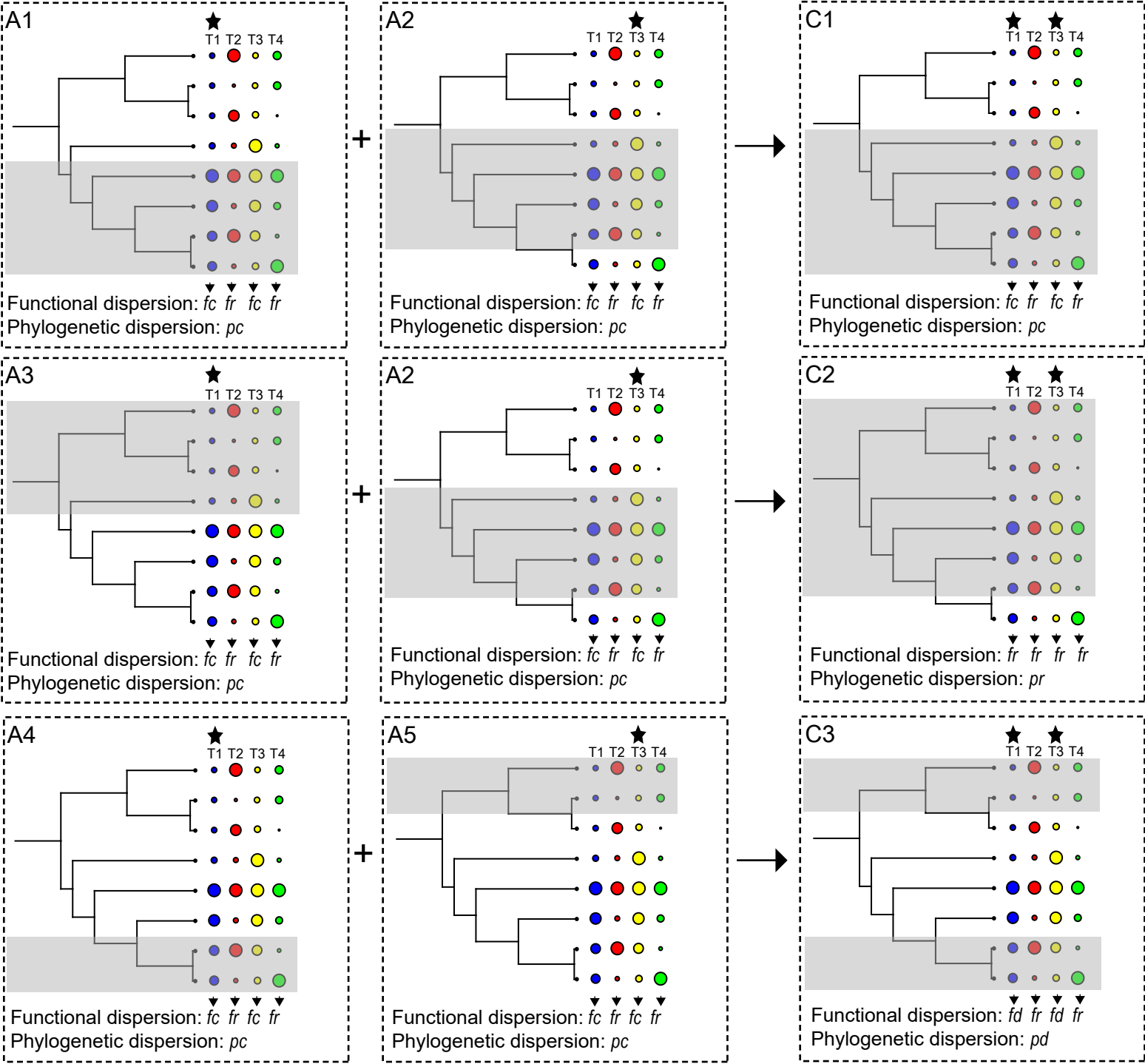


Simulated species, traits and phylogeny under environmental filtering effect in complex habitats

Scenario C contains two microhabitats Ai and Aj, predominated by phylogenetically conserved trait T1 or T3

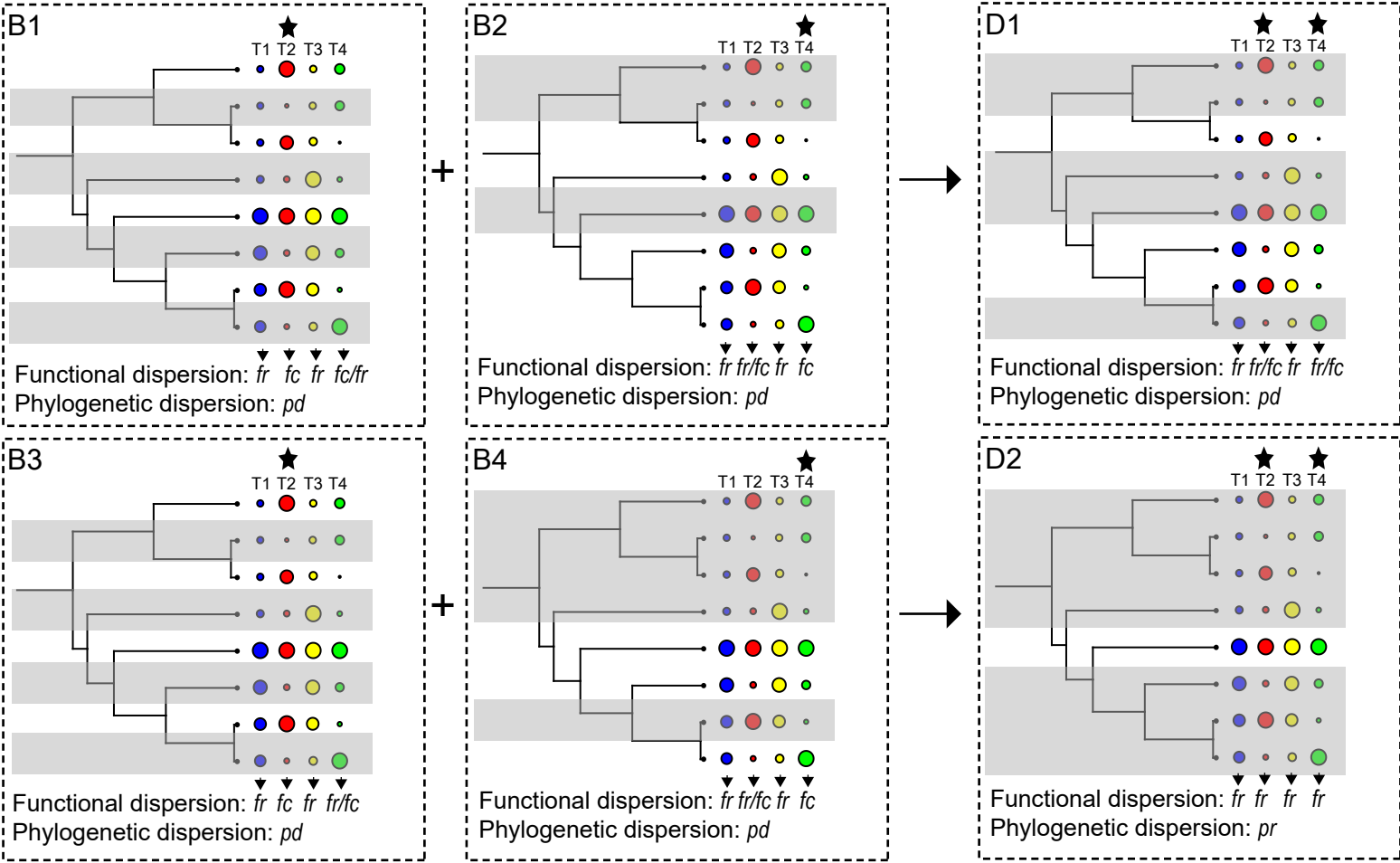


Due to environmental filtering within microhabitats acting on PreTrs T1 and T3, species within A1 and A2 are both clustered on phylogeny. If retained species are similar in two microhabitats, phylogenetic dispersion and PreTrs (T1 and T3) in C1 are expected to be clustered; AssTrs (T2 and T4) are expected to be functional random.

If retained species in two microhabitats occupy different subregions on the tree, phylogenetic dispersion and PreTrs (T1 and T3) and AssTrs (T2 and T4) are all expected to be random.

If retained species in two microhabitats occupy distant subregions on the tree, phylogenetic dispersion and PreTrs (T1 and T3) will perform functionally dispersed, whereas AssTrs (T2 and T4) should present random dispersion.

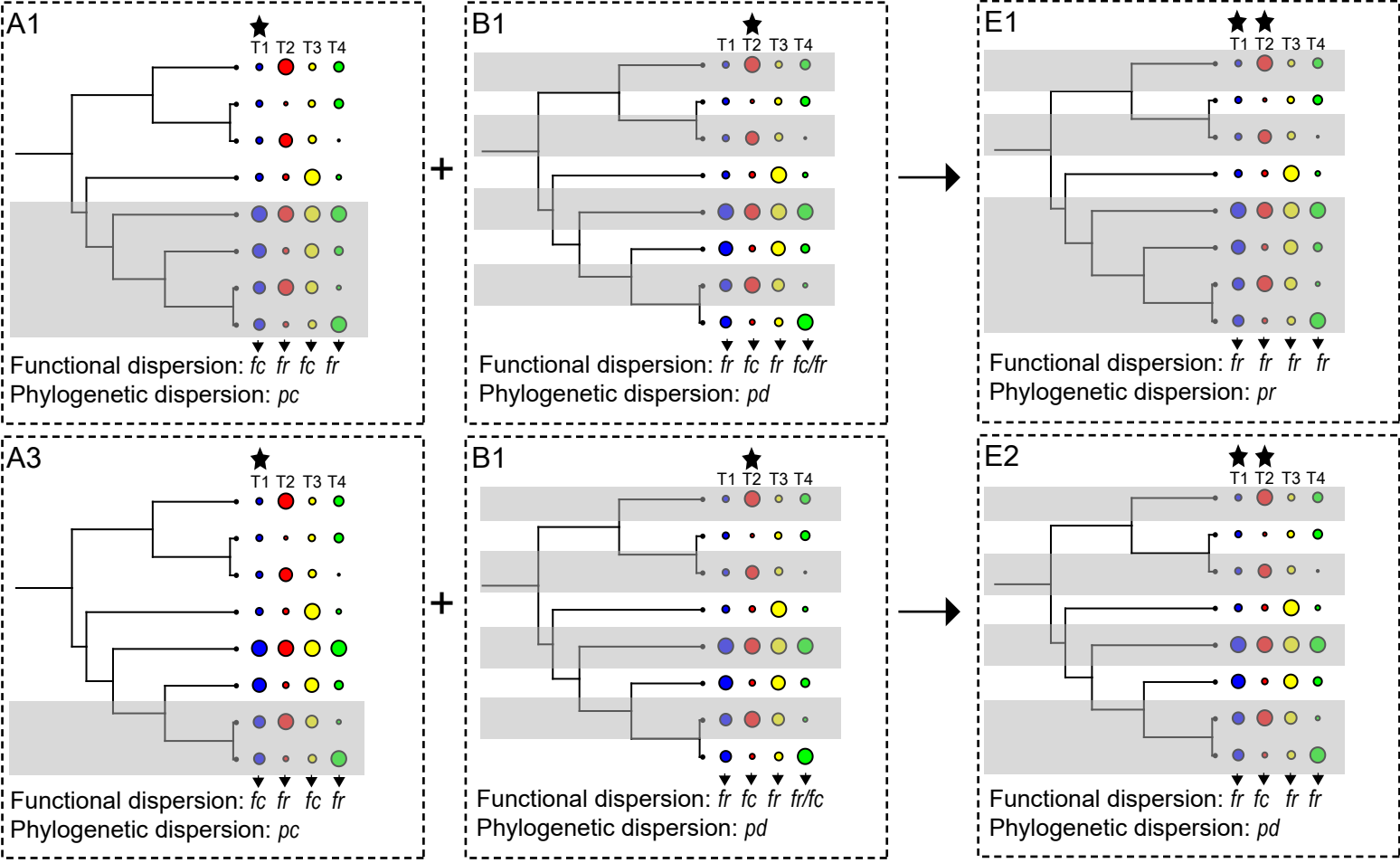
Scenario D contains two microhabitats Bi and Bj, predominated by phylogenetically convergent trait T2 or T4, respectively



Resulting from filtering effect within microhabitats B1 and B2, species are deserved to be dispersed on phylogeny. If retained species are similar in two habitats or one belongs to another, phylogenetic dispersion of D1 is expected to be dispersed; PreTrs (T2 and T4) are expected to be functionally clustered or random; AssTrs (T1 and T3) ought to be functional random.

If retained species in two microhabitats occupy different subregions on the tree, phylogenetic dispersion, PreTrs (T2 and T4) and AssTrs (T1 and T3) are all expected to be random.

Scenario E contains two microhabitats Ai and Bj, which are predominated by phylogenetically conserved T1 or phylogenetically convergent T2, respectively.



Environmental filtering effect is dominantly mediated by phylogenetically conserved trait T1 in A1 and convergent trait T2 in B1. Species are deserved to be phylogenetically clustered in A1 and dispersed in B1. If retained species in A1 occupy a relative large lineage on phylogeny, phylogenetic dispersion and functional dispersion of all traits in E1 are expected to be random.

If retained species in A3 occupy a relatively small lineage on the tree, species in E2 are deserved to be dispersed on phylogeny which is similar to B1. Therefore, the functional dispersion in E2 is expected to be dispersed for T2, but random for the rest trait (T1, T3 and T4).