**Palm functional trait responses to local environmental factors in the Colombian Amazon**

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**SUPPLEMENT 4**



**Figure 1**. Distribution of trait values across the tips of a phylogeny obtained from Faurby et al. (2016). LF: lifeform (⭘ : solitary, ⚫ :cespitose); GF: growth form (⚫ : erect, ⭘ : acaulescent, 🞎 : climbing); StH: maximum stem height; LN: maximum number of leaves; RL: maximum leaf rachis length; PeL: maximum petiole length; FD: maximum fruit diameter; SN: seed number. For continuous traits, circle sizes are scaled linearly between minimum and maximum trait values. The phylogeny is represented as 150 randomly sampled trees from the posterior distribution provided by Faurby et al. (2016). Scale bar in million years.

**Table 1.** Phylogenetic signal of the included traits (LF: lifeform; GF: growth form; StH: maximum stem height; LN: maximum number of leaves; RL: maximum leaf rachis length; PeL: maximum petiole length; FD: maximum fruit diameter; SN: seed number). For categorical traits, phylogenetic signal was calculated as the deviation of observed mean pairwise phylogenetic distance from a null distribution, which was generated by randomly reshuffling taxon names 999 times. For continuous traits, phylogenetic signal was calculated as Blomberg’s K (Blomberg & Garland 2002), compared to a null distribution generated by randomly reshuffling taxon names 999 times. All analyses were carried out for 1000 phylogenetic trees sampled from the posterior distribution of trees of Faurby et al. (2016). 95% HPD refers to the boundaries of the 95% highest posterior density interval of the values inferred across the 1000 sampled trees.

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| **Trait** | **MPD Z-score(mean [95% HPD])** | **Blomberg’s K (mean [95% HPD])** | **P (mean [95% HPD])** |
| LF: cespitose | -2.78 [-2.91 – -2.64] | - | **0.005** [**0.002** – **0.009**] |
| GF: climbing | -2.86 [-3.05 – -2.17] | - | **0.002** [**0.001** – **0.003**] |
| GF: acaulescent | 0.37 [0.30 – 0.43] | - | 0.708 [0.678 – 0.735] |
| StH | - | 0.28 [0.15 – 0.43] | 0.203 [**0.005** – 0.546] |
| LN | - | 0.35 [0.17 – 0.49] | 0.091 [**0.001** – 0.335] |
| RL | - | 0.79 [0.53 – 1.08] | **0.009** [**0.001** – **0.014**] |
| PeL | - | 0.56 [0.40 – 0.75] | **0.007** [**0.001** – **0.008**] |
| FD | - | 0.25 [0.15 – 0.38] | 0.275 [0.054 – 0.571] |
| SN | - | 1.88 [1.72 – 2.02] | **0.001** [**0.001** – **0.002**] |

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**Figure 2.** Metacommunity phylogenetic signal of the studied traits (LF: lifeform; GF: growth form; StH: maximum stem height; LN: maximum number of leaves; RL: maximum leaf rachis length; PeL: maximum petiole length; FD: maximum fruit diameter; SN: seed number). Circles and solid black lines show the observed R2 of a model relating community averaged trait values to an increasing number of phylogenetic eigenvectors. Categorical traits were coded as 1 for the focal state (e.g. cespitose habit) and 0 otherwise. Solid grey lines show the expected values given no phylogenetic signal, obtained by randomizing species names 999 times. Only when observed values fall outside the grey lines, traits are significantly phylogenetically structured across communities. This analysis was conducted using a Maximum Clade Credibility tree calculated from 1000 trees sampled from the posterior distribution of Faurby et al. (2016).

**References**

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