

Figure 1. Six study sites in Hong Kong with three types (MPA : Cape D'Aguilar [CDA, west]/Tung Ping Chau [TPC, east]; mariculture : Lamma [LM, west]/Sai Kung [SK, east]; sewage : Peng Chau [PC, west]/Center Island [CI, east]) and their environmental impacts. (a) Phase I (Seeding): 28 ARMS deployed (14/site) in MPAs for 12 months; 2 ARMS/site (dashed outlines) sampled. (b) Phase II (resistance): 4 ARMS translocated from MPAs to impacted sites (mariculture: LM/SK, sewage: PC/CI). After 12 months, half of the ARMS (dashed outlines) were sampled. (c) Phase III (resilience): remaining ARMS returned to original MPAs; all ARMS sampled after 6 months. (d) Heatmap of water quality during Phase II, normalized by regional means (east/west). Red/blue indicate values above/below the mean (dissolved oxygen inverted).

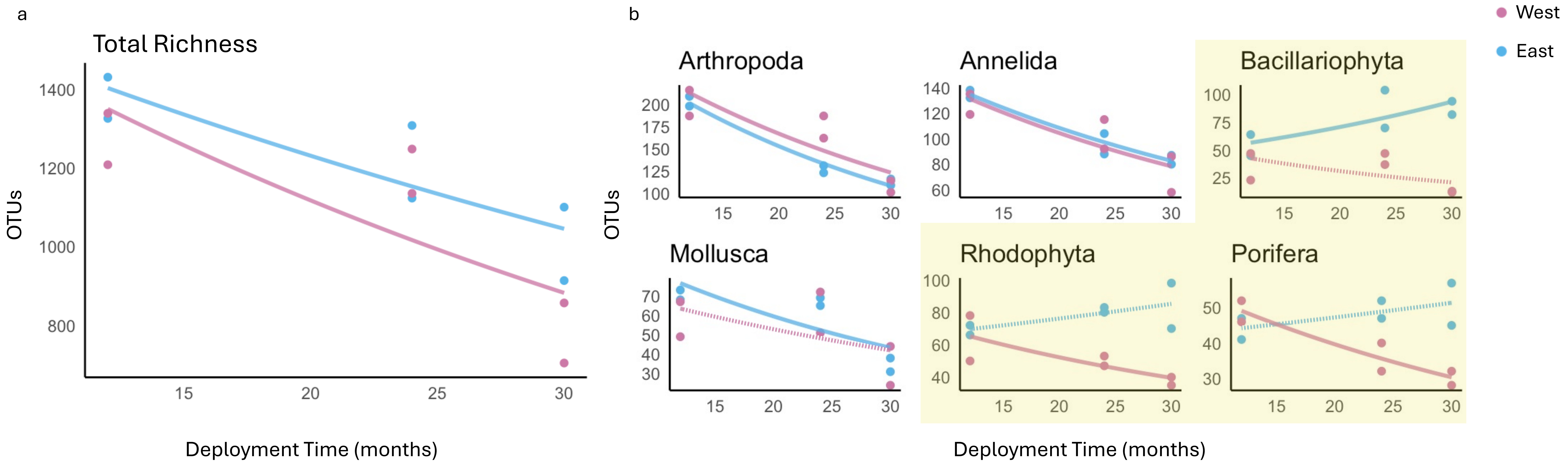


Figure 2. (a) OTUs in east (TPC, blue) and west (CDA, purple) MPAs over three phases: seeding (12 months), resistance (24 months), and resilience (30 months). Richness declines progressively in both MPAs. (b) Phylum-level richness trajectories for the six most abundant taxa. Sessile taxa (Bacillariophyta, Rhodophyta, Porifera; yellow boxes) exhibit different successional patterns between MPAs: East communities (TPC) sustain stable or increasing richness, while west (CDA) declines. All trends modeled with Negative Binomial regression. Dash lines indicated the log-rate slope was not statistically significant ($p>0.05$).

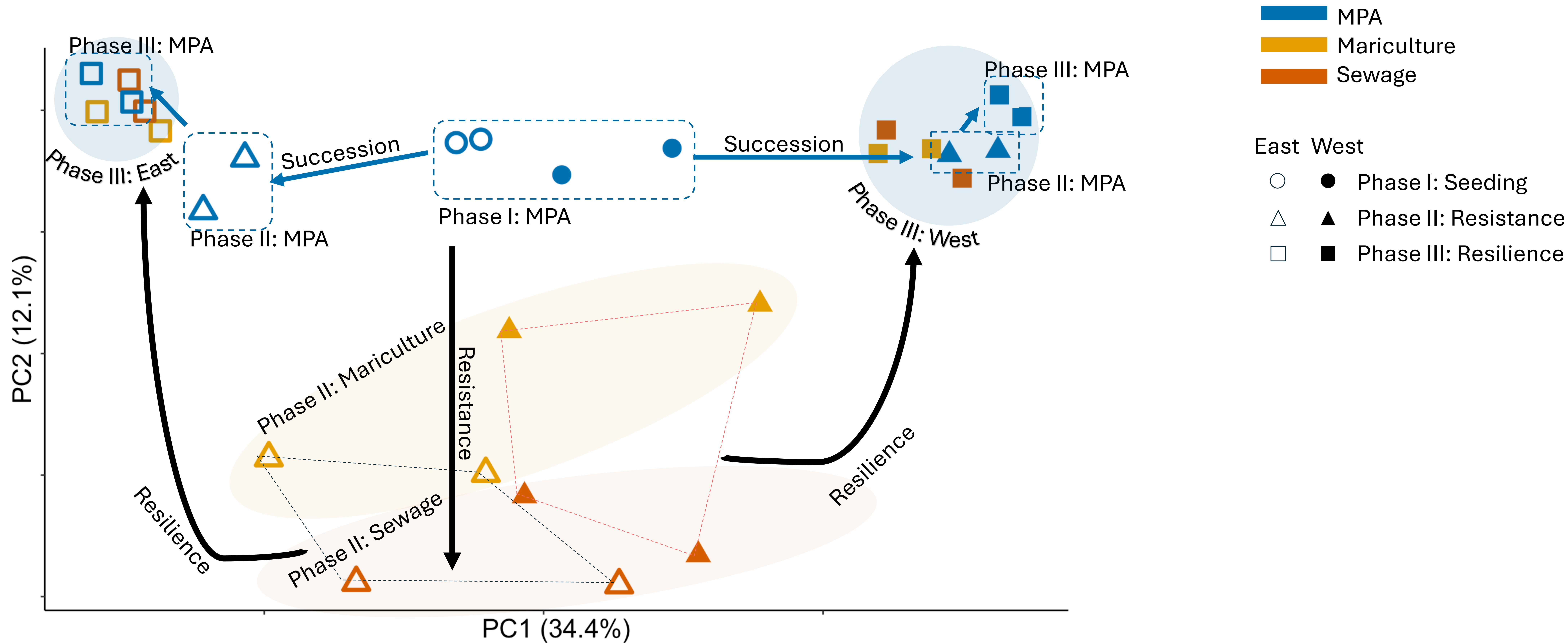


Figure 3. PCoA of all ARMS (Bray-Curits metric). Each point represents one community in different sites (MPA: blue, mariculture: yellow, sewage: red) from different phase (phase I: circle, phase II: triangle, phase III: square) across the east (hollow shape) and the west (solid shape). **Succession** was indicated by blue shapes in the top part of the plot where it started in the middle (circles) in the seeding phase, developing sideward through the resistance phase (triangles), and reached to both top corners (squares); communities translocated to the stressed sites during **resistance** phase moved downward with sewage communities on the bottom; after all communities were translocated back to the two MPAs in the **resilience** phase, all communities from the same seeding site clustered together on the two top corners. Note that in the west, phase II MPA communities (green triangles) were clustered together with all the resilience communities (top right) but the pattern is different in the east (top left).

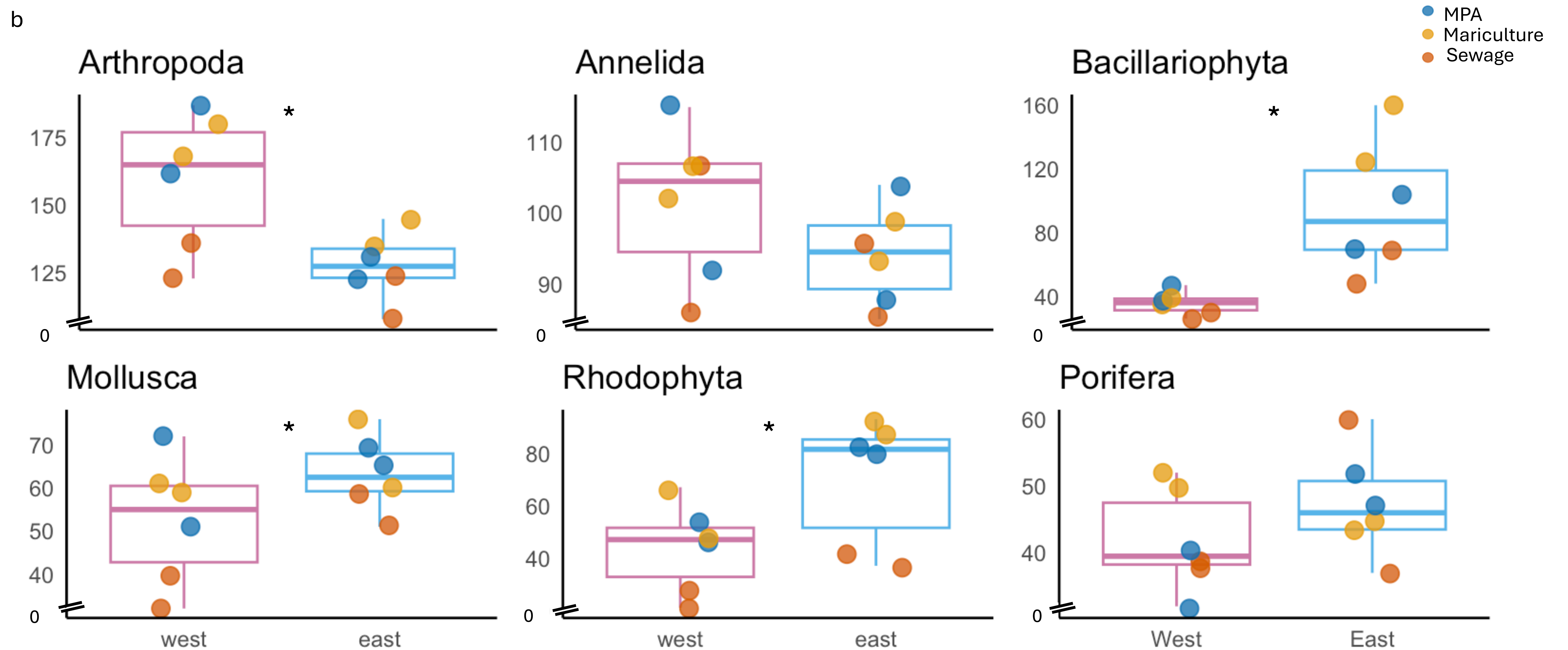
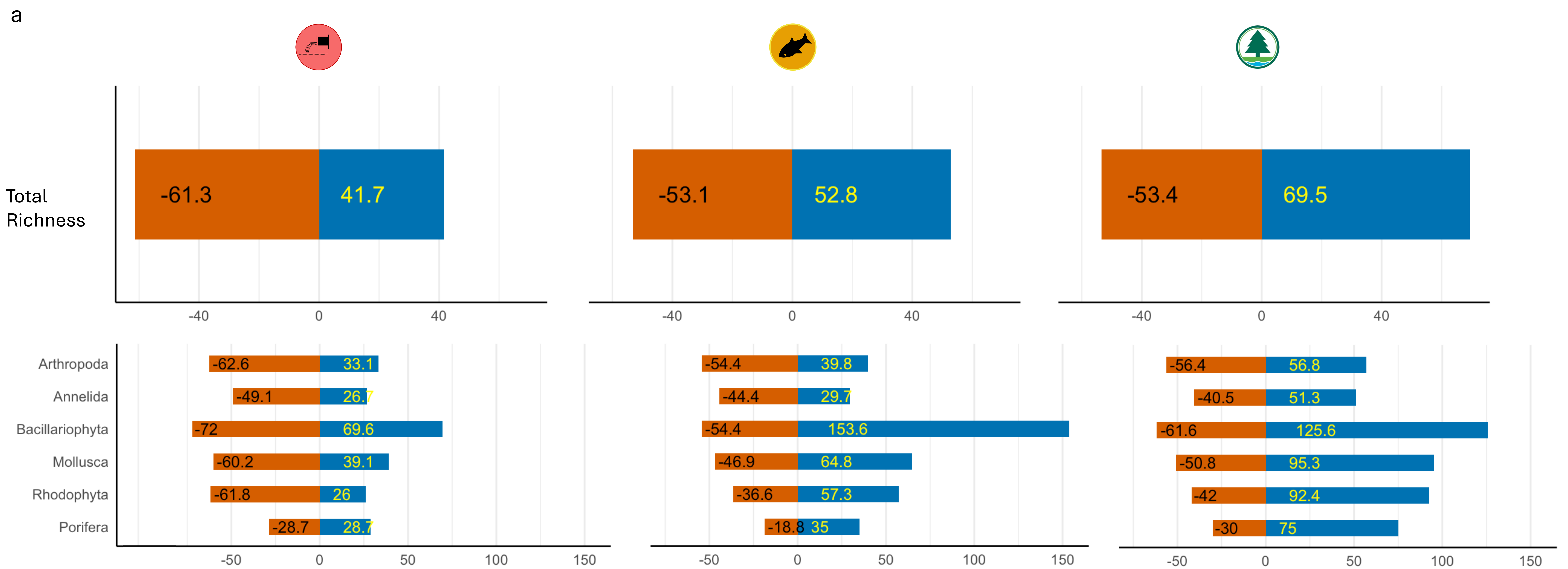


Figure 4. Changes in alpha diversity after resistance phase. (a) percentage total species richness loss (red) and gain (blue) of the resistance communities over the seeding communities (top); percentage species richness of the top six abundant phyla loss (red) and gain (blue) of the resistance communities over the baseline communities (bottom). (b) species richness difference over east and west by phyla. Asterisk indicate significant differences between east and west.

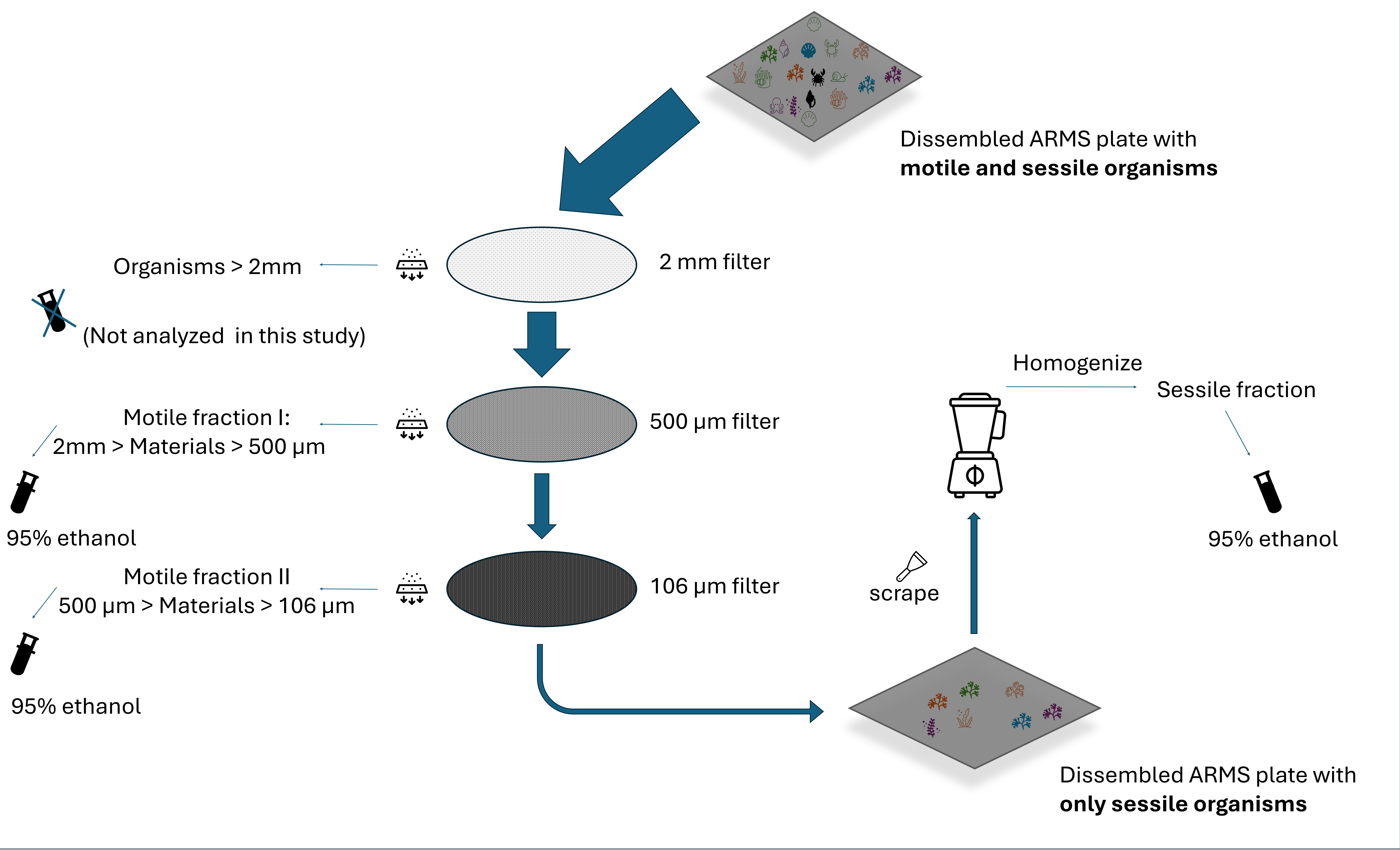
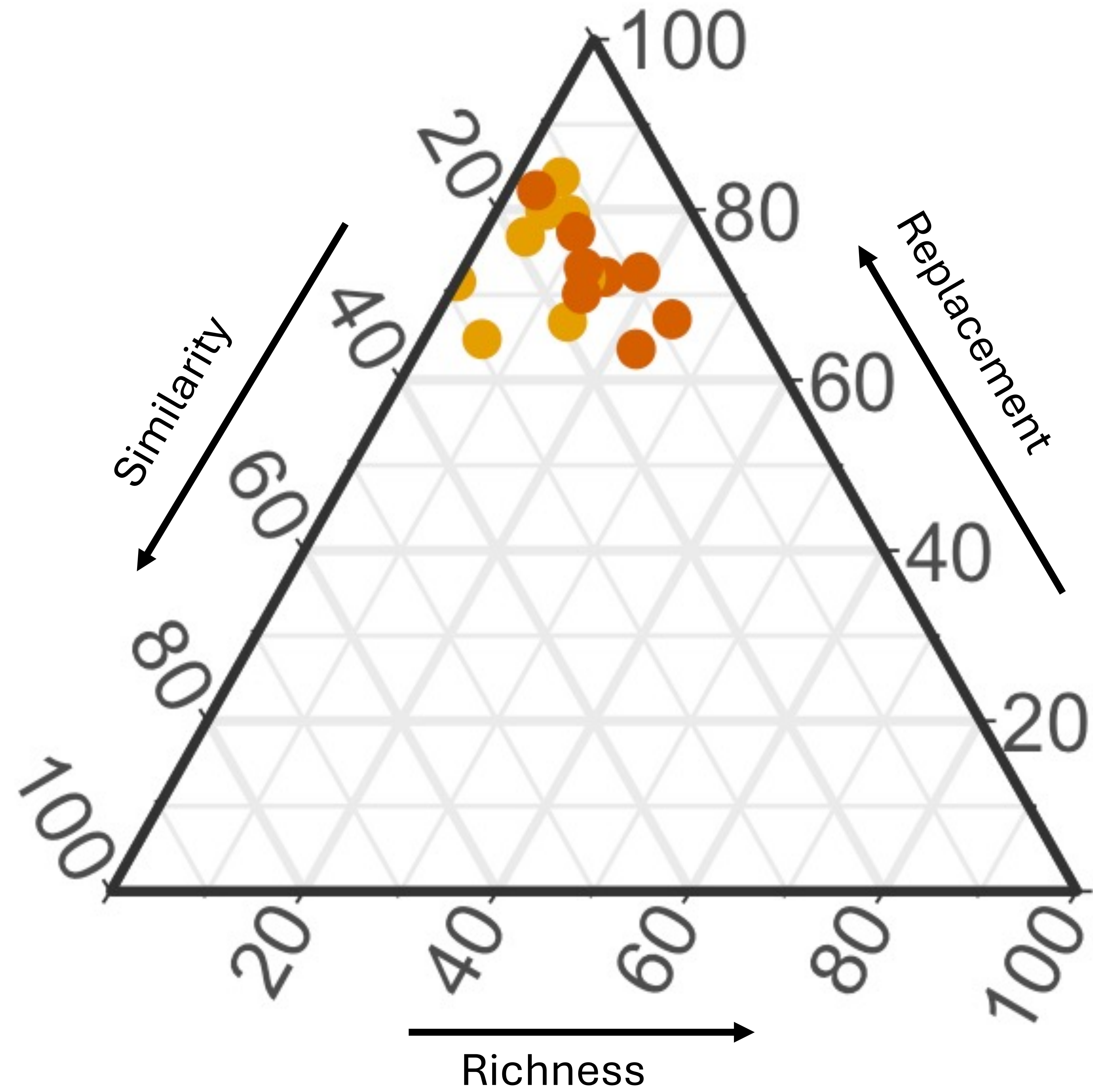


Figure S1. Post-disassembling, individual ARMS plates (top) were rinsed with filtered sea water to remove any motile organism and remaining debris. Dislodged materials were then sieved through a filter set of three (2 mm, 500 µm, 106 µm). Organisms over 2mm were not analyzed in this work. Motile fraction I and II were then preserved in 90% ethanol for later downstream processing. Sessile organisms retained on the plate were then scraped off and put though a blender to homogenize (sessile fraction), and then preserved with 95% ethanol.

Phase II: Resistance

Stressed communities vs MPA communities



Phase III: Resilience

Stressed communities vs MPA communities

● Mariculture

● Sewage

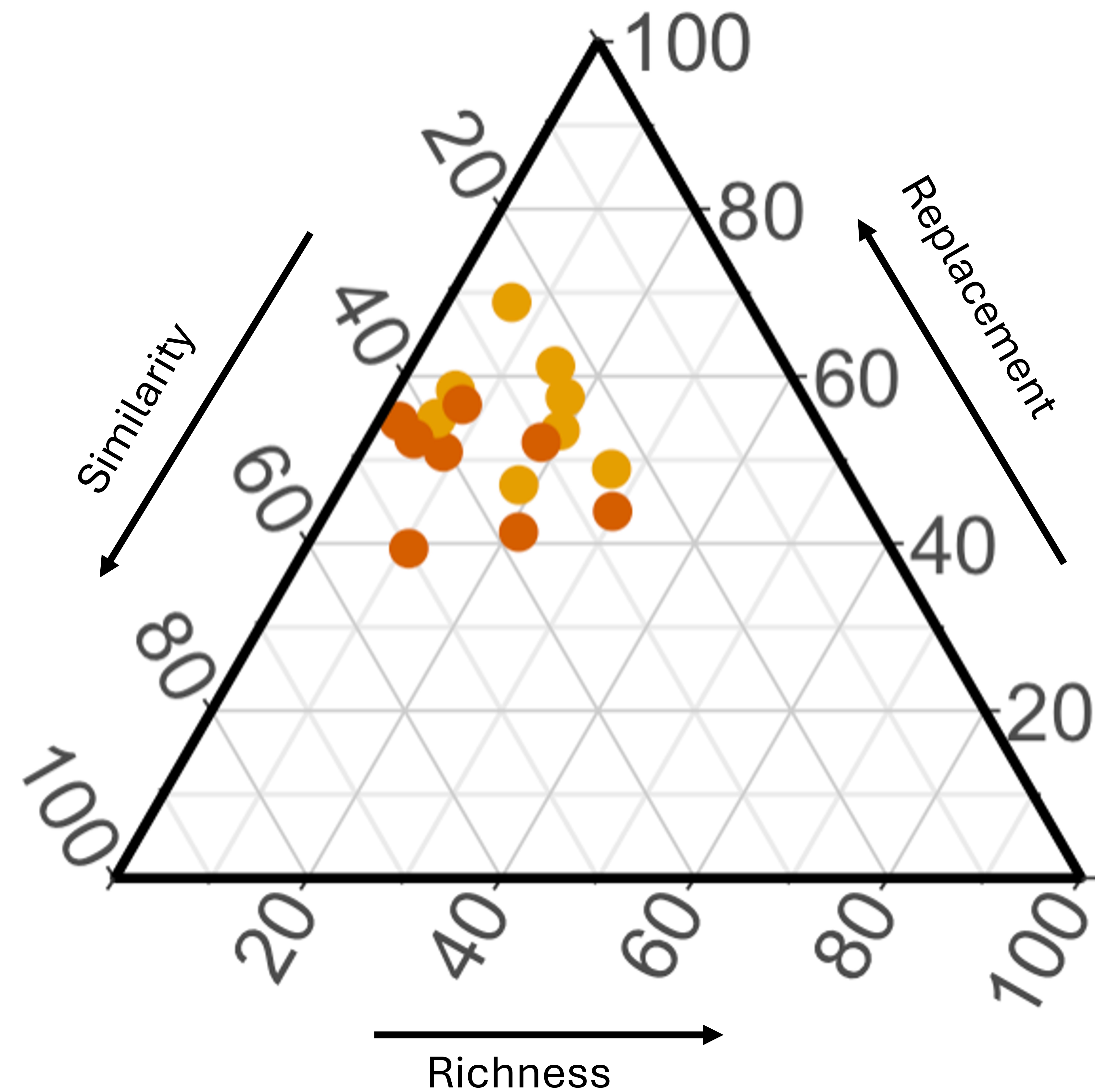


Figure S2. Ternary plots of beta diversity components (species replacement [β_{rp}], richness difference [β_{rich}]) during resistance (left) and resilience right) between stressed communities and MPA communities.