



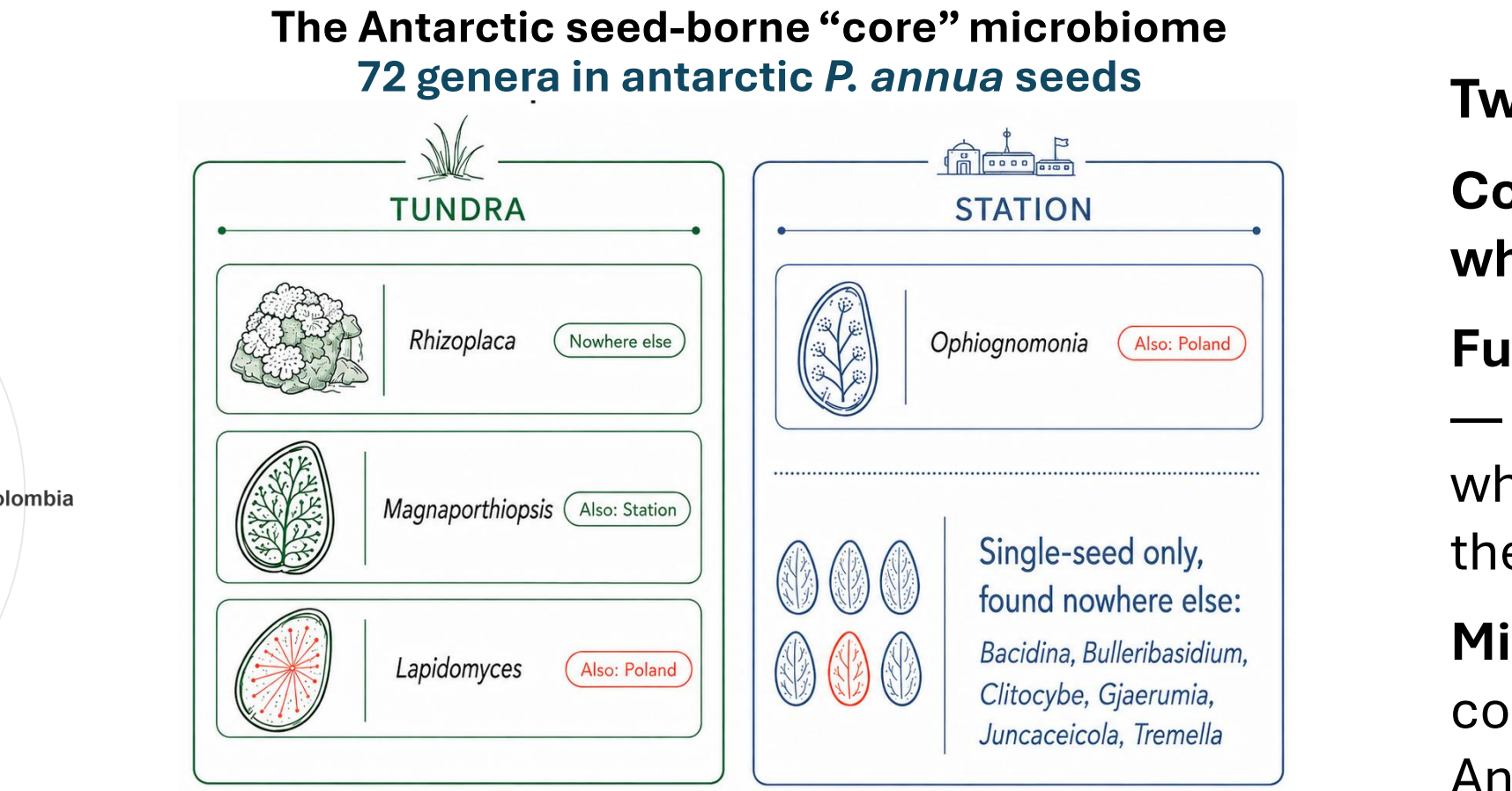
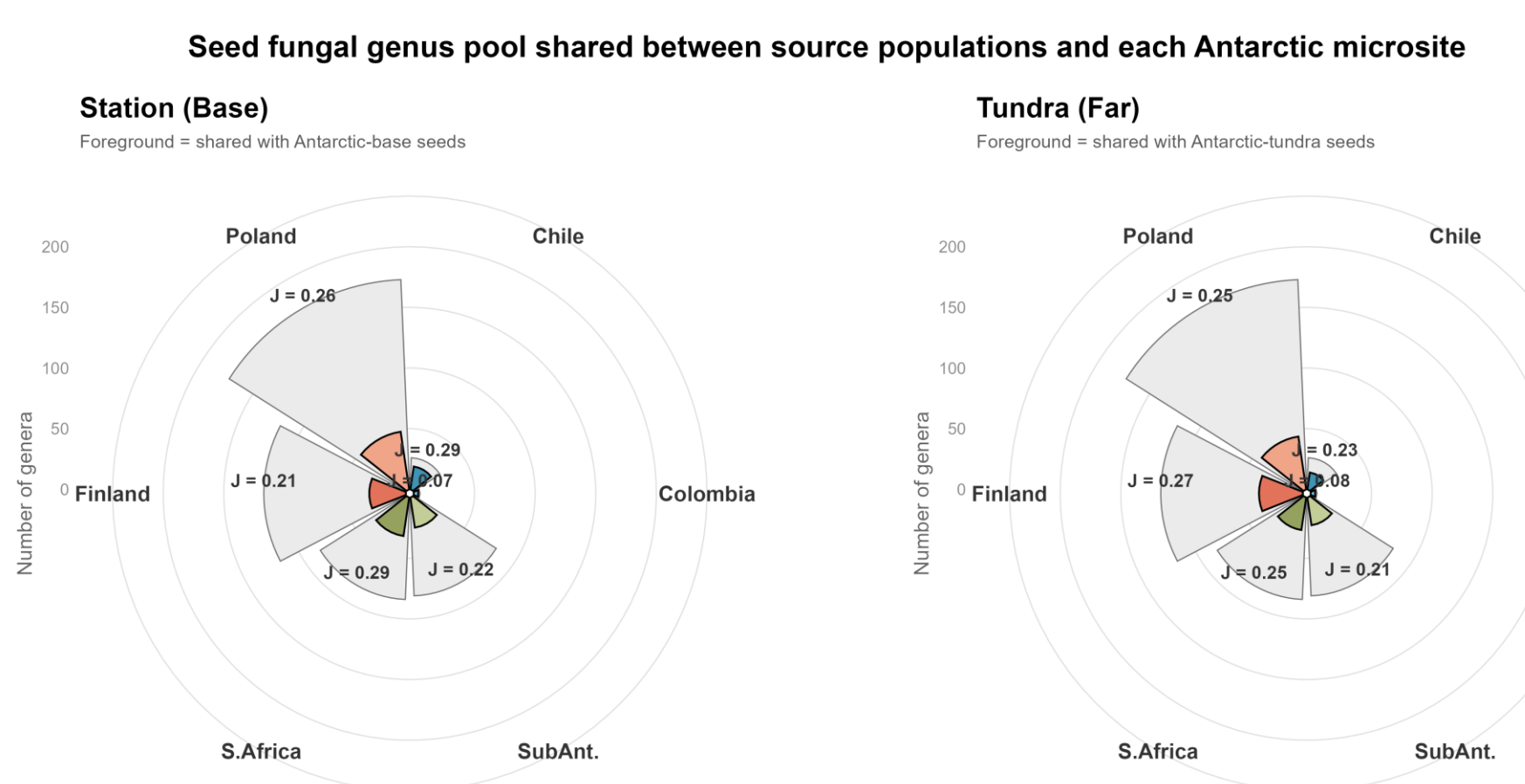
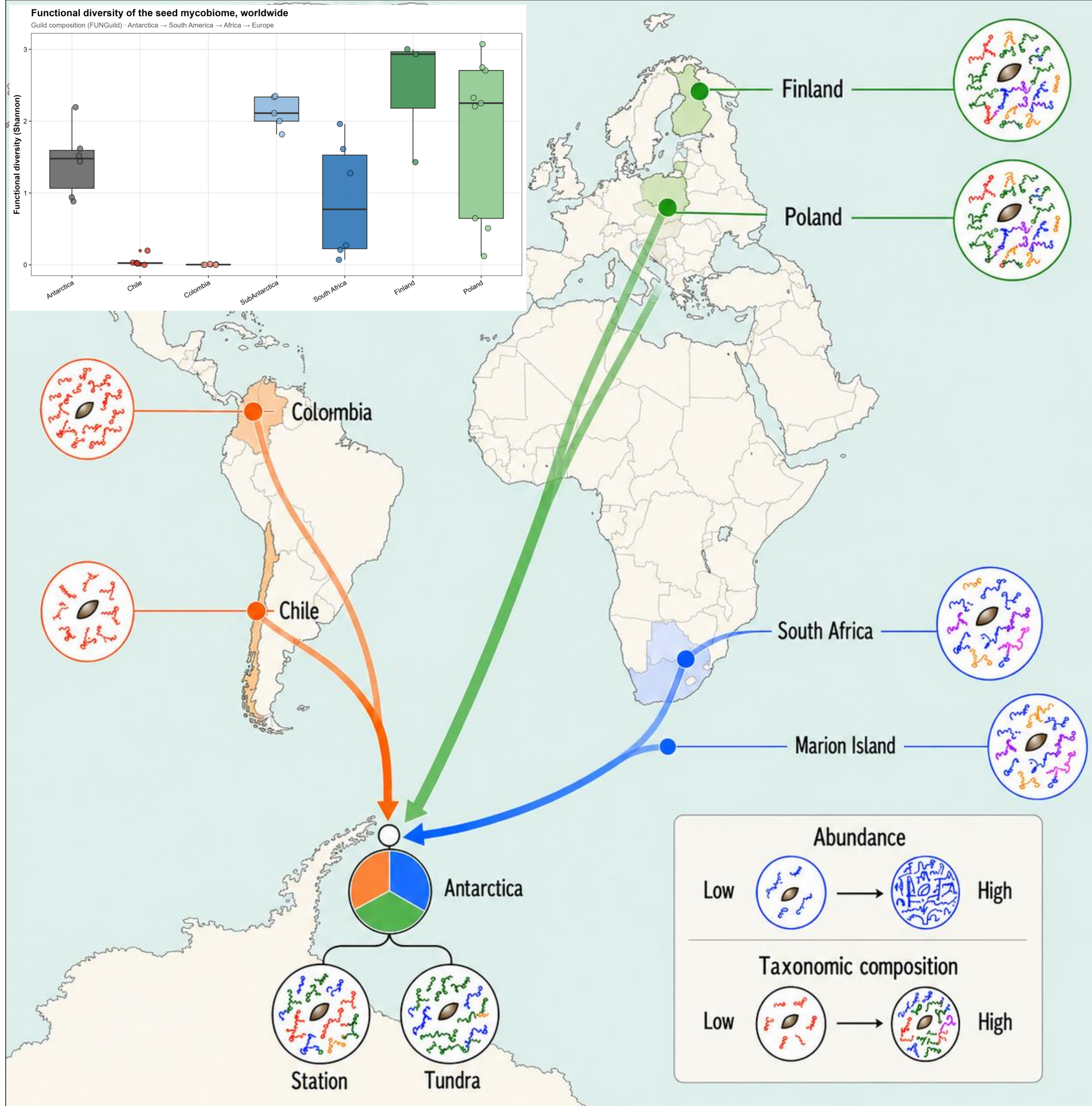
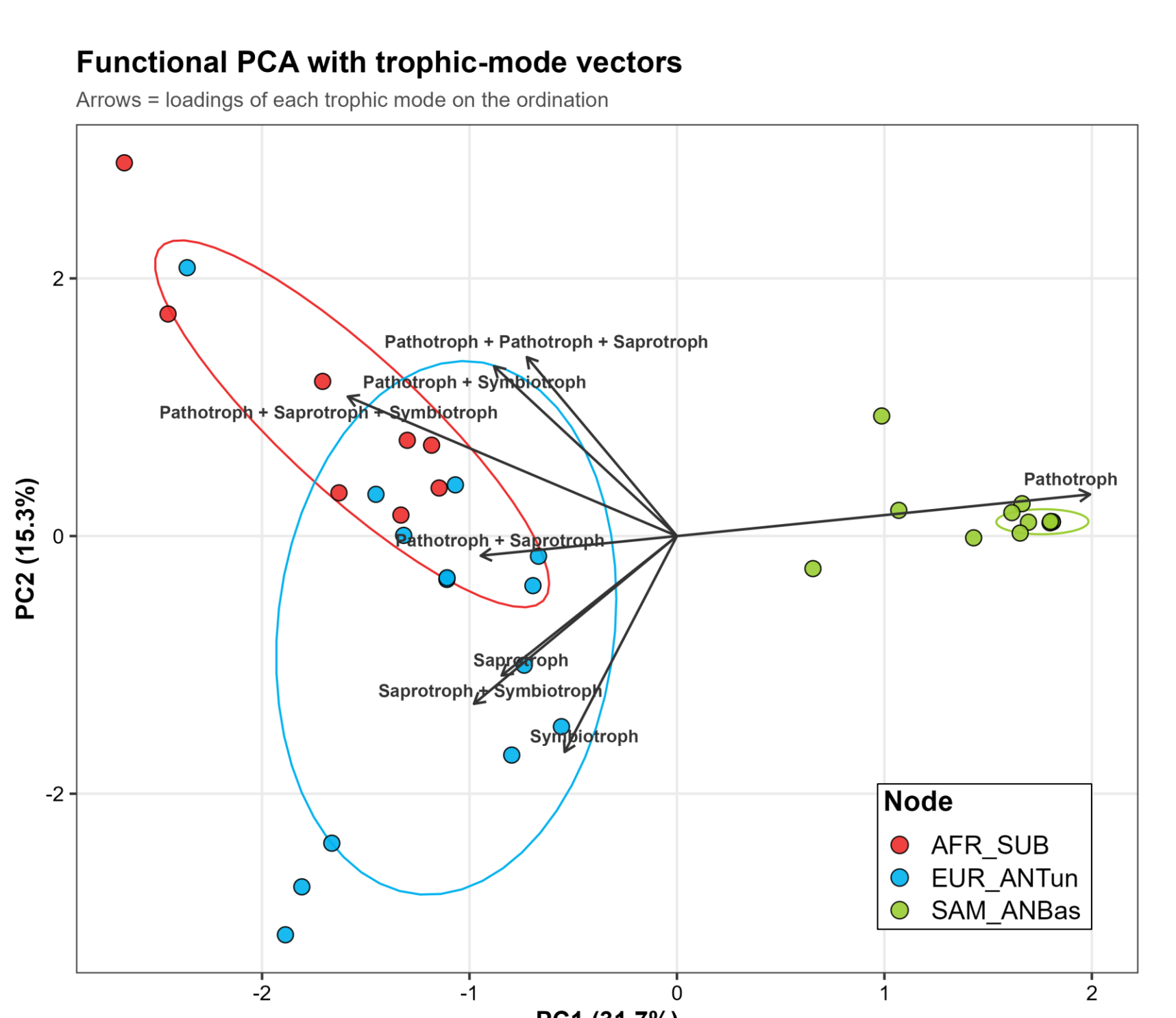
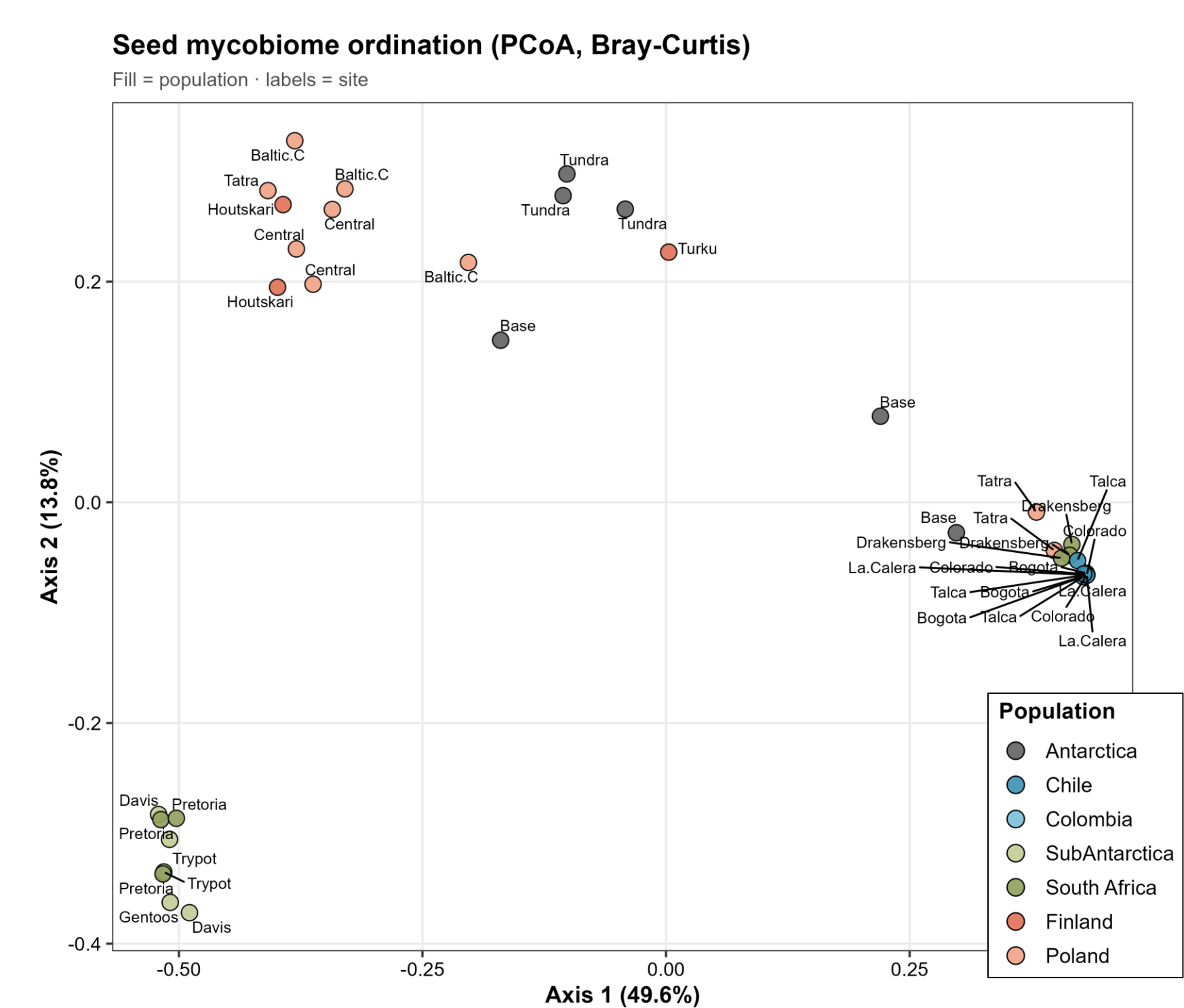
Project “Anillo” ATE-250059 is funded by the *Agencia Nacional de Investigación y Desarrollo de Chile* (ANID).

The Antarctic seed microbiome of the invasive *Poa annua* in global context: evidence of multi-origin assembly and environmental filtering

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Does Antarctica's invasive *Poa annua* carry a distinctive seed mycobiome – and can it be traced back to global source populations? *Poa annua* is one of the world's most successful plant invaders, and one of the very few vascular plants established in Antarctica. Its seeds carry a fungal microbiome that may travel with it. We profiled this seed mycobiome across seven source populations on four continents and at two Antarctic microsities – a disturbed research station and natural tundra – to ask whether invasion success is linked to a distinctive fungal signature, and whether that signature can be traced to specific global origins. Seed-associated fungal communities were profiled by ITS metabarcoding across 41 samples from 7 populations (Chile, Colombia, South Africa, sub-Antarctic Marion Island, Finland, Poland, Antarctica) and collapsed to 249 fungal genera.



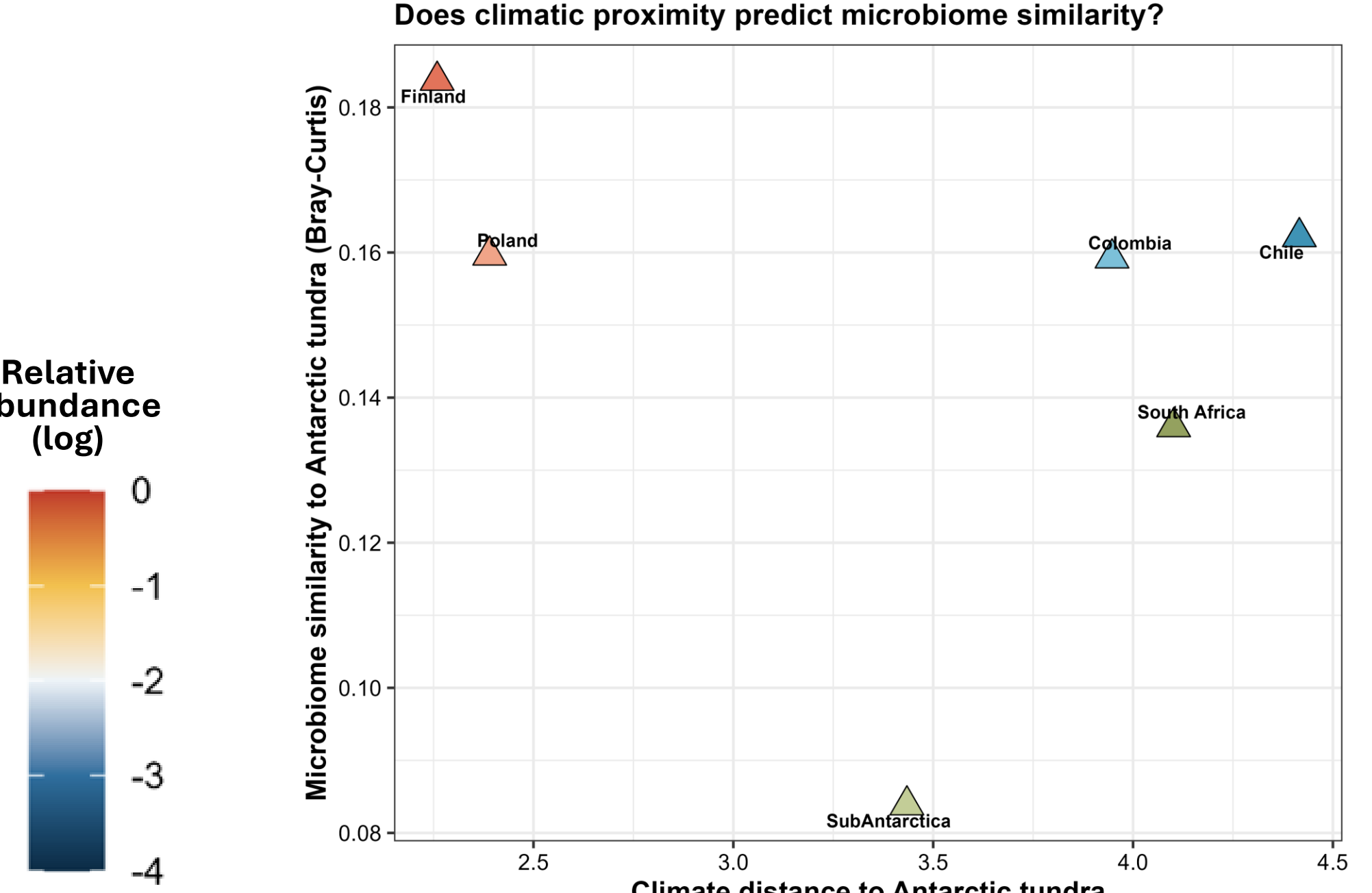
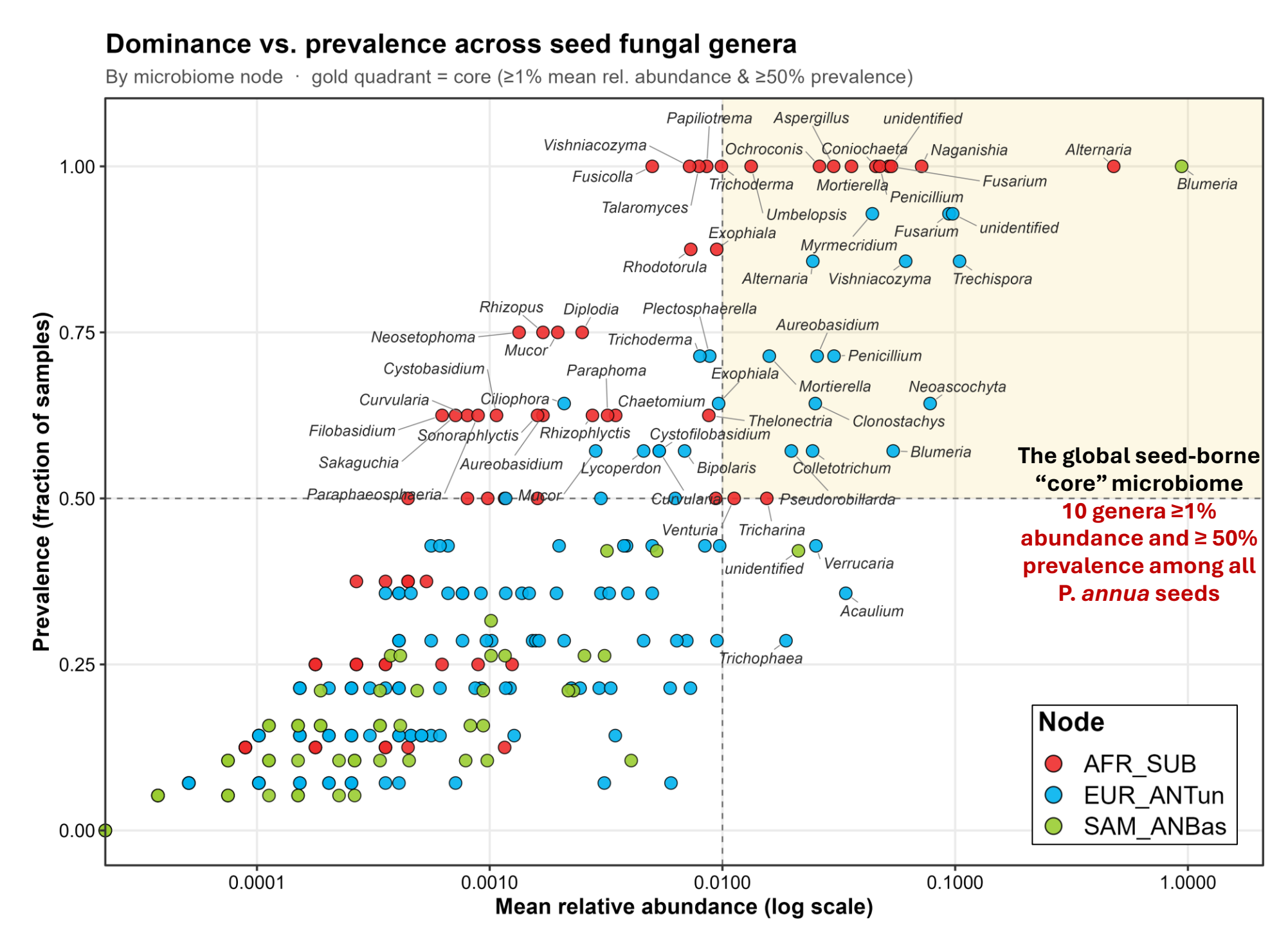
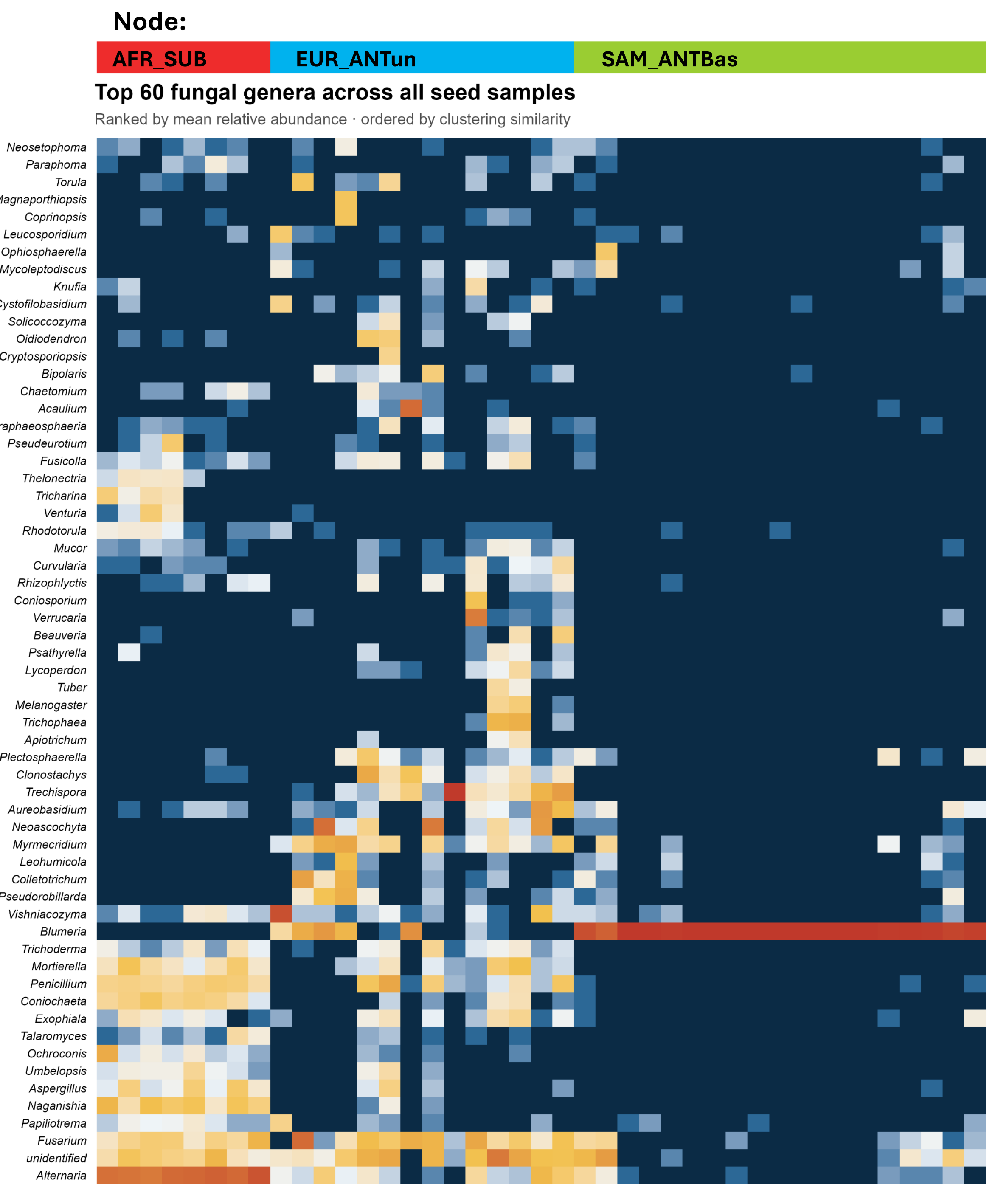
Two families of figures appear throughout: **compositional** and **functional**. **Compositional figures** (PCoA, heatmap, dominance-prevalence, Bray-Curtis flower plot) describe **who is there** — which fungal genera are present and in what relative abundance. **Functional figures** (guild/trophic-mode PCA, Shannon functional diversity) describe **what they do** — the ecological roles (pathotroph, saprotroph, symbiotroph...) those genera play, regardless of which taxa are performing them. The two PCA panels side by side (top-left) are these two views of the **same samples** — same points, different ordination. **Microbiome nodes** (color-coded throughout): three recurrent groupings recovered from compositional clustering — **AFR_SUB** (South Africa + sub-Antarctic) · **EUR_ANTun** (Europe + Antarctic tundra) · **SAM_ANBas** (South America + Antarctic station)



The **"core" seed mycobiome**: in the dominance-prevalence plot, the gold-shaded quadrant ($\geq 1\%$ mean relative abundance *and* present in $\geq 50\%$ of samples) marks the genera we call the **core mycobiome of the *Poa annua* seed** — present and abundant regardless of population or node. Everything outside that box is population- or node-specific rather than universal.

The **taxonomic/functional asymmetry**: *compositionally*, Antarctic seeds cluster with South America and Europe — the node structure itself is built on this. But *functionally*, the Antarctic guild profile looks closer to Europe and Africa, suggesting that taxonomically different source communities can converge on similar functional roles once established in Antarctica. Composition and function are not telling quite the same story.

A potential **"filtering signal", post-arrival**: within Antarctica, the natural tundra mycobiome looks more symbiotic and more specialist than the disturbed station mycobiome — consistent with filtering by the colder, more natural tundra environment, and with the cold-associated genera (e.g. *Magnaporthopsis*, *Typhula*-type taxa) found there. This trend is for now just indicative



Research team:



Financial support:



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