Supplementary material

We developed a methodological approach to calculate the mean age of communities by join the information provided by an ancestral area reconstruction (Figure S1 A), species occurrence in communities and the bioregion at which each community are located (Figure S1 B). Figure S1 represents a hypothetical example to illustrate the calculation of mean age of three communities (Comm 1, Comm 2 and Comm 3) that present the occurrence of five species. Each node in the tree is represented by its ancestral state provided by the ancestral area reconstruction (bioregion A, B and C in Figure S1 A), in this example we assume that each node can made up to 3 bioregions. The first step comprises the calculation of arrival ages for each species in each community. Community 1 present species S4 and S5, in which all the ancestors of both species diversified inside biome A (Node 6 and Node 7), that is the same biome in which both species and ancestors occurred. In this case the arrival age for both species were set as 2 myr (Figure S1 C, line 1). Community 2 (bioregion B) present species S1, S2 and S3. The first two species arrived in bioregion B after the last event of speciation (Node 9), therefore, we assume that this comprises a recent event of historical dispersal, setting the arrival age the value of 0.00001. The last species (S3) arrived in bioregion B 1myr ago (Node 8). Finally, Community 3, located at bioregion C, present species S1 and S2 that both arrived in bioregion C 0.5 myr ago. We can calculate the average values for each line of matrix containing arrival ages (Figure S1 C) obtaining mean age for each community. In this example Community 1 is the oldest (2 myr), followed by Community 2 (0.66 myr) and the Community 3 (0.5 myr).



Figure S1: Hypothetical example illustrating the calculation of mean age of three communities (Comm 1, Comm 2 and Comm 3) that present the occurrence of five species (S1, S2, S3, S4 and S5). The information needed to obtain the arrival age of species in communities and mean age of assemblages (C) are an ancestral character reconstruction (A), a matrix of species occurrence and the bioregions in which each community are located (B).