**Electronic Supplemental Material:**

**Living in stable**

**social groups is associated with reduced brain size in woodpeckers (*Picidae*)**

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**ESM1**

Additional details of method: Measurement of specimens

Brain volumes were measured by filling the endocranial cavity with yellow mustard seeds through the foramen magnum; all foraminae were plugged using Groomstick. The seeds were subsequently weighed and volumes constructed using a weight-volume curve. This method has been shown to have strong correlations with measures of fresh brain volume (1) and is not subject to changes caused by freezing, desiccation or perfusion (2). Where the original weight was recorded with the museum specimen, this was used; otherwise the mean body mass values from the CRC handbook of avian body masses (3) were used. Measurements for *Mulleripicus pulverulentus* were kindly provided by staff at the Smithsonian National Natural History Museum and the Delaware Natural History Museum.

Social systems of “Group-living” woodpeckers

In some cases, the relationships among group members are unknown, beyond their prolonged associations (e.g. *Sasia africana*, *Picus erythropygius*) or tendency to nest in loose colonies (*Colaptes campestris, Melanerpes striatus*). Helpers at the nest are described in *Picoides borealis*, where a breeding site in a coniferous tree is defended by drilling holes in the trunk, producing a sheet of resin over the trunk which cannot be climbed by snakes. Both *Melanerpes flavifrons* and *M.cruentatus* are cooperative breeders, often nesting in loose colonies with sometimes several adult helpers at a nest. Cooperation reaches a peak in *Melanerpes formicivorus*, the Acorn Woodpecker of the USA, which nests colonially and where up to 10 helpers have been recorded at a nest, both polygynous and polygynandrous breeding is found, and in which groups amass and defend “granaries” of up to 50,000 acorns pushed into holes they excavate in a dead tree.

**Additional analysis using Bayesian Markov-Chain Monte Carlo (MCMC) methods**

Using a maximum clade credibility tree to conduct PGLS regression analyses does not account for the possibility of phylogenetic uncertainty, which requires Bayesian methods [1]. In order to check the robustness of our results while accounting for phylogenetic uncertainty, we re-ran our main PGLS analyses across the complete posterior sample of 3000 phylogenies using Bayesian Markov chain Monte Carlo (MCMC) methods in BayesTraits (Version 2, [2,3]). We estimated the posterior probability distributions for parameters including regression coefficients (β), model R2 and phylogenetic signal (λ). We report average values for parameters and the percentage of posterior estimates above (+ve) or below (-ve) zero (we report whichever of these two percentages was greatest). We determined *a priori* that >97.5% of posterior estimates for regression coefficients above or below zero would be interpreted as ‘strong evidence’ for a statistical relationship between variables (equivalent to a 2-tailed test at the 5% level). As for our main analyses using PGLS regression, we used log-transformed brain volume as the dependent variable, social organization as a categorical independent variable on three levels (solitary, pair living, group living), and a log-transformed measure of body size was included as a covariate to adjust for allometric scaling effects on brain size.

We ran the MCMC chains for 2,000,000 iterations, sampling every 500 generations, following a burnin period of 50,000 iterations. Uninformative uniform prior distributions were used for regression coefficients (-100, +100). Acceptance rates were auto-fitted, chains were visually inspected for convergence, and all effective sample sizes were >2500. As in the PGLS regression, we found strong evidence for reduced brain volume relative to body size in group living species relative to solitary species (average β: -0.08, 99% β -ve). The evidence for reduced brain volume in group living species relative to pair living species did not exceed our *a priori* defined threshold for strong evidence, but did receive 93% posterior support (average β: -0.06, 93% β -ve), and we did not find strong evidence of a difference in brain volume between pair living species relative to solitary species (average β: -0.02, 74% β -ve). As reported in the main analysis, there was an overall negative trend between brain volume and social complexity. There was also strong evidence that body weight predicted brain volume (average β: 0.67, 100% β +ve). The model R2 was 0.78 and phylogenetic signal (λ) was estimated as 0.73.

1 Rubolini, D., Liker, A., Garamszegi, L. Z., Møller, A. P., & Saino, N. (2015). Using the BirdTree. org website to obtain robust phylogenies for avian comparative studies: A primer. *Current Zoology*, *61*(6), 959-965.

2 Pagel, M., & Meade, A. (2006). Bayesian analysis of correlated evolution of discrete characters by reversible‐jump Markov chain Monte Carlo. *The American Naturalist*, *167*(6), 808-825.

3 Pagel, M., & Meade, A. 2014 BayesTraits (Version 2.0). Reading, UK. [www.evolution.rdg.ac.uk](http://www.evolution.rdg.ac.uk)