Biosynthesis gene cluster-containing species drive microbial community stability under thermal stress through enhanced ecological cohesion

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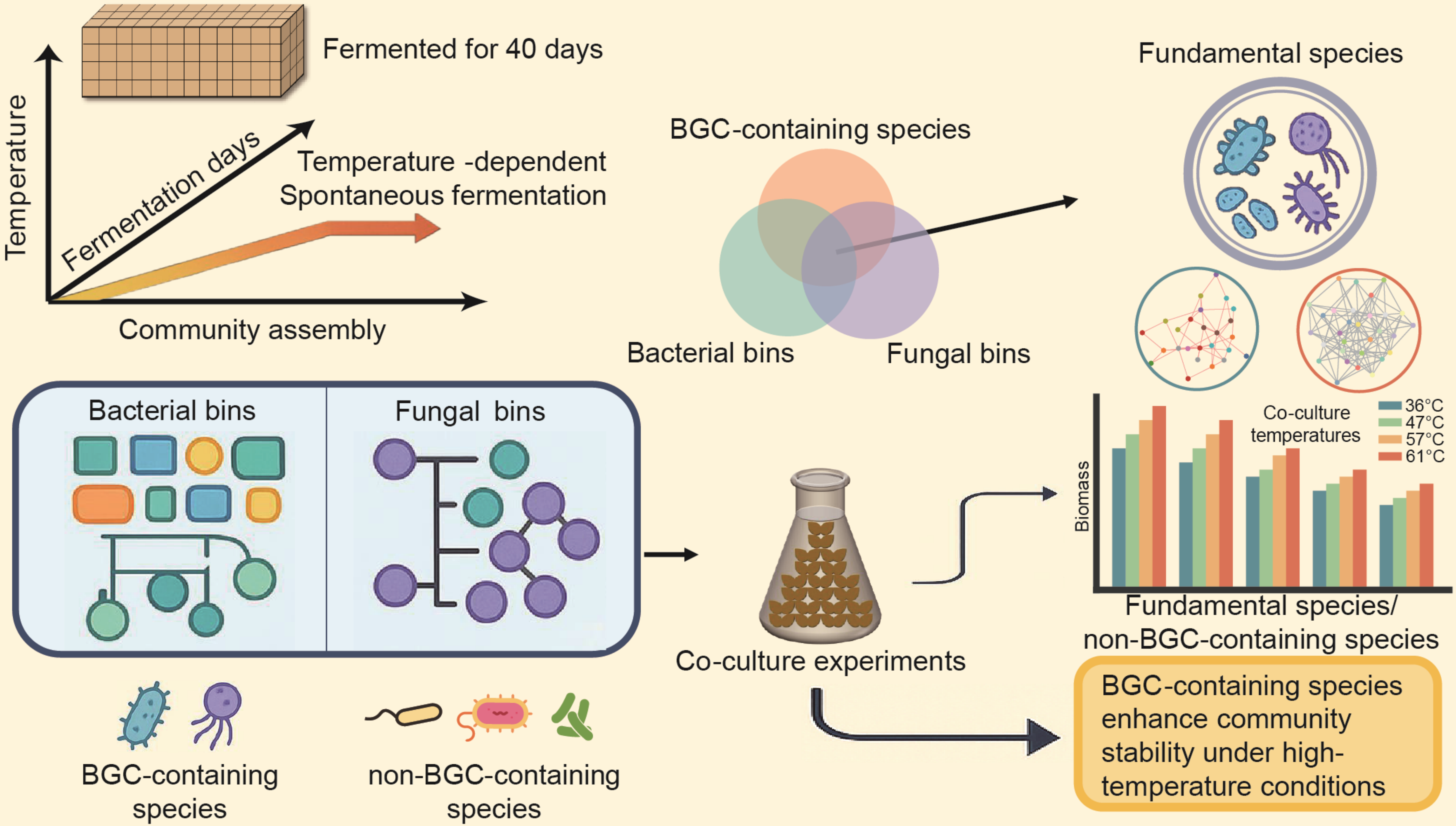
Introduction



Fermented for 40 days

Temperature -dependent
Spontaneous fermentation

BGC-containing species

Bacterial bins

Fungal bins

Fundamental species

Bacterial bins

Fungal bins

BGC-containing species

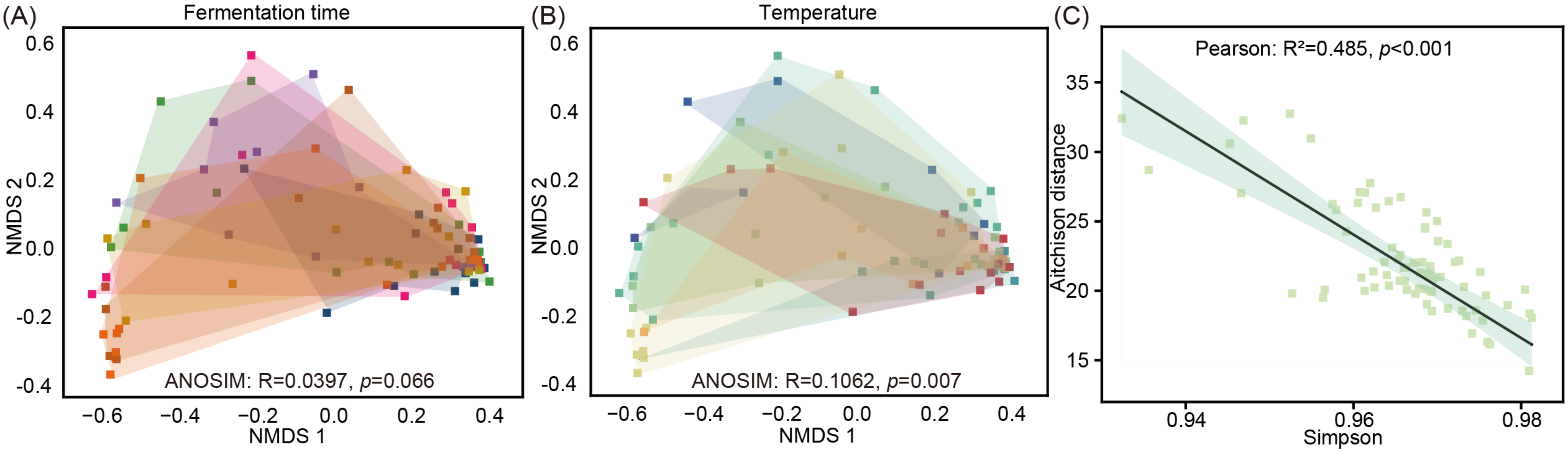
non-BGC-containing species

Co-culture experiments

Fundamental species/
non-BGC-containing species

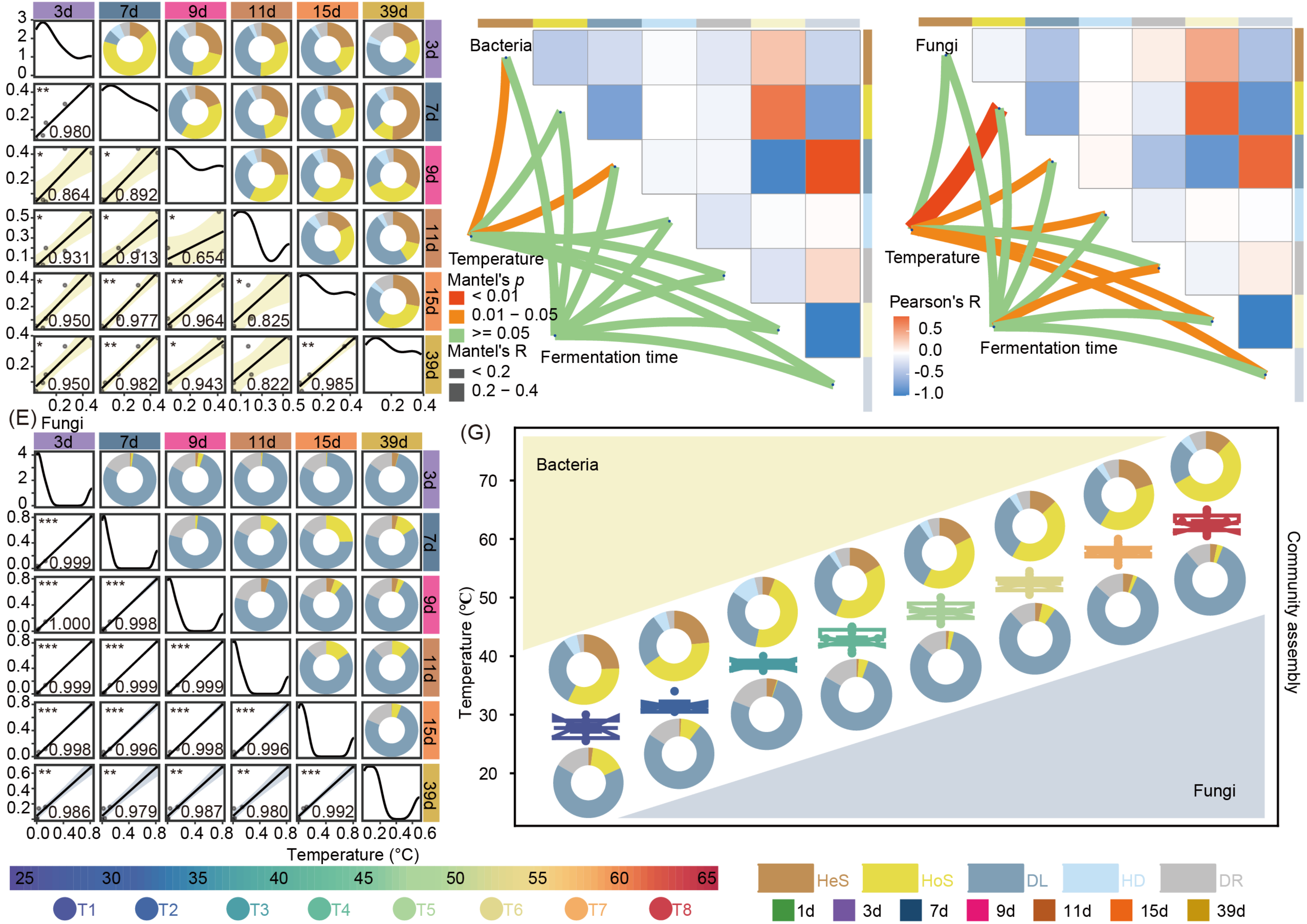
BGC-containing species enhance community stability under high-temperature conditions

Influence of time and temperature on microbial assembly processes



- ☐ **Temperature, rather than fermentation time**, was the primary driver of community variation during *Daqu* fermentation.
- ☐ Aitchison distance was negatively correlated with the Simpson index, indicating that as α-diversity declined, β-dissimilarity increased, consistent with **stress-driven community differentiation and reconstruction along divergent assembly** trajectories.

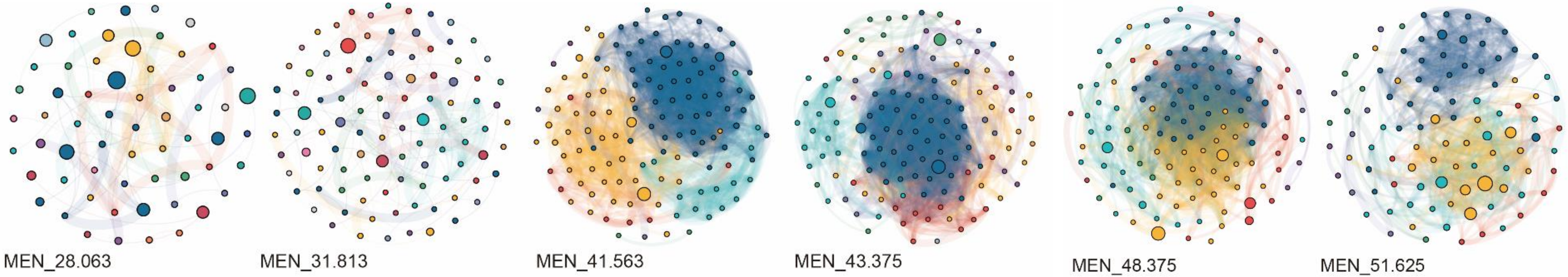
Influence of time and temperature on microbial assembly processes

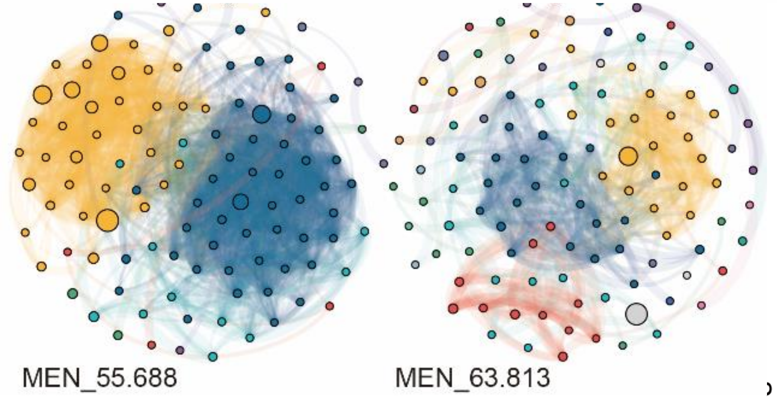


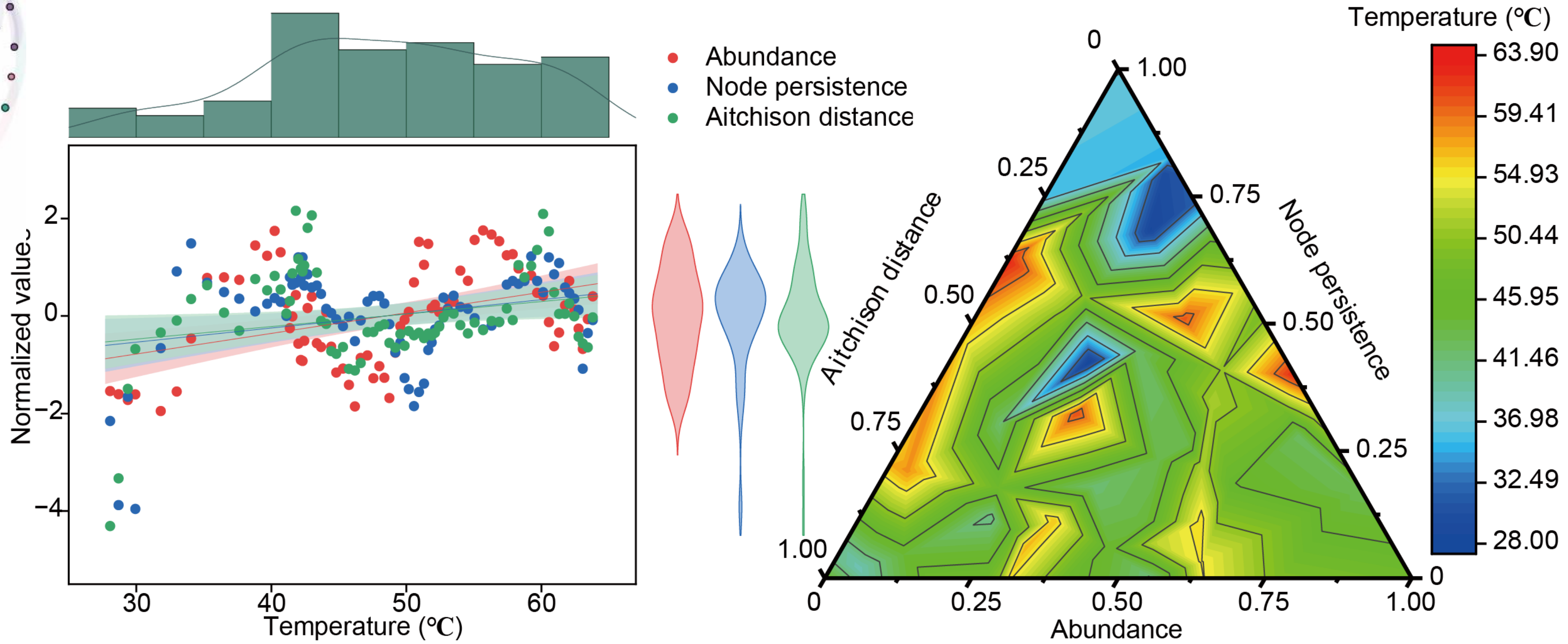
☐ Temperature was the dominant driver of community assembly during fermentation, as community structure and α-diversity varied significantly with temperature but not with time, and partial Mantel **tests linked assembly processes to temperature rather than time or acidity**.

☐ **iCAMP/Mantel analyses** showed **stage-specific** reallocation of assembly mechanisms across the temperature gradient.

Microbial communities and phylogenetic groups under high temperatures

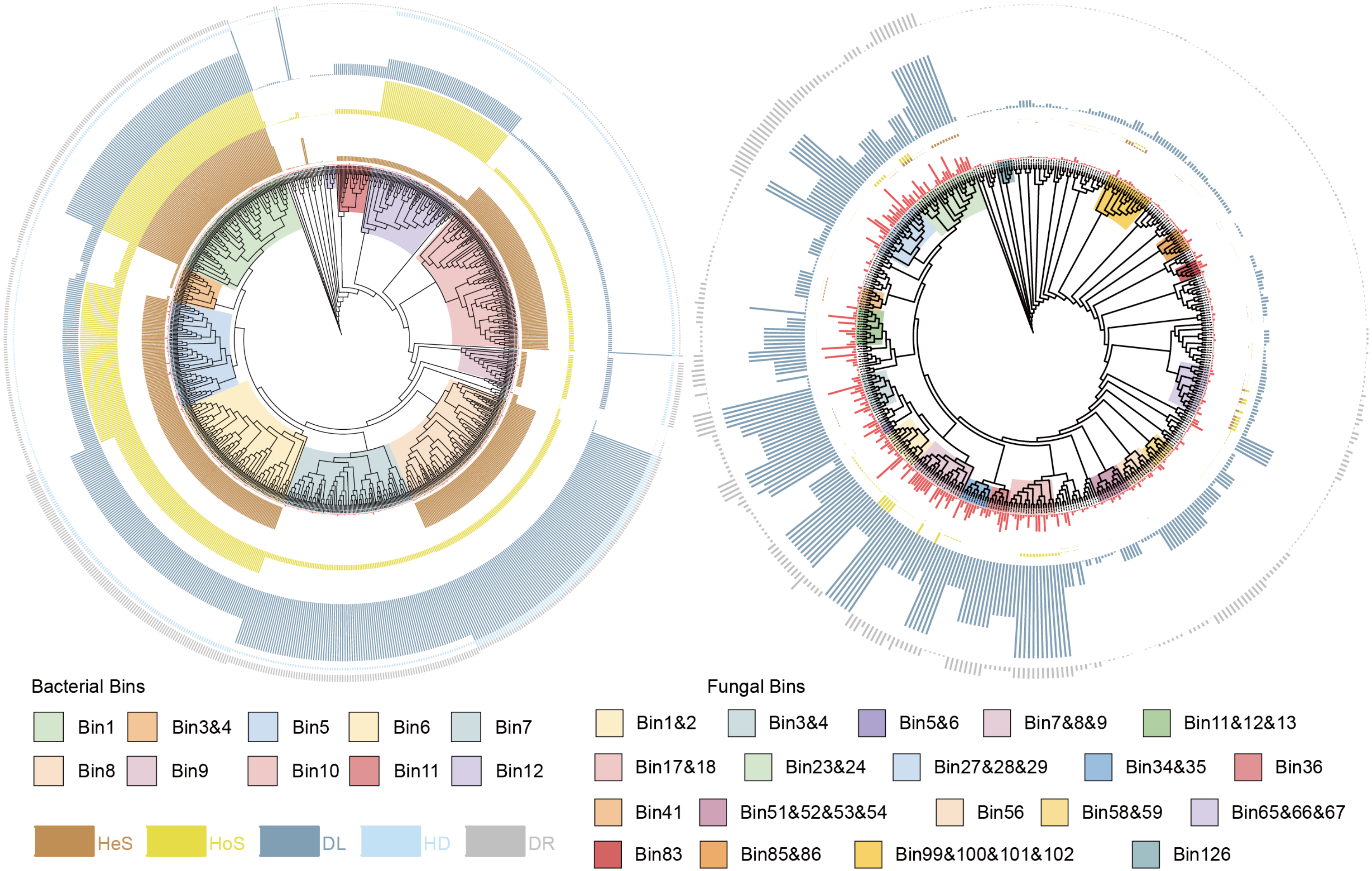






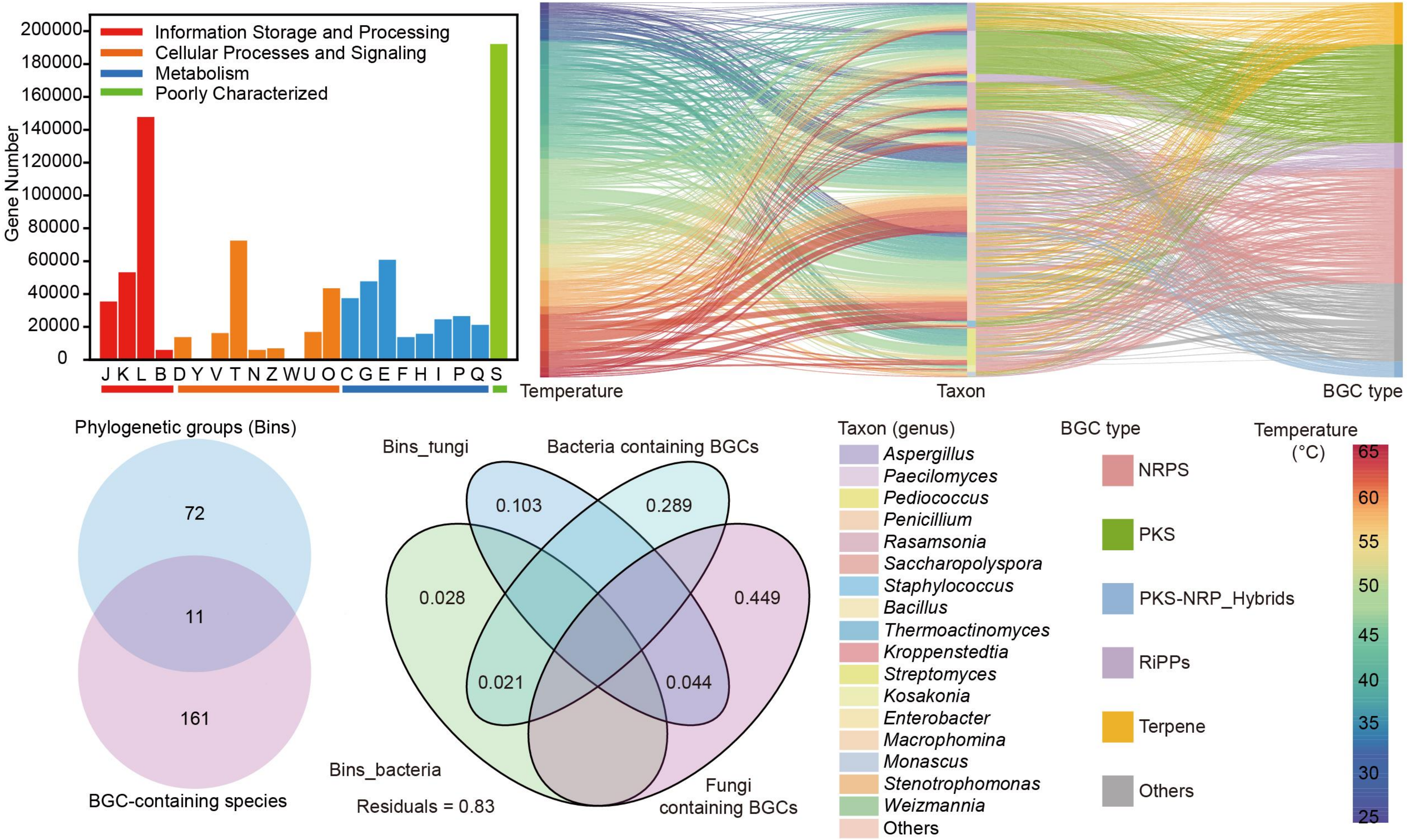
- ☐ **76 MENs were built using adjacent-temperature samples**, with richness and total abundance largely stable across networks.

Microbial communities and phylogenetic groups under high temperatures



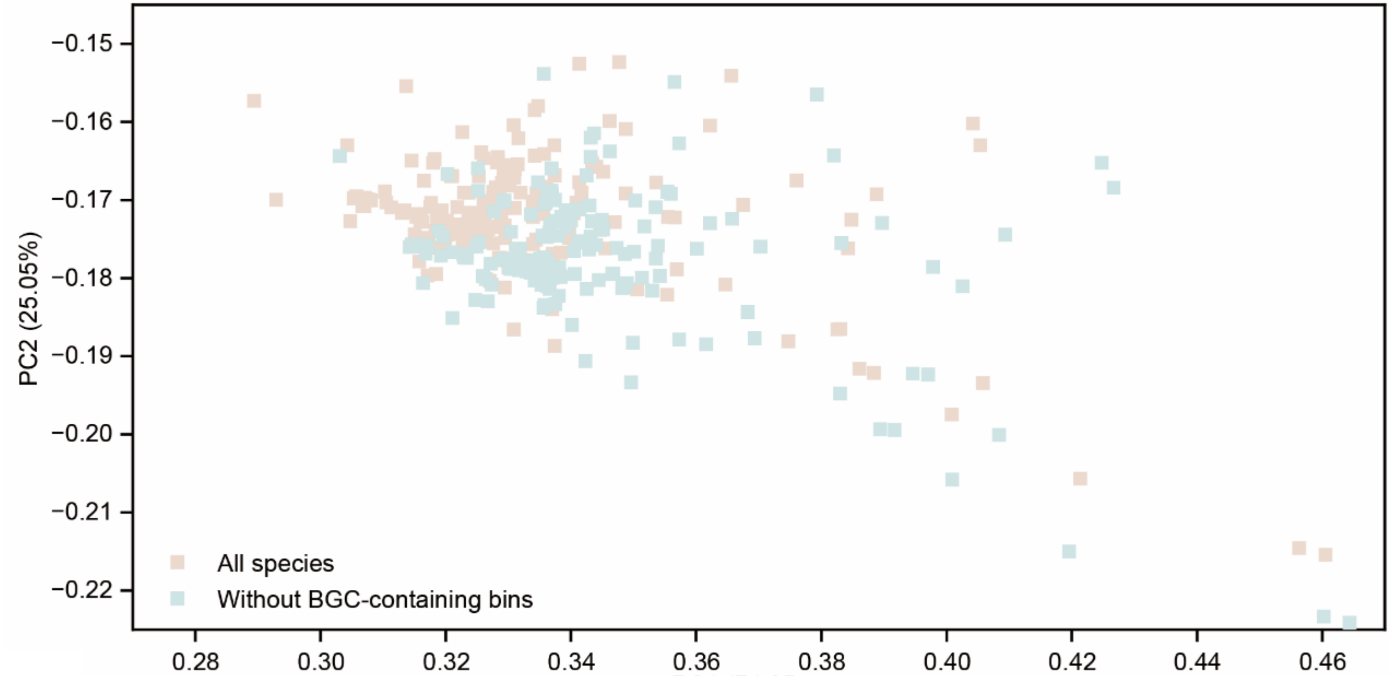
☐ β-dissimilarity increased and node persistence changed, suggesting heat-driven **node loss and network reorganization**.

BGC-containing bins in microbial community stability at high temperatures

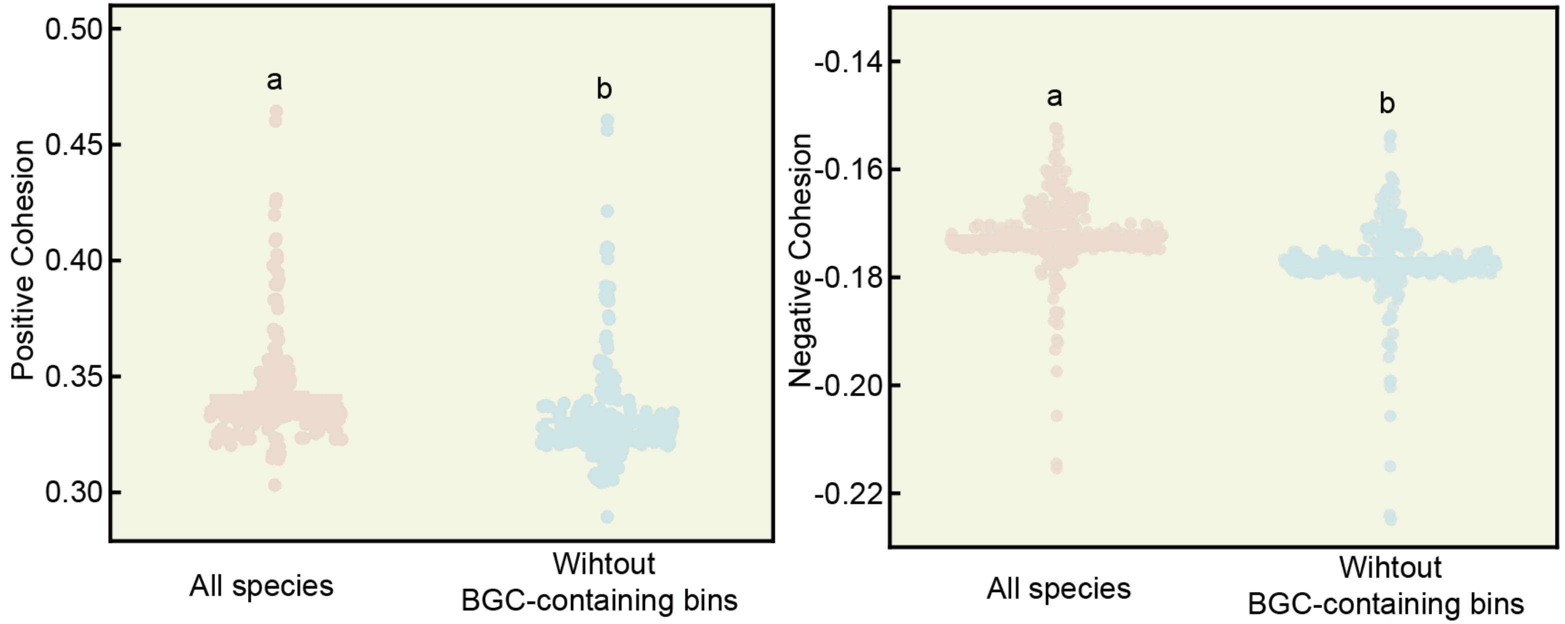


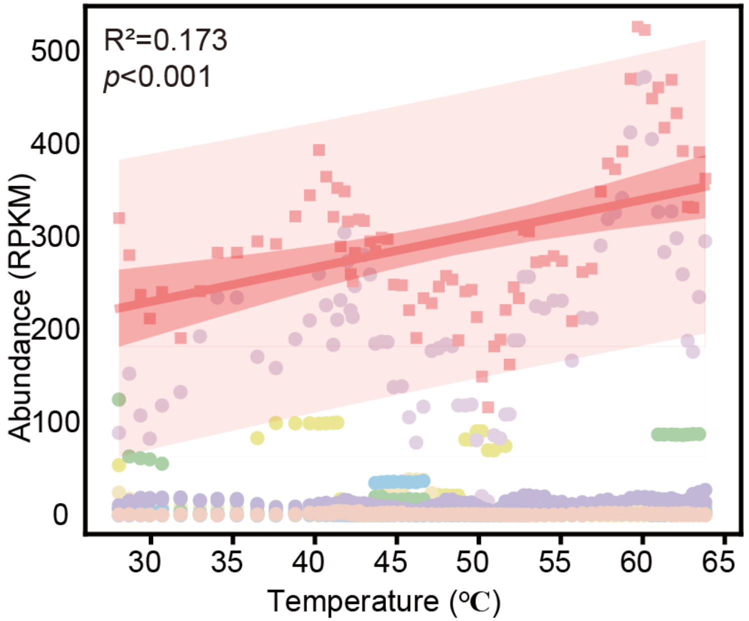
- ☐ eggNOG annotation showed metabolism-related functions were prominent, and **secondary-metabolism genes** increased with temperature.

BGC-containing bins in microbial community stability at high temperatures

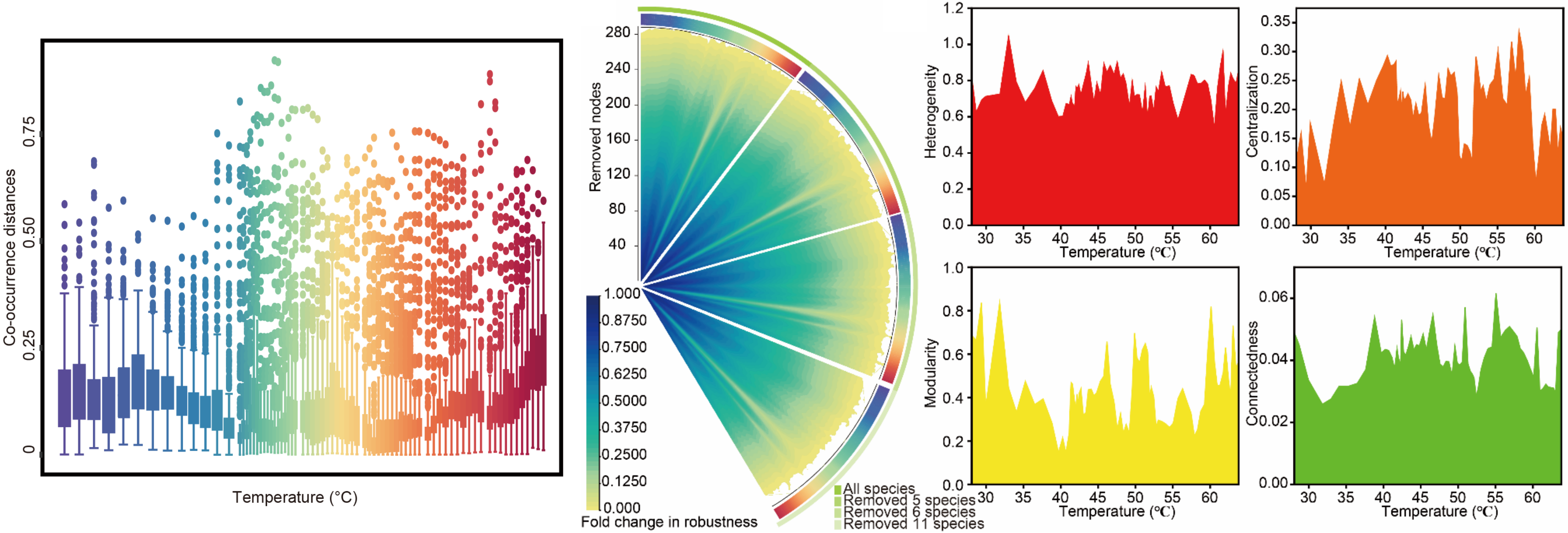


- ☐ Across **17 dominant genera**, we detected **1,413 BGCs**, mainly from *Paecilomyces* and *Aspergillus*.
- ☐ 11 BGC-containing bins explained 80.38% of assembly variation, and they **increased positive cohesion while reducing negative cohesion**.





Correlation between microbial adaptability and BGC-containing bins

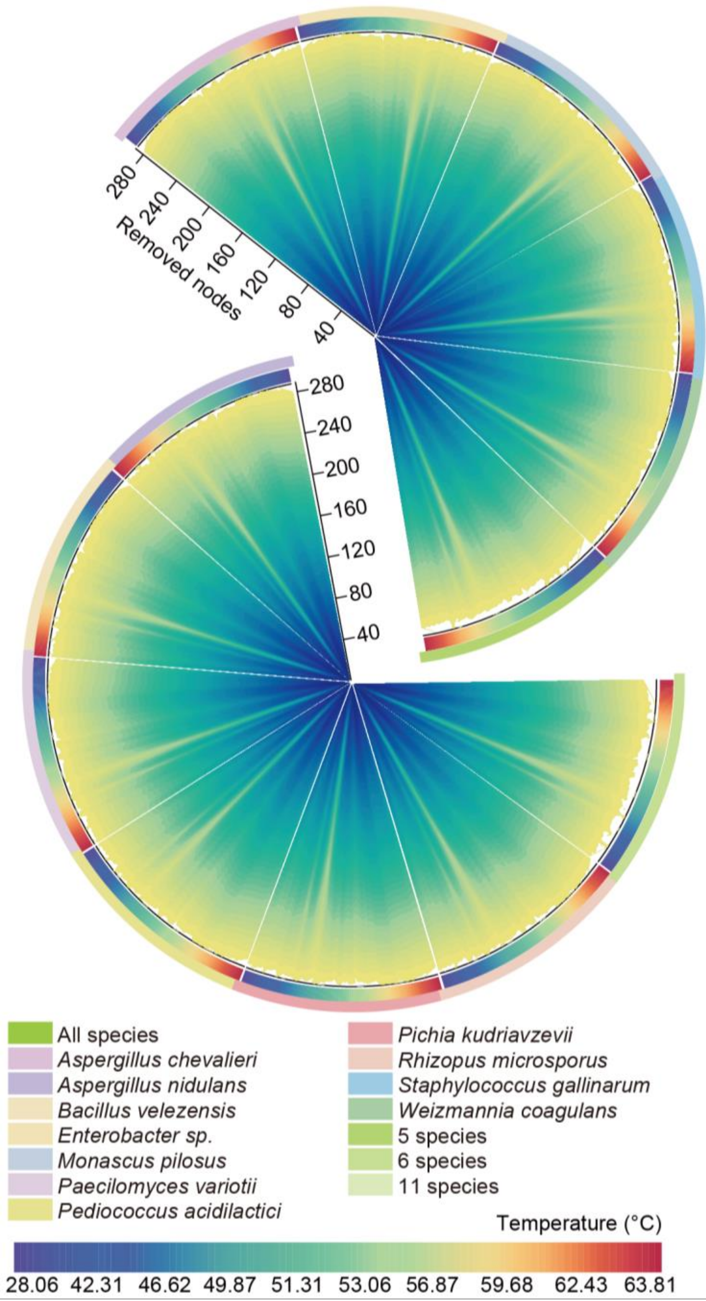


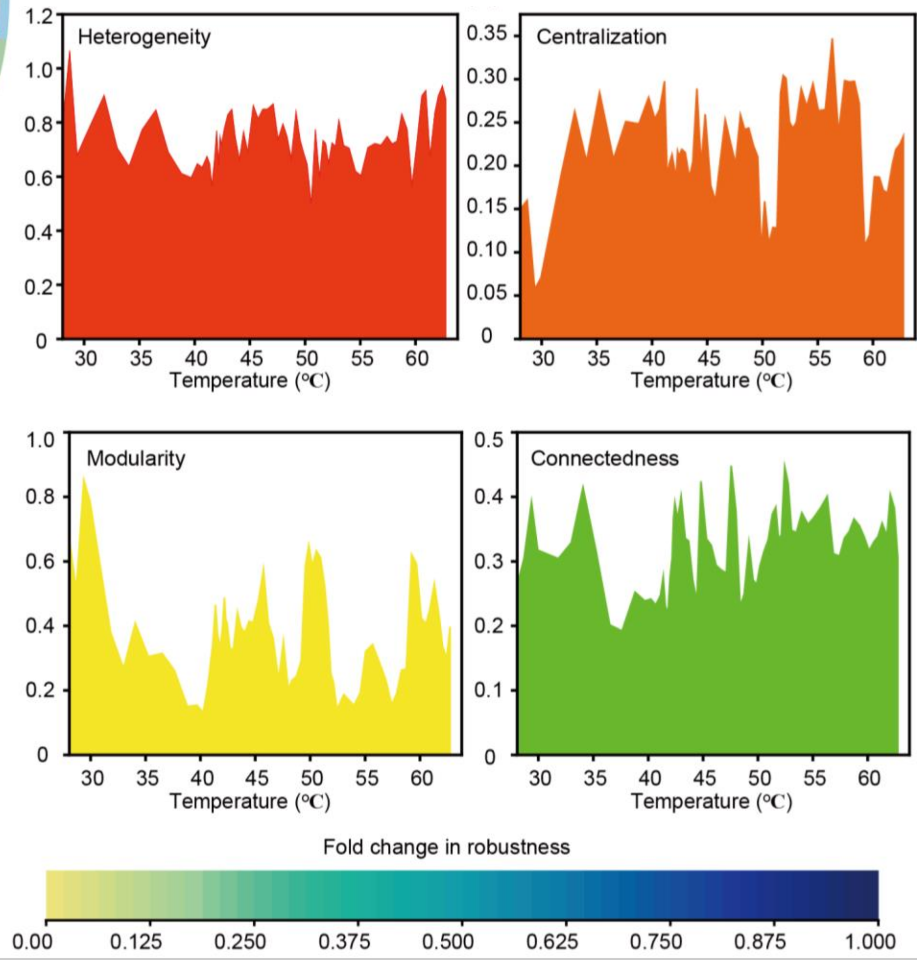
☐ As temperature rose (especially **51–61°C**), **co-occurrence distance increased while α-diversity declined**, alongside higher abundance of BGC-containing bins.

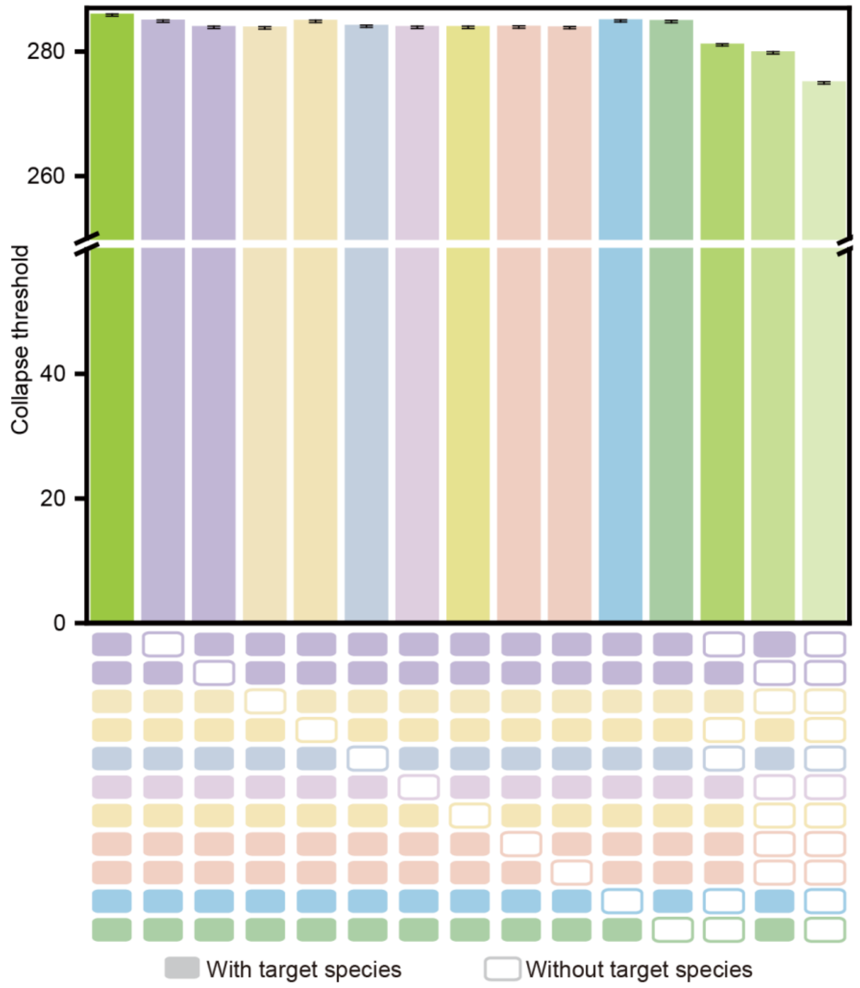
☐ Baseline community robustness and network topological indices declined from 41.56 to 51.31 ° C and then increased from 51.31°C onward, indicating that **rising temperature reshapes the community**.

Correlation between microbial adaptability and BGC-containing bins

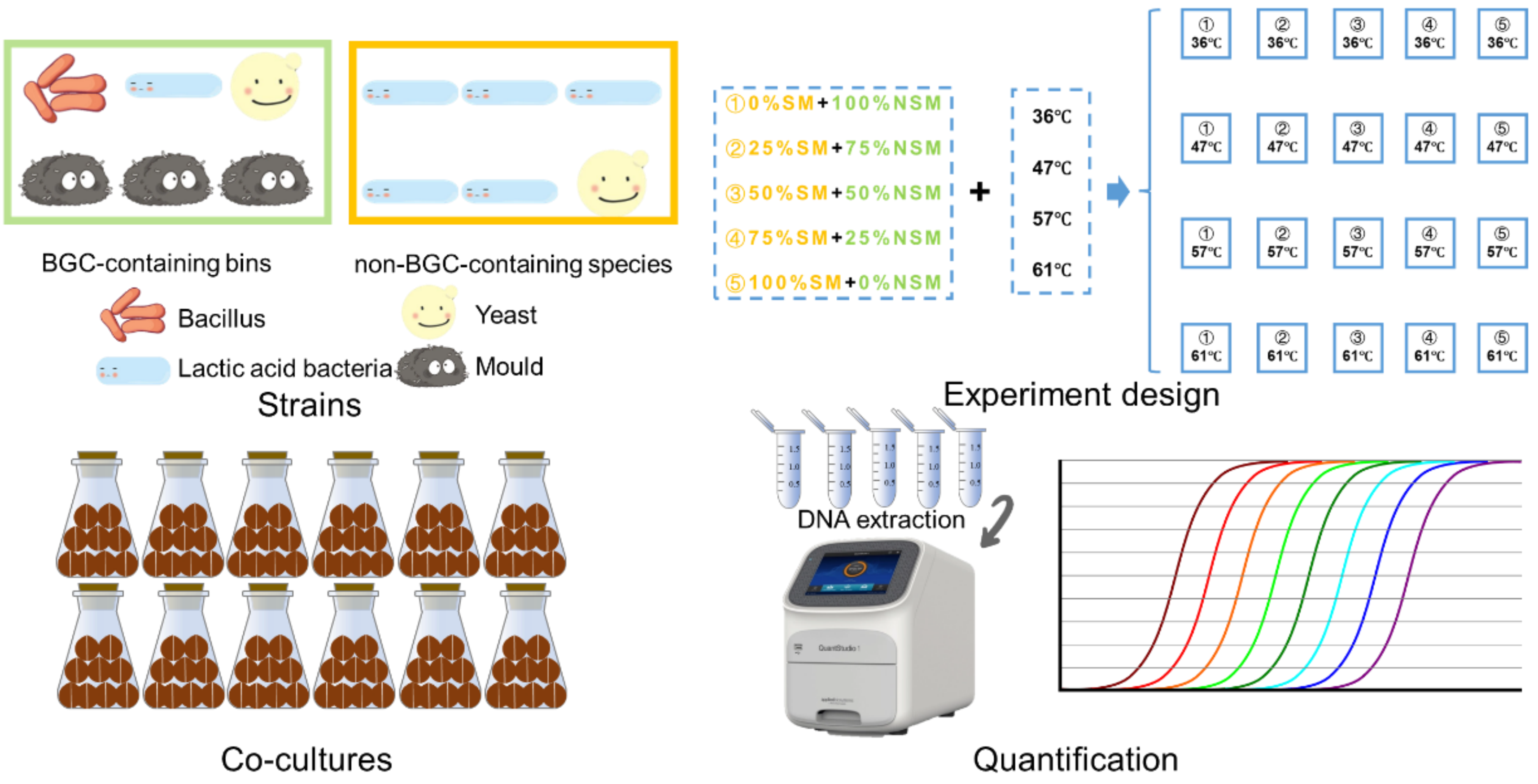
- Removal simulations showed the fundamental species caused the strongest stability loss—markedly **reducing robustness and collapse threshold**—therefore we define them as **fundamental species**

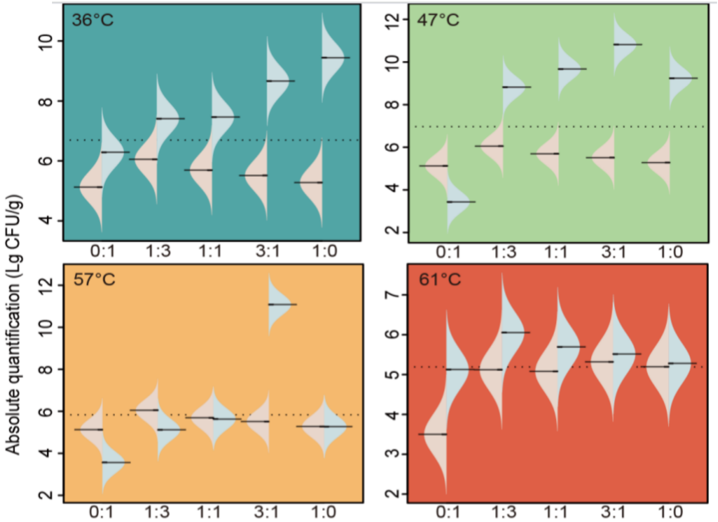


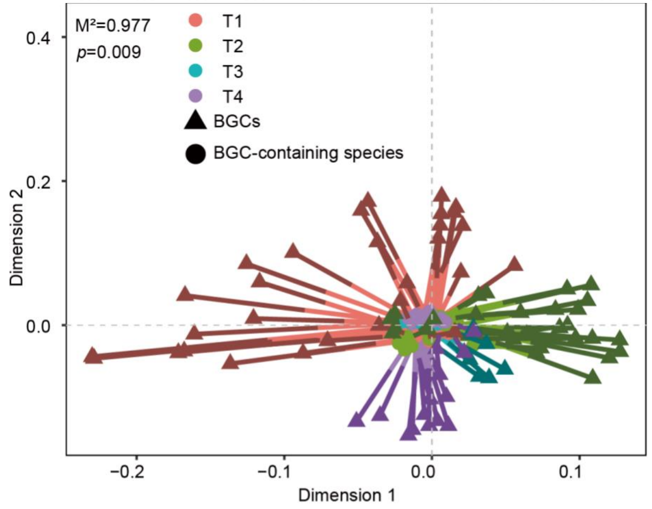




The role of the biomass of BGC-containing bins in maintaining microbial stability



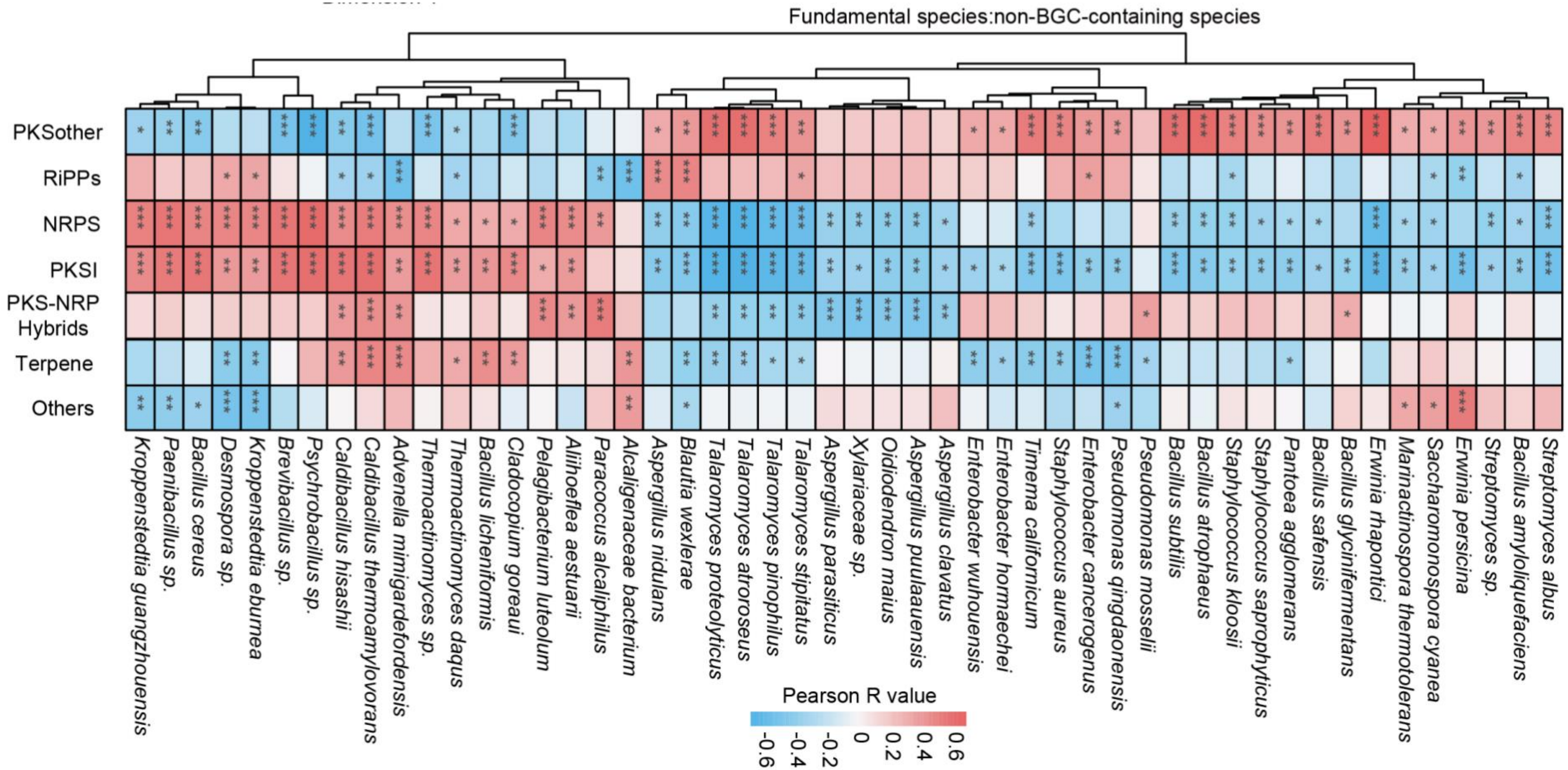




☐ **Procrustes/correlation** analyses showed BGC stability effects were largely driven by **BGC-containing bins**; 90.3% (149/165) significantly shaped community BGC content.

☐ **SynComs** confirmed that adding fundamental species increased total biomass across 36–61℃ (typically >50%, up to >215%) compared with communities without them.

The role of the biomass of BGC-containing bins in maintaining microbial stability



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- ☐ **SynComs** confirmed that adding fundamental species increased total biomass across 36–61℃ (typically >50%, up to >215%) compared with communities without them.
- ☐ Fundamental species enhance **heat tolerance, cohesion, and stability** during heating.

Summary

- Temperature acts as both a “destroyer” and a “reconstructor” during spontaneous *Daqu* fermentation, driving stage-specific ecological regimes.
- By integrating iCAMP with molecular ecological network analyses, we show that BGC-containing species strengthen interactions and cohesion to stabilize networks under thermal stress, and we identify six “fundamental species” with disproportionate effects on robustness and collapse threshold
- Loss of these fundamental species weakens interactions and destabilizes the community, whereas their presence supports recovery and functional persistence.
- SynCom co-culture validation shows consistent, temperature-dependent biomass advantages (≥50.08%), supporting BGC-associated fundamental species as stability nchors in thermally stressed fermentation ecosystems.

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