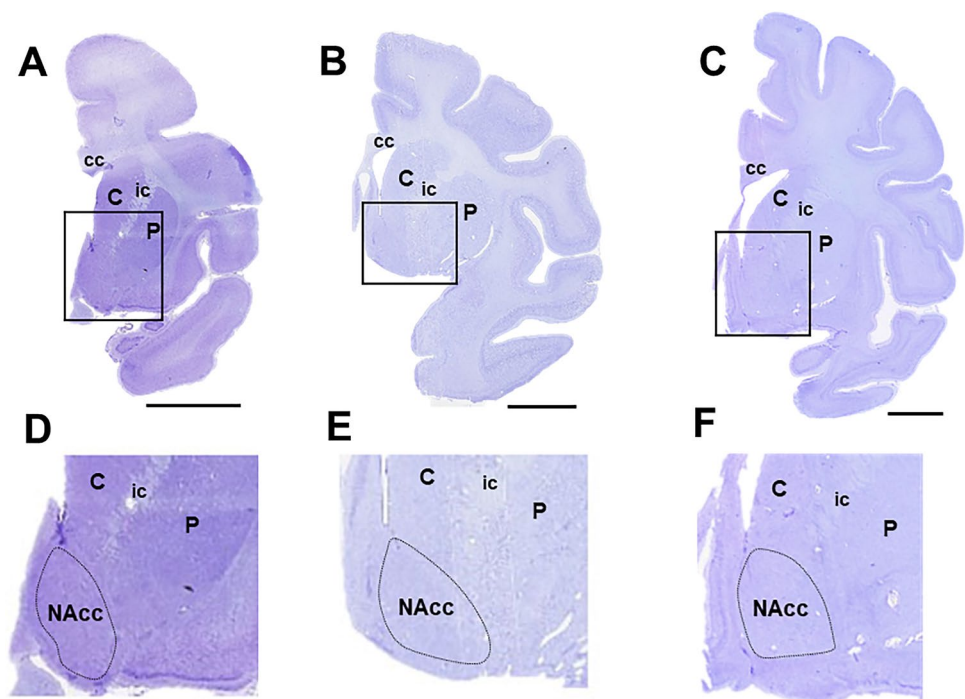
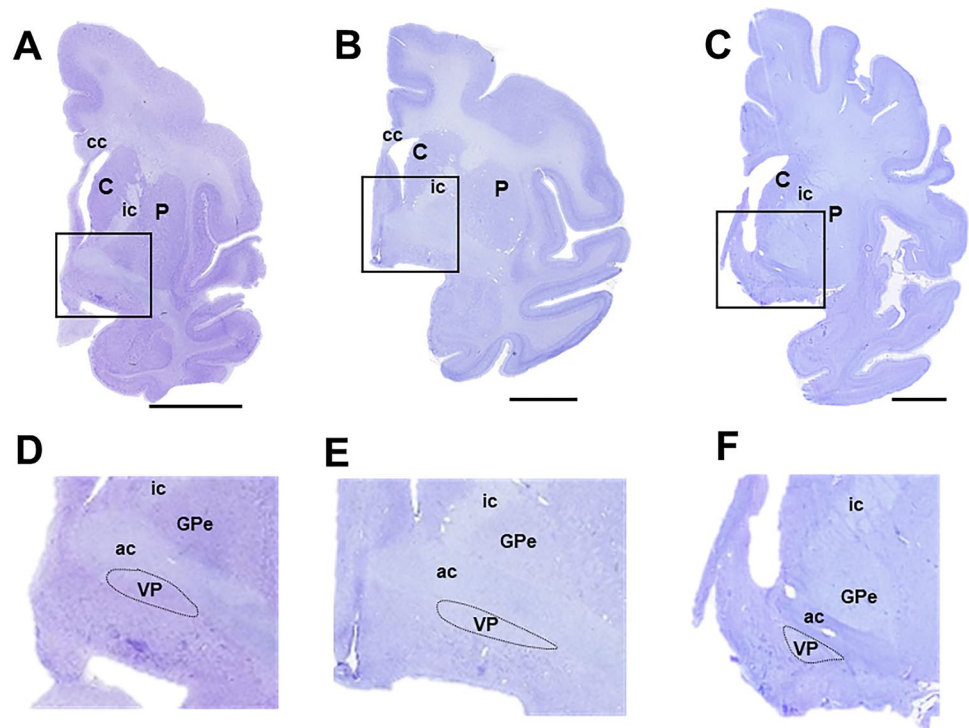


Fig. 2 Nissl-stained coronal sections showing the ventral pallidum (VP) in capuchin (A, D), macaque (B, E), and chimpanzee (C, F). The regions outlined in A, B, and C are shown at higher resolution in D, E, and F, respectively. *ac* anterior commissure, *C* caudate nucleus; *cc*, corpus callosum, *ic* internal capsule, *GPe* external globus pallidus, *P* putamen, *VP* ventral pallidum. Scale bar = 1 cm for panels A, B, and C



Sampling grids were optimized for each specimen, with an average grid of $496 \times 401 \mu\text{m}$ (range 106×66 – 1632×1092). Axons were marked, where they intersected the outline of the hemisphere. Axon length density (ALv) was calculated as the total fiber length (μm) divided by the planimetric measurement (μm^3) of the reference volume sampled. Based on subsampling results, three sections per region per individual were quantified to reliably provide coefficients of error of less than 0.10. The section sampling interval ranged from 1 in 5 for smaller brains to 1 in 20 for larger brains. The mean number of sampling sites in the NAcc per individual was 29 ± 5 (s.d.) with an average of 131 ± 38 axon intersections counted per region. The mean number of sampling sites in the VP per individual was 28 ± 6 with an average of 72 ± 40 axon intersections counted per region. The Gundersen coefficient of error (CE, $m = 1$) was 0.06 ± 0.03 .

Neuron density (Nv) and glial density (Gv) were assessed in adjacent Nissl-stained sections using the optical fractionator probe. While neuron densities were quantified for the purpose of standardizing the comparative data, glia densities were also collected at the same time. The ratio of glia to neurons (G/N) has been used to examine cell type composition across species and brain region (Sherwood et al. 2006). Nv and Gv are reported as the estimated population divided by the planimetric volume (μm^3). The NAcc and VP were outlined at $4\times$ magnification and neurons and glia were manually counted under a

$40\times$ objective (N.A. 0.75) with a counting frame of $50 \times 50 \mu\text{m}$. As there is a significantly large range in the size of the specimens in this comparative sample, sampling grids also varied in size with an average of $550 \times 459 \mu\text{m}$ (range 78×111 – 1280×1702). The optical disector height was $7 \mu\text{m}$ with a 2% guard zone. Section thickness was measured at every 5th sampling site and the average mounted section thickness for Nissl-stained sections was $13.4 \pm 4.9 \mu\text{m}$. The Gundersen CE ($m = 1$) was 0.07 ± 0.003 for Nv and 0.06 ± 0.01 for Gv. Neurons were identified by the presence of a large, lightly stained nucleus and a distinct nucleolus, accompanied by lightly stained dendritic processes. Glia cells do not possess a visible nucleolus or dendritic processes. Due to the difficulty in differentiating astrocytes, oligodendrocytes, and microglia in Nissl-stained sections, all glia were included. Nv and Gv were calculated as the sum of neurons or glia counted, respectively, within the sum of optical disectors divided by the product and volume of the disector (e.g., Sherwood et al. 2006).

Because the specimens included in this study are derived from species with vastly different brain sizes, we used the ratio of ALv/Nv for comparative analysis among species. Using neuron density as a denominator provides a variable that accounts for the fact that axons are innervating neurons regardless of brain size. In addition, glia densities (Gv) and glia-to-neuron ratios were evaluated for each region across species.

Statistical analysis

We used IBM SPSS software, TIBCO Statistica Academic and R to analyze the data. Among-species differences were evaluated using analysis of variance (ANOVA) in the NAcc and VP separately. The dependent variables were TH ALv/Nv, Nv, Gv, and glia-to-neuron ratio (G/N). A Brown–Forstye correction was applied when Levene’s test for homogeneity of variance was significant. Significant results were evaluated using Fisher’s least significant difference (LSD) post hoc tests. Prior to among-species analyses, separate independent sample *T* tests were used to test for differences between sexes in each species. The results from these analyses were non-significant ($p > 0.05$ for all); therefore, sexes were pooled.

Additional analyses to determine allometric scaling relationships with brain weight were performed using R studio software (R core Team, Vienna, Austria, version 4.0.2). Species mean data were evaluated using phylogenetic generalized least squares (PGLS) to calculate scaling slopes while accounting for the covariance structure of evolutionary relatedness. In these analyses, *Aotus* spp.

individuals were pooled with *Aotus trivirgatus*. Phylogenetic analysis of covariance (pANCOVA) was used to test whether human values were significantly different from what would be expected for their brain size (Smaers and Rohlf 2016). PGLS and pANCOVA were performed for NAcc and VP data separately. The dependent variables were TH ALv/Nv, Nv, Gv, and glia-to-neuron (G/N) ratio, while the independent variable was brain weight. The level of significance (α) was set at 0.05 for all statistical tests.

Results

Among-species analyses

TH ALv/Nv

Figures 3, 4, 5 and 6 provide examples of TH immunohistochemical staining of the NAcc and VP for all species. Immunostaining was robust for all individuals used in this study. Notably, there are differences among species and between regions for the number and size of TH-ir

Fig. 3 High-magnification photomicrographs of TH-ir axons in the NAcc in marmoset (A), tamarin (B) owl monkey (C), capuchin (D), rhesus macaque (E), pig-tailed macaque (F), chimpanzee (G), bonobo (H), and human (I). Scale bar in I = 25 μ m

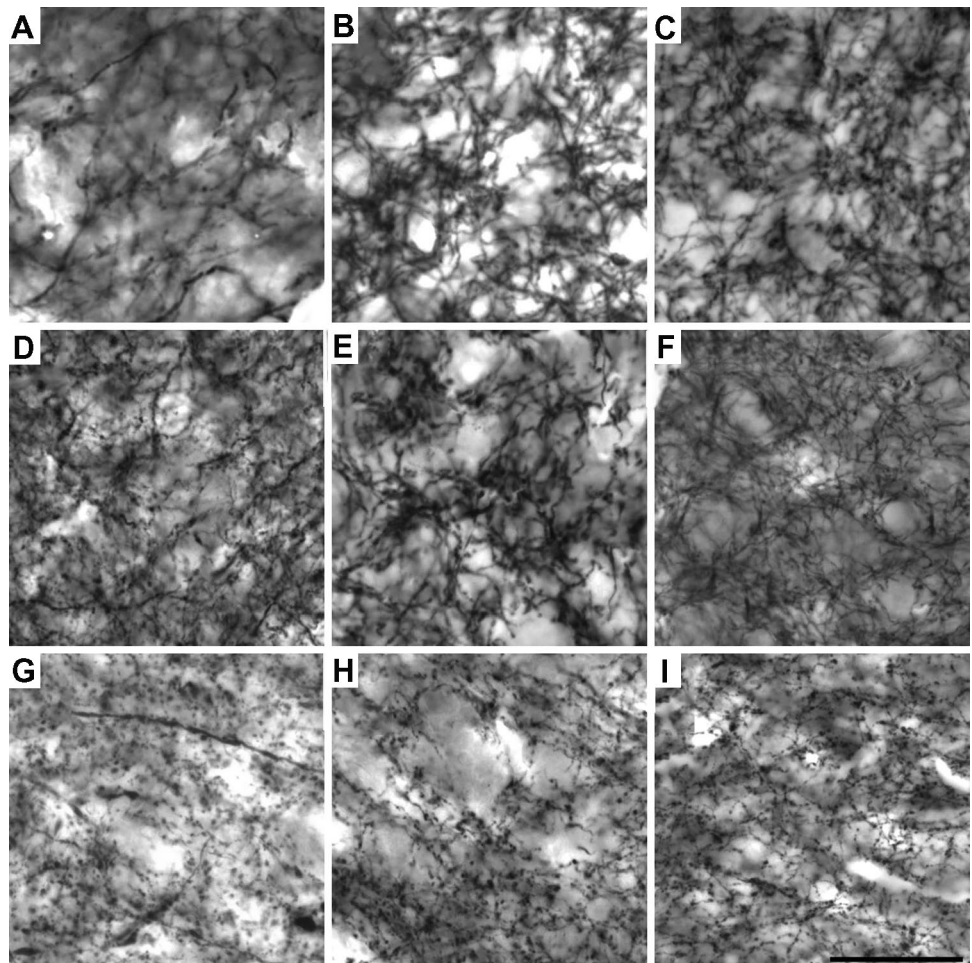
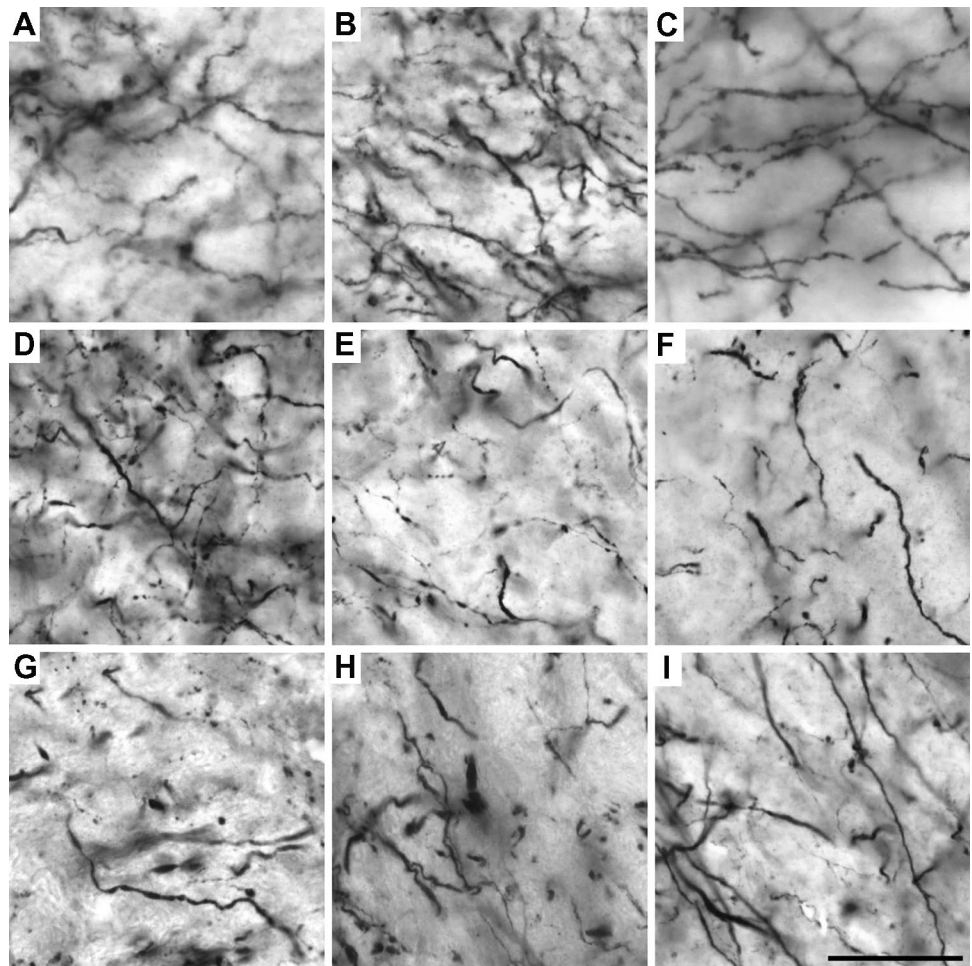


Fig. 4 High-magnification photomicrographs of TH-ir axons in the VP in marmoset (A), tamarin (B), owl monkey (C), capuchin (D), rhesus macaque (E), pig-tailed macaque (F), chimpanzee (G), bonobo (H), and human (I). Scale bar in I = 25 μ m



varicosities and axons. Generally speaking, axons were finer and with a higher concentration of smaller varicosities in the NAcc. TH-ir axons within the VP were thicker with larger, although more widely spaced, varicosities. Tables 2 and 3 provide summary data for all variables by species. ANOVA analysis revealed a significant difference among species for TH ALv/Nv in the NAcc ($F_{8,40}=6.25$, $p<0.025$; Fig. 7). Post hoc analyses indicated that humans possess significantly higher TH ALv/Nv in the NAcc relative to all nonhuman primate species ($p<0.05$ for all). Our next analysis used PGLS to examine allometric scaling of TH ALv/Nv against brain weight while accounting for phylogenetic relatedness in the comparative sample. The PGLS regression indicated a significant positive scaling relationship across the primates between TH ALv/Nv and brain weight for the NAcc ($df=10$, regression slope $b=0.24$, 95% CI 0.13–0.35, $p=0.0006$; Fig. 8). pANCOVA demonstrated that human TH ALv/Nv in the NAcc was significantly higher than expected from the overall primate scaling trend ($df=3$, $F=7.73$, $p=0.021$).

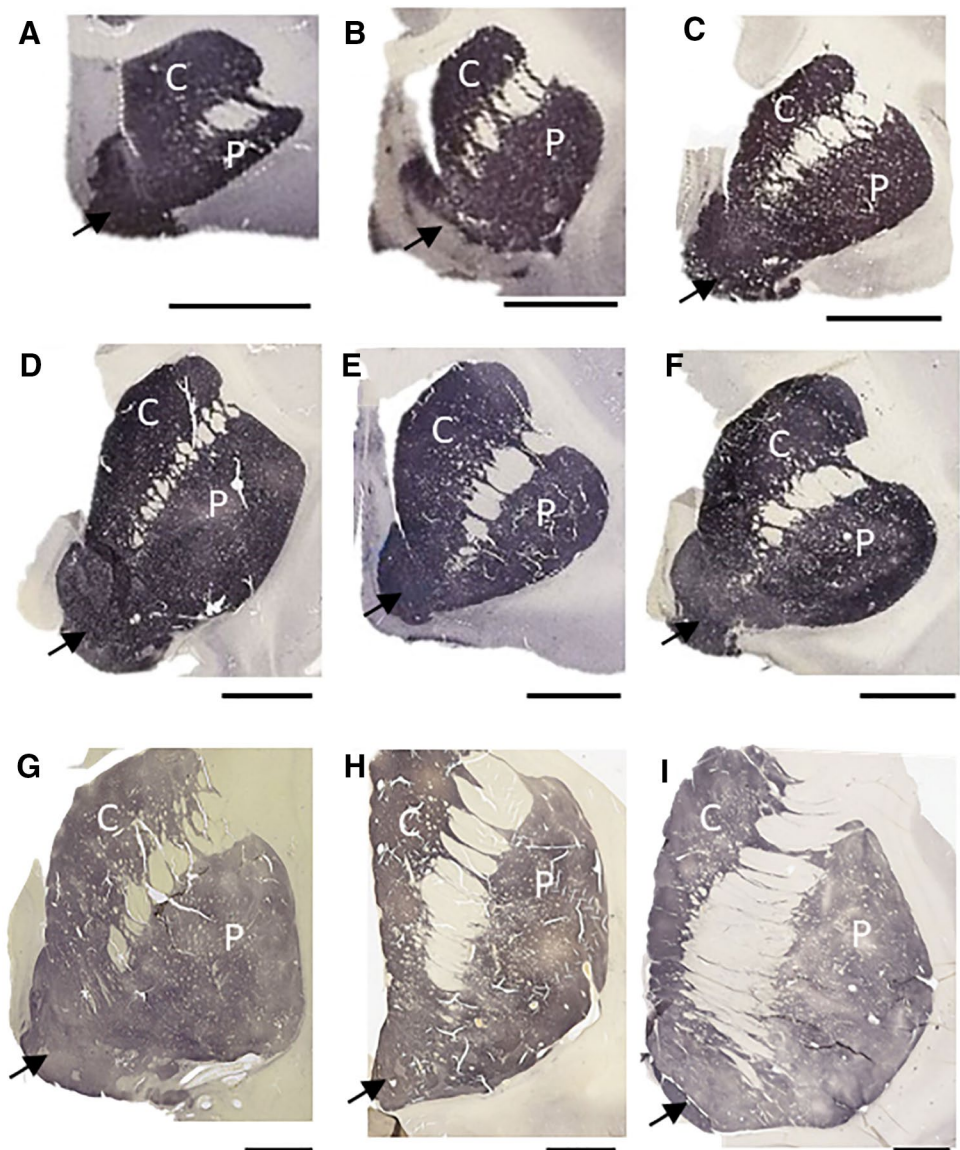
TH ALv/Nv in the VP was also significantly different among species ($F_{8,38}=5.35$, $p<0.025$; Fig. 7), with

humans having significantly higher ALv/Nv than non-human primate species ($p<0.05$ for all). PGLS analysis showed that TH ALv/Nv in the VP displayed a significant positive scaling relationship ($df=10$, regression slope $b=0.26$, 95% CI 0.17–0.36, $p=0.0001$; Fig. 8). Human TH ALv/Nv in the VP was relatively high, with pANCOVA finding the human value approaching a conventional level for statistical significance in deviating from primate scaling predictions ($df=3$, $F=3.84$, $p=0.082$).

Neurons and Glia

NAcc Nv results revealed a significant difference among species ($F_{8,40}=4.60$, $p<0.025$; Fig. 7). Post hoc analyses indicated that marmosets possessed significantly higher neuron density than all other species. Humans possessed significantly lower neuron density compared to tamarins, bonobos, and owl monkeys. A significant effect of species was also detected for VP Nv ($F_{8,38}=7.98$, $p<0.025$; Fig. 7). Post hoc analyses showed that marmosets have higher neuron densities relative to all species except owl monkeys (all p values <0.05). Owl monkeys have higher

Fig. 5 Low-power photomicrographs showing TH-immunostained sections containing the NAcc. The NAcc is indicated by arrows. Note that there is not an obvious distinction between the shell and core regions of the NAcc. *C* caudate nucleus, *P* putamen. Scale bars = 0.5 cm



densities relative to capuchins and all catarrhines (all p values < 0.05). Tamarins display significantly increased neuron density compared to pig-tailed macaques, bonobos, and humans. Capuchins exhibit a significantly lower neuron density than did other platyrrhines. No differences were detected among catarrhines (all p values > 0.05). Interestingly, a species difference was not detected for NAcc Gv ($F_{8,40} = 1.348$, $p > 0.025$; Fig. 7) or VP Gv ($F_{8,38} = 1.790$, $p > 0.025$; Fig. 7).

NAcc G/N ratio analyses revealed significant differences among species ($F_{8,40} = 3.233$, $p < 0.025$; Fig. 7). Post hoc analyses indicated that humans displayed a significantly higher G/N ratio than all other species except capuchins. Capuchins had a significantly higher G/N ratio than all other platyrrhine monkeys. VP G/N analyses were significantly different among species ($F_{8,38} = 4.28$, $p < 0.025$; Fig. 4).

Humans possess a significantly higher G/N ratio than all other species except pig-tailed macaques and bonobos. Both species display a higher G/N ratio compared to all platyrrhines.

PGLS analyses (Fig. 9) indicated significant negative scaling between Nv and brain weight in the NAcc ($df = 10$, regression slope $b = -0.19$, 95% CI -0.31 to -0.07 , $p = 0.0062$) and the VP ($df = 10$, regression slope $b = -0.29$, 95% CI -0.42 to -0.15 , $p = 0.0009$). In contrast, there was no relationship between Gv and brain weight in the NAcc ($df = 10$, regression slope of $b = 0.02$, 95% CI -0.08 to 0.13 , $p = 0.6374$) or the VP ($df = 10$, regression slope $b = -0.07$, 95% CI -0.16 to 0.02 , $p = 0.0964$). The G/N ratios in each region, consequently, displayed positive allometric scaling: NAcc ($df = 10$, regression slope $b = 0.40$, 95% CI 0.23 – 0.57 , $p = 0.0003$)

Fig. 6 Low-power photomicrographs showing TH-immunostained sections containing the VP. The VP is indicated by arrows and is easily identifiable in all sections with its distinct borders. *C* caudate nucleus, *P* putamen, *ac* anterior commissure. Scale bars = 0.5 cm

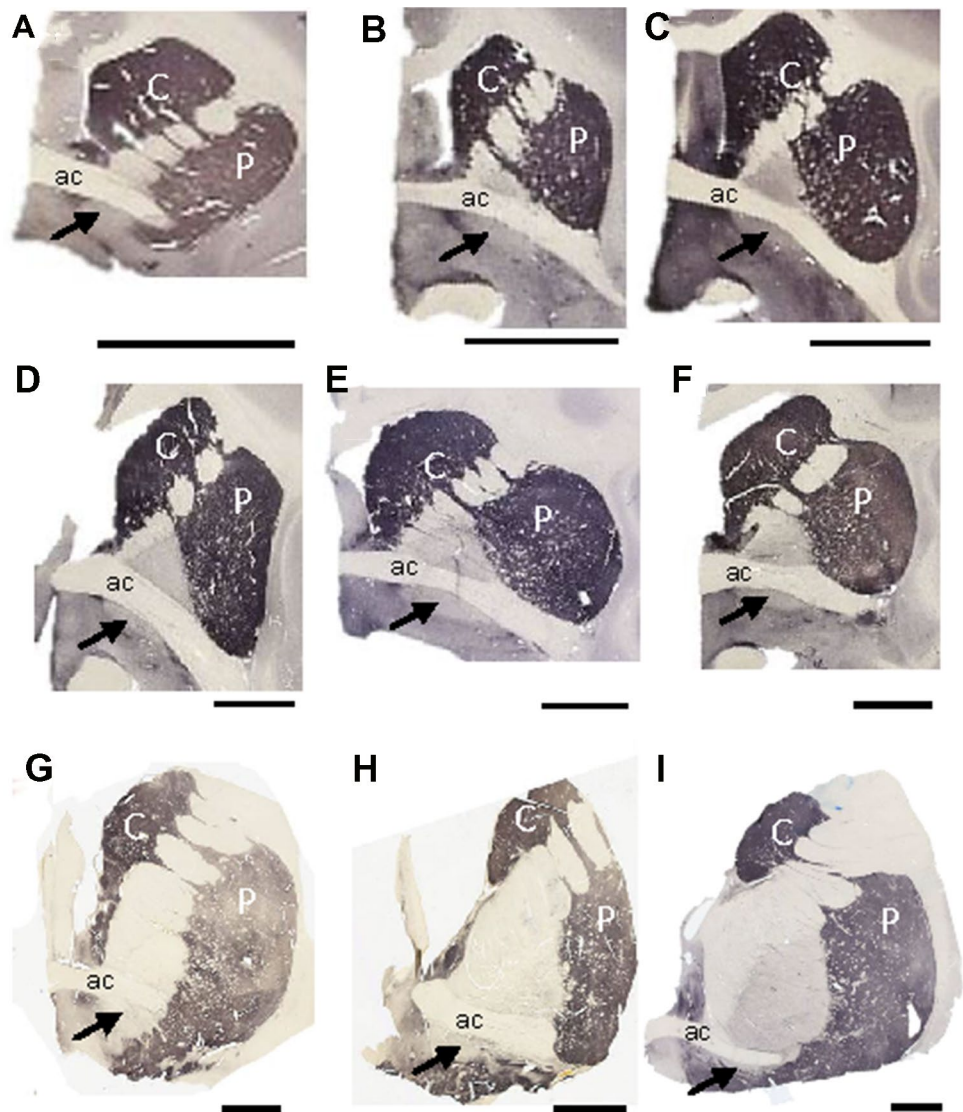
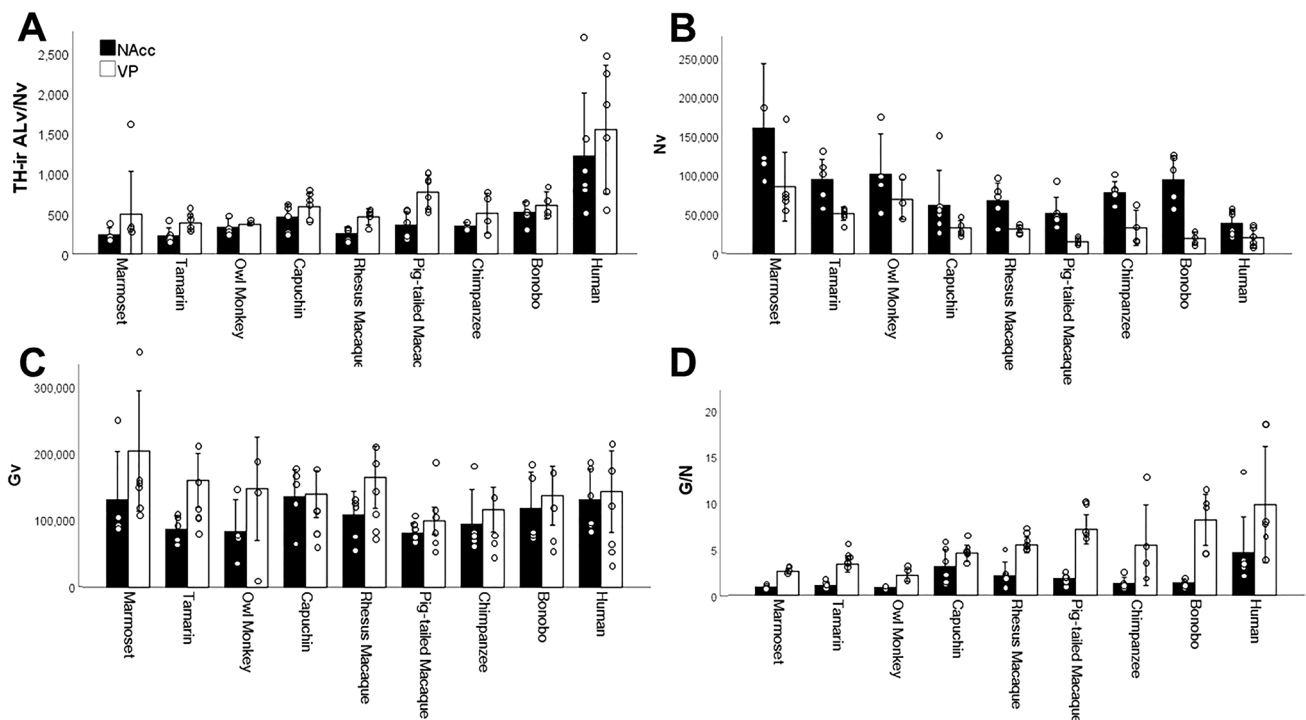


Table 2 Summary data for TH axon length density (ALv), neuron density (Nv), TH ALv/Nv, glia density (Gv), and glia to neuron ratio (G/N) for each species in the nucleus accumbens (NAcc)

Genus	TH ALv ($\mu\text{m}/\mu\text{m}^3$)	Nv (neurons/ μm^3)	TH ALv/Nv	Gv (glia/ μm^3)	G/N
<i>Callithrix</i> spp.	35,359,503 \pm 13,126,716	159,788 \pm 81,939	241.29 \pm 90.13	133,260 \pm 73,634	.85 \pm .15
<i>Saguinus oedipus</i>	20,456,808 \pm 6,463,875	94,391 \pm 25,711	229.34 \pm 99.55	88,419 \pm 20,584	1.02 \pm .43
<i>Aotus</i> spp.	30,569,387 \pm 7,253,895	101,139 \pm 51,251	337.91 \pm 109.9	84,868 \pm 48,672	.81 \pm .10
<i>Cebus apella</i>	29,610,015 \pm 15,075,605	61,559 \pm 44,520	467.69 \pm 167.4	137,895 \pm 41,112	3.00 \pm 1.76
<i>Macaca mulatta</i>	17,766,455 \pm 7,115,746	67,524 \pm 22,498	256.58 \pm 84.69	110,359 \pm 35,704	2.01 \pm 1.44
<i>Macaca nemestrina</i>	17,355,095 \pm 7,203,398	51,287 \pm 20,536	363.78 \pm 172.9	82,575 \pm 15,091	1.74 \pm .51
<i>Pan troglodytes</i>	26,979,932 \pm 2,958,398	77,714 \pm 14,057	352.70 \pm 47.35	96,138 \pm 52,820	1.24 \pm .62
<i>Pan paniscus</i>	47,311,086 \pm 13,961,461	94,127 \pm 30,620	526.67 \pm 135.1	120,157 \pm 55,220	1.30 \pm .40
<i>Homo sapiens</i>	38,852,153 \pm 10,445,364	38,804 \pm 17,699	1242.2 \pm 801.5	133,250 \pm 47,120	4.43 \pm 3.73

Table 3 Summary data for TH axon length density (ALv), neuron density (Nv), TH ALv/Nv, glia density (Gv), and glia to neuron ratio (G/N) for each species in the ventral pallidum (VP)

Genus	TH ALv ($\mu\text{m}/\mu\text{m}^3$)	Nv (neurons/ μm^3)	TH ALv/Nv	Gv (glia/ μm^3)	G/N
<i>Callithrix</i> spp.	38,424,091 \pm 35,379,311	82,282 \pm 43,706	502.97 \pm 545.66	207,626 \pm 91,768	2.49 \pm .27
<i>Saguinus oedipus</i>	19,557,066 \pm 4,767,129	51,120 \pm 8,495	391.60 \pm 112.07	162,862 \pm 41,059	3.23 \pm .83
<i>Aotus</i> spp.	25,716,375 \pm 8,383,588	69,253 \pm 25,266	374.53 \pm 17.37	150,104 \pm 78,724	2.08 \pm .66
<i>Cebus apella</i>	19,984,428 \pm 8,288,468	33,029 \pm 9,107	598.78 \pm 169.3	141,935 \pm 35,705	4.39 \pm .84
<i>Macaca mulatta</i>	14,832,980 \pm 4,566,302	31,472 \pm 4,827	468.96 \pm 103.66	167,385 \pm 47,208	5.25 \pm .83
<i>Macaca nemestrina</i>	11,345,480 \pm 2,104,688	15,333 \pm 4,712	783.93 \pm 215.62	101,138 \pm 20,833	6.87 \pm 1.52
<i>Pan troglodytes</i>	12,877,586 \pm 1,564,131	32,984 \pm 22,449	515.25 \pm 252.51	118,253 \pm 34,197	5.21 \pm 4.20
<i>Pan paniscus</i>	11,379,280 \pm 3,935,412	19,540 \pm 7,938	615.71 \pm 171.88	139,552 \pm 44,864	7.84 \pm 2.66
<i>Homo sapiens</i>	24,707,901 \pm 10,494,620	20,522 \pm 12,709	1579.37 \pm 817.6	145,732 \pm 62,153	9.44 \pm 6.05

**Fig. 7** Bar graphs showing mean TH-ir ALv/Nv (TH-ir positive axon length density/neuron density; **A**), Nv (estimated neuron population/planimetric volume in μm^3 ; **B**), Gv (estimated glia population/planimetric volume in μm^3 ; **C**), and glia to neuron (G/N) ratio (**D**) in the NAcc and VP by species. The open circles represent individual values. Error bars show ± 1 SD

and VP ($df=10$, regression slope of $b=0.21$, 95% CI 0.11–0.32, $p=0.001$). pANCOVA analysis indicated that humans do not differ from the overall primate trend in neuron and glia densities of NAcc and VP, or for G/N ratio in VP. However, the human G/N ratio in the NAcc did depart significantly from the overall primate trend in being elevated ($df=3$, $F=6.35$, $p=0.033$).

metric volume in μm^3 ; **C**), and glia to neuron (G/N) ratio (**D**) in the NAcc and VP by species. The open circles represent individual values. Error bars show ± 1 SD

Discussion

DA transmission in the ventral striatum, and specifically in the NAcc, plays a major role in behavioral flexibility. It is important to note that in many studies, the ventral striatum and NAcc are treated as the same structure although there are clear distinctions between the two regions (e.g., Haber and McFarland 1999; Haber et al. 2006). The ability to

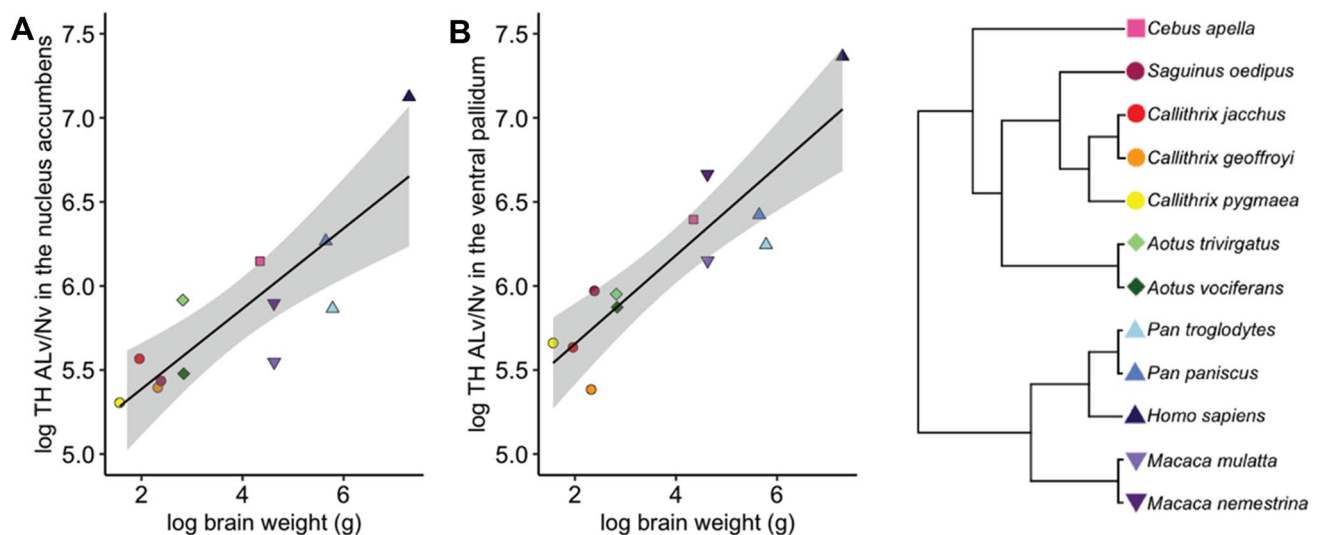


Fig. 8 PGLS regressions of TH ALv/Nv (TH-ir positive axon length density/neuron density) against brain weight shown with 95% confidence intervals for nucleus accumbens (A) and ventral pallidum (B).

The phylogenetic tree in this figure provides the color/shape legend for species values in all plots of PGLS analyses

evaluate different levels of reward, especially those involving value versus risk, as well as simultaneously reducing the likelihood of adverse outcomes, are essential components of developing goal-directed behavior, especially in the context of group living (Haber 2014). DA released from the VTA into the NAcc mediates incentive salience, especially the motivation to behave in a particular way in response to certain stimuli (Báez-Mendoza et al. 2013; Báez-Mendoza and Schultz 2013). Although the roles of DAergic pathways in modulating cognition, social behavior, and personality in both human and other primates are yet to be fully explored, these systems likely impact social organization, reproductive strategies, and foraging patterns.

Here, we present the results of a comparative analysis of DAergic innervation, Nv, Gv, and G/N ratios in the NAcc and VP in a large sample of haplorrhine primates, including humans. Consistent with previous reports that examined other brain regions in comparative samples of mammals, we found an inverse relationship between neuron density and brain weight and no correlation of glia density with brain size (e.g., Haug 1987; Herculano-Houzel 2014; Sherwood et al. 2006; see Fig. 9). G/N ratios increased allometrically with brain weight in both areas and these scaling patterns were similar to what has been reported for cortex. Interestingly, humans possessed a significantly increased G/N ratio within the NAcc relative to the other primates in our sample (see Fig. 7). This resulted from a combination of both decreased neuron density and increased glia density within this region. Classically, the G/N ratio has been considered to be a measure of metabolic support (Hawkins and Olszewski 1957); however, it is possible that developmental constraints

and variation in neuron size may drive inter-species differences (Herculano-Houzel 2014).

Humans were also distinguished in having significantly higher DAergic innervation in both the VP and NAcc compared to other primates (see Figs. 7 and 8), even while accounting for overall brain size and phylogenetic relatedness in our comparative sample. This pattern is consistent with the uniquely human neurochemical profile previously reported for the dorsal striatum, suggesting evolutionary reorganization of the human striatum (Raghanti et al. 2018). This unique striatal neurochemistry includes increases in TH-containing neurons and axons in the dorsal and middle caudate nucleus, and differential expression of multiple DA-related genes compared to those in rodents and nonhuman primates (Inoue-Murayama et al. 2002; Miller and Madras 2002; Raghanti et al. 2018; Sousa et al. 2017). The increased G/N ratio of human NAcc, a region critical to the brain's reward pathway, combined with greater DAergic innervation, may prove to have played a significant role in our unique vulnerability to addiction and psychiatric disorders, including depression and anxiety (Calvey 2019; Mavridis 2015).

We originally anticipated that humans and other monogamous and semi-monogamous primates would share increased DA within one or both regions of interest based on previous studies conducted in rodent species (Aragona et al. 2006; Curtis et al. 2006). However, owl monkeys, marmosets, and tamarins did not exhibit increased DA relative to non-monogamous species in our study. While this deviates from what we expected from work conducted in prairie voles, it is consistent with what has been reported for titi monkeys (*Callicebus cupreus*). Hostetler (2017)

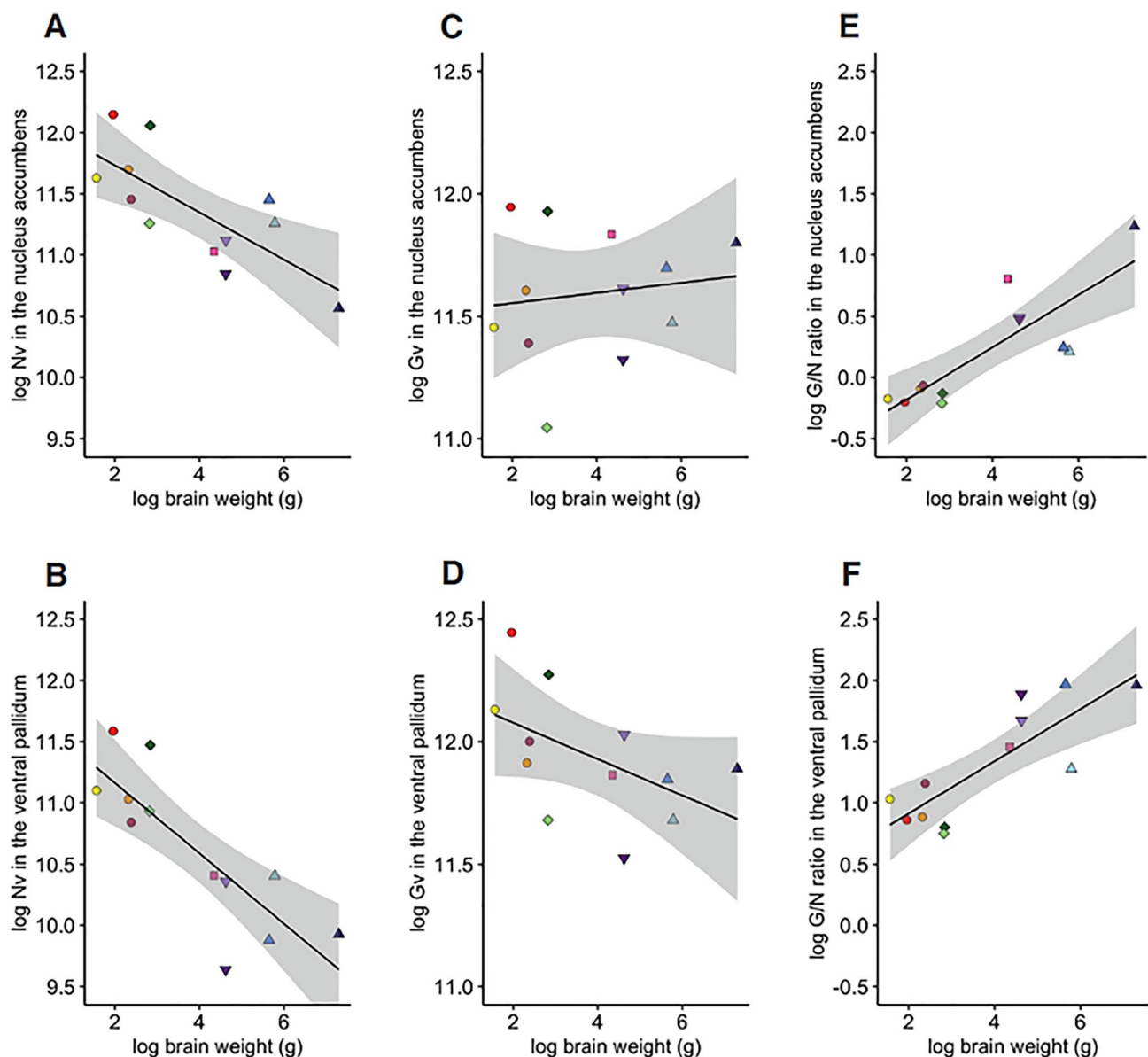


Fig. 9 PGLS regressions against brain weight shown with 95% confidence intervals for Nv (estimated neuron population/planimetric volume in μm^3) in the nucleus accumbens (A) and ventral pallidum (B), Gv (estimated glia population/planimetric volume in μm^3), in

the nucleus accumbens (C) and ventral pallidum (D), and G/N ratio in the nucleus accumbens (E) and ventral pallidum (F). The phylogenetic tree in this figure provides the color/shape legend for species values in all plots of PGLS analyses

examined DA binding (to the D1 receptor) in male titi monkeys after their pairing with a female and found an increase in the lateral septum, but not in the NAcc or other regions implicated in the prairie vole model of monogamy. While features of the neuroanatomical substrates that regulate monogamy are likely conserved among mammals (Young and Wang 2004), these results highlight the need for further development of nonhuman primate and other models for gaining a more comprehensive understanding of how neurobiology modulates behaviors across species (Phillips et al. 2014; Preuss 2019). In particular, our ability to

distinguish whether monogamous marmosets, tamarins, and owl monkeys display a particular DAergic profile in the NAcc and ventral pallidum would have been improved if we had additional non-monogamous platyrrhine primates besides capuchins for our outgroup comparisons. Furthermore, inclusion of monogamous primate species phylogenetically closer to humans (e.g., gibbons and siamangs) may provide additional resolution.

We previously argued that a change in neurochemistry, including a more DA-dominated striatum, may have been pivotal in the evolution of the human lineage by supporting

an increased sensitivity to social and environmental cues as well as decreased within-group aggression (Raghanti et al. 2018). Such changes may have been coincident with the emergence of bipedality and the reduction of the canine (the social tooth) > 4 million years ago (e.g., Holloway 1967; Lovejoy 2009). The sectorial canine complex refers to the continual honing of the upper canine's critical shearing capacity that maintains it as a potential weapon (e.g., Holloway 1967; Lovejoy 2009). The striatum plays a major role in social behaviors, particularly those involved in social reward (e.g., Baez-Mendoza et al. 2013). Research in nonhuman primates, rodents, and cats has demonstrated that relative activity levels of dorsal versus ventral striatal regions contributes to individual personality style (e.g., exploratory behaviors, sensitivity to social and environmental cues, extraversion, etc.) (see van den Bos 2015; Van der Bercken and Cools 1982 for reviews). Individuals with increased relative activity in the dorsal striatum were more internally motivated with a high degree of autonomy and a more superficial knowledge of their environment, and were more aggressive, dominant, and less responsive to social events. Individuals with increased activity in the ventral striatum were less aggressive and more externally driven, with a greater interest in their environment. They were also highly responsive to social stimuli (reviewed in van den Bos 2015; Van der Bercken and Cools 1982).

Striatal neurochemistry has been linked to behaviors that are associated with these 'personality styles', including exploratory behaviors, sensitivity to social and environmental cues, and extraversion (e.g., Bergey et al. 2016; Cools et al. 1975; Jolly et al. 2008; Jolly et al. 2013; Higley et al. 1996; Raleigh et al. 1991; Rilling and Sanfey, 2011; Tanaka et al. 2004; Tanaka et al. 2007; Van den Bercken and Cools 1982). Increased DA shifts activity to the ventral striatum and its associated personality style, while decreased DA shifts activity to the dorsal striatum and its associated behaviors. Individual variation in personality styles and their effects on potential cooperative interaction could have been targets of selection in early human ancestral populations. Enhanced awareness of habitat, decreased aggression, and elevated social conformity are all associated with a DA-dominated striatum personality style, and each could have improved survivorship and reproductive success, thus ultimately undergoing strong selection (Raghanti et al. 2018). Moreover, further expansion of this personality style may have provided the cognitive flexibility and social intelligence underlying not only acquisition of language and speech, but also a strong tendency towards social conformity, altruism, and empathy—the suite of extraordinary characters that have come to define human uniqueness.

While personality style and social behaviors can be linked to current experimental data from primate and rodent species, it is important to note that these postmortem analyses cannot definitively link specific cognitive or behavioral characteristics with innervation patterns. This level of interpretation will require future research to allow a more complete understanding of the neuroanatomical bases of human versus nonhuman behaviors.

Acknowledgements This research was funded by the National Science Foundation (NSF BCS-1846201 to MAR and SMA-1542848 and EF-2021785 to CCS and WDH). Elaine Miller was supported by the National Science Foundation Graduate Research Fellowship Program (1746914). We would like to thank Dr. Richard S. Meindl for statistical advice. We are grateful to each of the following for the use of brain materials: The NIH NeuroBioBank, National Chimpanzee Brain Resource (NIH grant NS092988), NINDS Grants NS-402867 and NS0-73134, The Great Ape Aging Project (supported by NIH Grant AG014308), the National Primate Research Center at the University of Washington (NIH grant RR000166), the Oregon National Primate Research Center (NIH P51 OD011092), the Northwestern University Alzheimer's Disease Center Brain Bank (supported by Alzheimer's Disease Core Center Grant AG013854, from the National Institute on Aging to Northwestern University, Chicago, IL).

Author contributions KH and MAR contributed to the study conception and design. Material preparation, data collection and analysis were performed by KH, EM, CDS, KAP, WDH, PRH, CCS, COL, and MAR. The first draft of the manuscript was written by KH and MAR and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

Funding This research was funded by the National Science Foundation (NSF BCS-1846201 to MAR and SMA-1542848 and EF-2021785 to CCS and WDH). Elaine Miller was supported by the National Science Foundation Graduate Research Fellowship Program (1746914).

Availability of data and materials All raw data are available and will be posted in the National Chimpanzee Brain Resource website data repository (<https://www.chimpanzeebrain.org/data-repository>) and can be requested from the corresponding authors.

Code availability NA.

Declarations

Conflict of interest None.

Ethics approval Human postmortem brain samples meet the criteria for IRB Exemption 4 under DHHS regulations 45 CFR 46 (46.101). Because no living subjects are involved in this research, this proposal does not qualify for IACUC oversight. However, when alive, all nonhuman primates were housed at research or zoological institutions and were maintained in accordance with each institution's animal care and use guidelines.

Consent to participate NA.

Consent for publication NA.

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