June 2020

Press Report

Flora Borne

Nature, 3 June 2020

Selective prebiotic formation of RNA pyrimidine and DNA purine nucleosides

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Extant biology, in contrast to the proposed RNA world theory, features DNA as the central information-carrying molecule. This discrepancy between the RNA world and modern biology requires a 'genetic takeover' that invokes the power of primitive biosynthetic machinery and natural selection operating over millions of years, ultimately resulting in an ancestral biosynthetic route to DNA[16]. The superior hydrolytic stability and replication fidelity[17] of DNA could have resulted in selection of primitive organisms capable of synthesizing DNA, and thus its rise to prominence, but the feasibility of this evolutionary process in a pre-DNA world is debated[1]. To circumvent this potentially problematic transition, an RNA/DNA world has been proposed, in which nascent biology had access to both RNA and DNA building blocks from the outset, without requiring elaborate biosynthesis[18–20]. In such a world, heterogeneous polymers would have initially been most common, but polymers with increased homogeneity—and hence properties closer to that of either RNA or DNA—would have been selected for over their mixed counterparts[4].

rdial geochemical scenario. Here we demonstrate a high-yielding, completely stereo-, regio- and furanosyl-selective prebiotic synthesis of the purine deoxyribonucleosides: deoxyadenosine and deoxyinosine. Our synthesis uses key intermediates in the prebiotic synthesis of the canonical pyrimidine ribonucleosides (cytidine and uridine), and we show that, once generated, the pyrimidines persist throughout the synthesis of the purine deoxyribonucleosides, leading to a mixture of deoxyadenosine, deoxyinosine, cytidine and uridine. These results support the notion that purine deoxyribonucleosides and pyrimidine ribonucleosides may have coexisted before the emergence of life[5].

Science, June 2020

GENOMIC DUPLICATIONS

Exploring whole-genome duplicate gene retention with complex genetic interaction analysis

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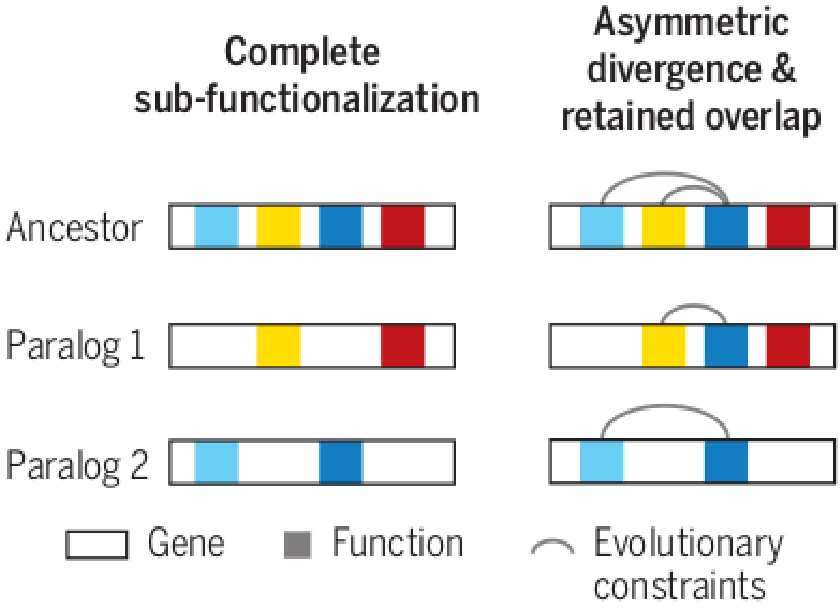
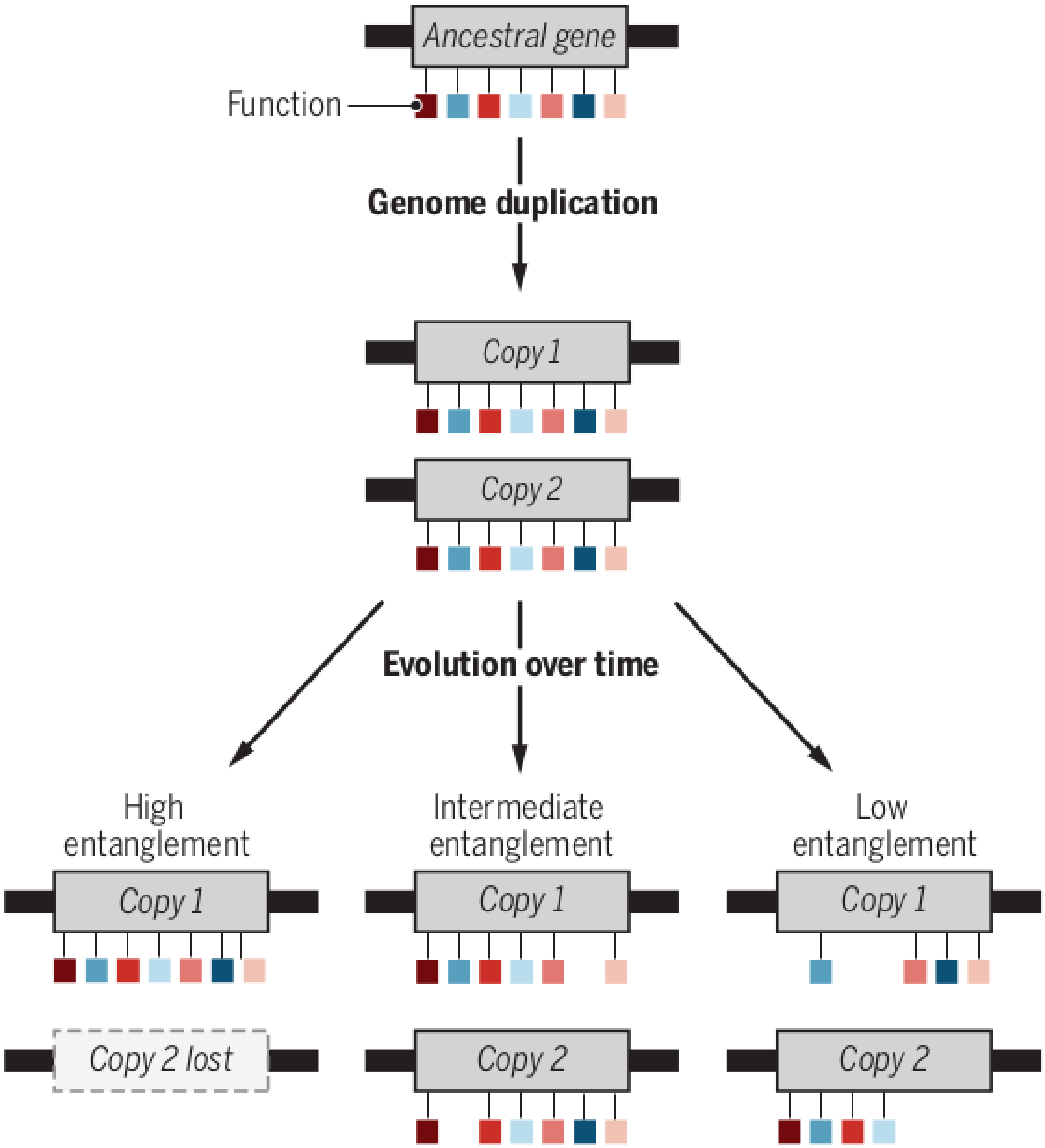
Whole-genome duplication has played a central role in the genome evolution of many organisms, including the human genome. Most duplicated genes are eliminated, and factors that influence the retention of persisting duplicates remain poorly understood. We describe a systematic complex genetic interaction analysis with yeast paralogs derived from the whole-genome duplication event. Mapping

We compared trigenic interactions for double-mutant query strains deleted for both members of nonessential paralog pairs to the corresponding digenic interaction profiles for each single-mutant sister gene, and we quantified a spectrum of functional redundancy among paralogs. A correlative analysis of the gene features suggests that the evolutionary trajectories of retained duplicated genes can be driven by genes encoding functionally and structurally constrained proteins, which we refer to as "entangled."

Structural and functional entanglement model of paralog divergence



Exploring whole-genome duplicate gene retention with complex genetic interaction analysis



CONCLUSION: We propose that the evolutionary fate of a duplicated gene is dictated by an interplay of structural and functional entanglement. Paralog pairs with high levels of entanglement are more likely to revert to a singleton state. In contrast, unconstrained paralogs will tend to partition their functions and adopt divergent roles. Intermediately entangled paralog pairs may partition or expand nonoverlapping functions while also retaining some common, overlapping functions, such that they can both adopt paralog-specific roles and maintain functional redundancy at an evolutionary steady state. ■

Ecology and Evolution, June 2020

Reproductive isolation caused by azoospermia in sterile male hybrids of *Drosophila*

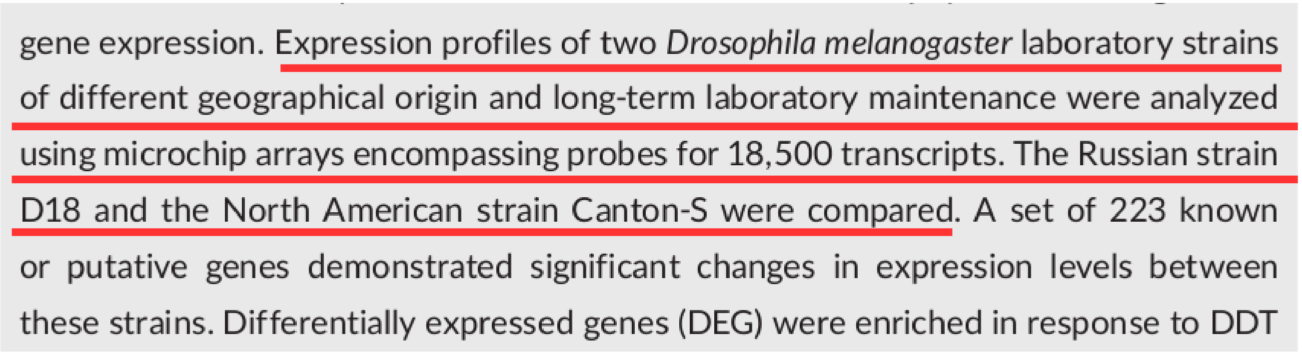
Hunter Davis | Nicholas Sosulski | Alberto Civetta

Recently diverged populations in the early stages of speciation offer an opportunity to understand mechanisms of isolation and their relative contributions. *Drosophila willistoni* is a tropical species with broad distribution from Argentina to the southern United States, including the Caribbean islands. A postzygotic barrier between northern populations (North America, Central America, and the northern Caribbean islands) and southern populations (South American and the southern Caribbean islands) has been recently documented and used to propose the existence of two different subspecies. Here, we identify premating isolation between populations regardless of their subspecies status. We find no evidence of postmating prezygotic isolation and proceeded to characterize hybrid male sterility between the subspecies. Sterile male hybrids transfer an ejaculate that is devoid of sperm but causes elongation and expansion of the female uterus. In sterile male hybrids, bulging of the seminal vesicle appears to impede the movement of the sperm toward the sperm pump, where sperm normally mixes with accessory gland products. Our results highlight a unique form of hybrid male sterility in *Drosophila* that is driven by a mechanical impediment to transfer sperm rather than by an abnormality of the sperm itself. Interestingly, this form of sterility is reminiscent of a form of infertility (azoospermia) that is caused by lack of sperm in the semen due to blockages that impede the sperm from reaching the ejaculate.

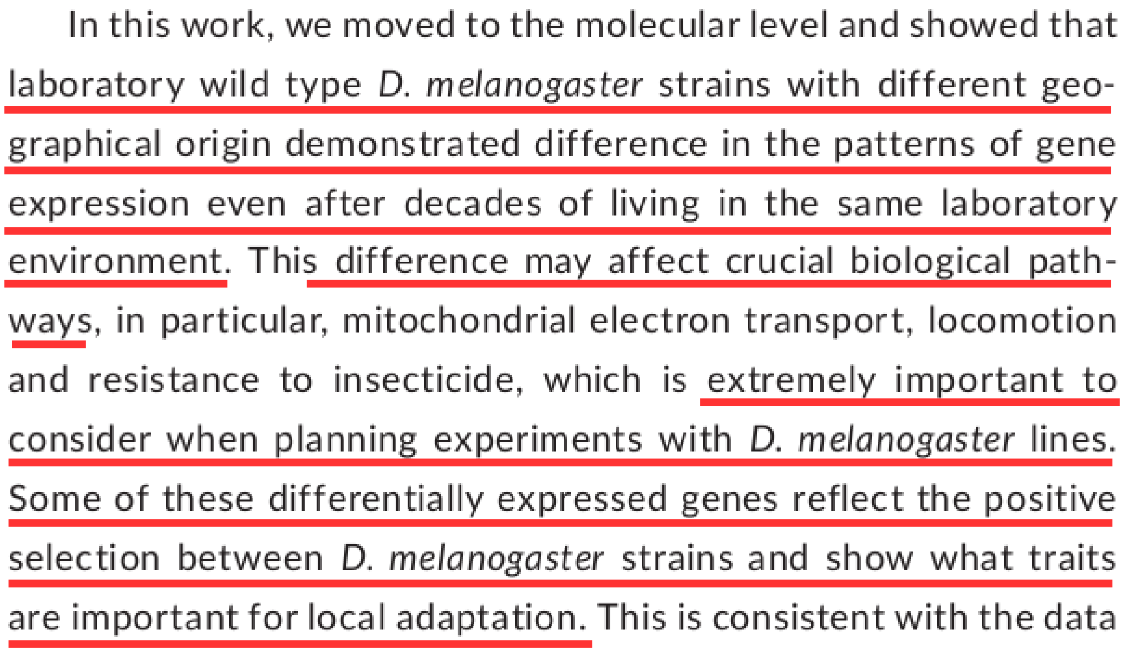
Ecology and Evolution, June 2020

Transcriptome analysis of *Drosophila melanogaster* laboratory strains of different geographical origin after long-term laboratory maintenance

Mikhail Zarubin[1] | Alena Yakhnenko[1,2] | Elena Kravchenko[1]



gene expression. Expression profiles of two *Drosophila melanogaster* laboratory strains of different geographical origin and long-term laboratory maintenance were analyzed using microchip arrays encompassing probes for 18,500 transcripts. The Russian strain D18 and the North American strain Canton-S were compared. A set of 223 known or putative genes demonstrated significant changes in expression levels between these strains. Differentially expressed genes (DEG) were enriched in response to DDT



In this work, we moved to the molecular level and showed that laboratory wild type *D. melanogaster* strains with different geographical origin demonstrated difference in the patterns of gene expression even after decades of living in the same laboratory environment. This difference may affect crucial biological pathways, in particular, mitochondrial electron transport, locomotion and resistance to insecticide, which is extremely important to consider when planning experiments with *D. melanogaster* lines. Some of these differentially expressed genes reflect the positive selection between *D. melanogaster* strains and show what traits are important for local adaptation. This is consistent with the data

Biorxiv, June 2020

Unravelling the genetic basis for the rapid diversification of male genitalia between *Drosophila* species

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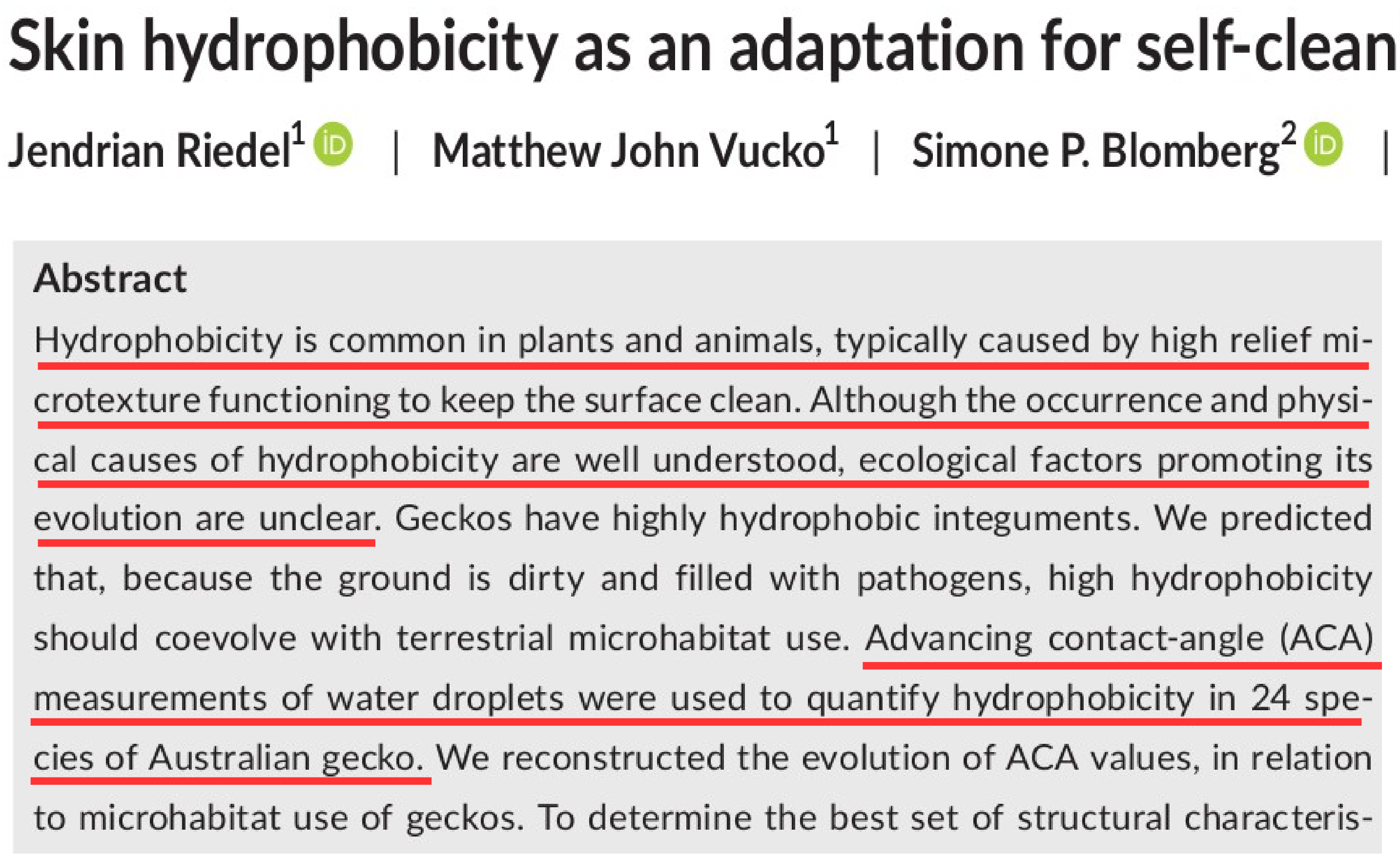
In the last 240,000 years, males of the *Drosophila simulans* species clade have evolved striking differences in the morphology of their epandrial posterior lobes and claspers (surstyli). These changes have most likely been driven by sexual selection and mapping studies indicate a highly polygenic and generally additive genetic basis. However, we have limited understanding of the gene regulatory networks that control the development of genital structures and how they evolved to result in this rapid phenotypic diversification. Here, we used new *D. simulans / D. mauritiana* introgression lines on chromosome 3L to generate higher resolution maps of posterior lobe and clasper differences between these species. We then carried out RNA-seq on the developing genitalia of both species to identify the genes expressed during this process and those that are differentially expressed between the two species. This allowed us to test the function of expressed positional candidates during genital development in *D. melanogaster*. We identified several new genes involved in the development and possibly the evolution of these genital structures, including the transcription factors Hairy and Grunge. Furthermore, we discovered that during clasper development Hairy negatively regulates *tartan*, a gene known to contribute to divergence in clasper morphology. Taken together our results provide new insights into the regulation of genital development and how this evolves between species.

Ecology and Evolution, June 2020

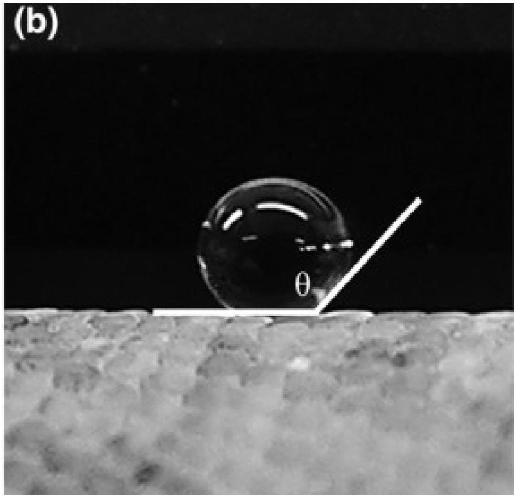


Skin hydrophobicity as an adaptation for self-cleaning in geckos

Jendrian Riedel[1] | Matthew John Vucko[1] | Simone P. Blomberg[2] | Lin Schwarzkopf[1]

Abstract

Hydrophobicity is common in plants and animals, typically caused by high relief microtexture functioning to keep the surface clean. Although the occurrence and physical causes of hydrophobicity are well understood, ecological factors promoting its evolution are unclear. Geckos have highly hydrophobic integuments. We predicted that, because the ground is dirty and filled with pathogens, high hydrophobicity should coevolve with terrestrial microhabitat use. Advancing contact-angle (ACA) measurements of water droplets were used to quantify hydrophobicity in 24 species of Australian gecko. We reconstructed the evolution of ACA values, in relation to microhabitat use of geckos. To determine the best set of structural characteris-



Contact angle

Skin hydrophobicity as an adaptation for self-cleaning in geckos

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. All species were highly hydrophobic (ACA > 132.72°), but terrestrial species had significantly higher ACA values than arboreal ones. The evolution of longer spinules and smaller scales was correlated with high hydrophobicity. These results suggest that hydrophobicity has coevolved with terrestrial microhabitat use in Australian geckos *via* selection for long spinules and small scales, likely to keep their skin clean and prevent fouling and disease.

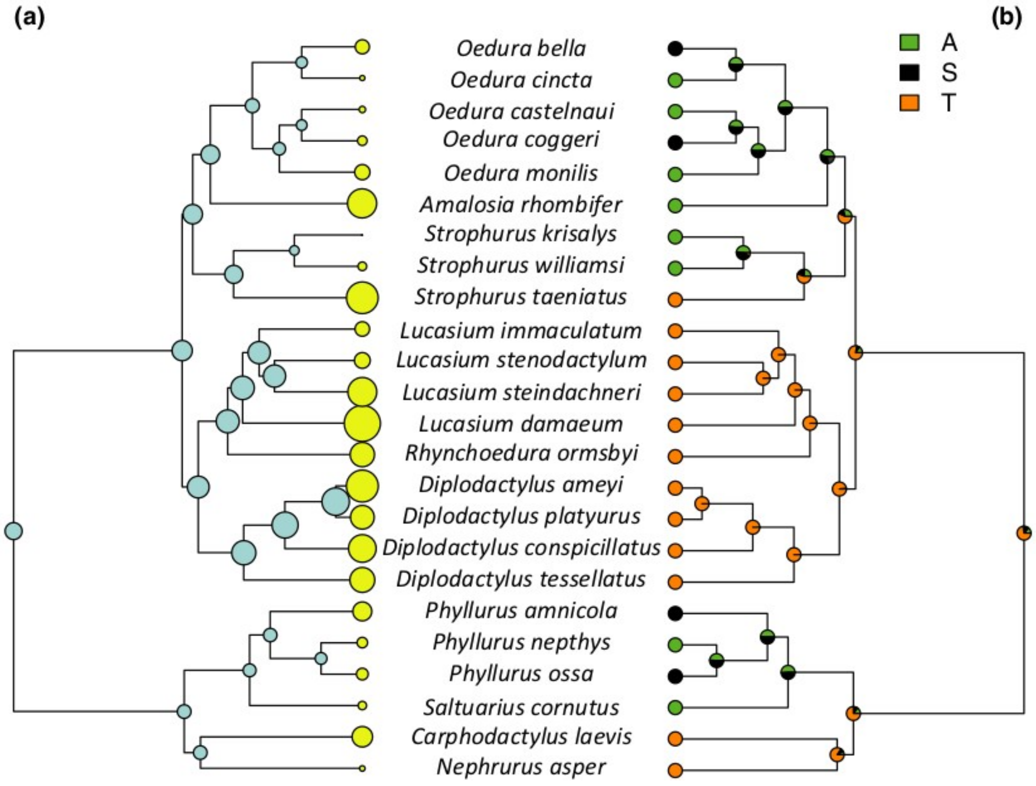

FIGURE 3 Reconstructed ancestral states of hydrophobicity (a) and microhabitat use (b). For hydrophobicity, the size of the dots correlates with the ACA measurements for the species of this study (yellow dots) and reconstructed for the nodes (blue dots). For microhabitat use, the dots correspond to the reconstructed probability of microhabitat use for nodes: A (green), arboreal; S (black), saxicoline; T (orange), terrestrial. Note the correspondence between brown nodes (terrestrial species) and large yellow circles (hydrophobic species)

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