



21st Evolutionary Biology Meeting at Marseilles

September 26th – 29th, 2017



Convergent Evolution: concepts, database, road map and case studies

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Most of the authors studying convergent evolution think about the apparition of a similar phenotype in two evolutionary independent lineages (Conway Morris 2003 , McGee 2011, Losos 2011 , Gordon et al 2015). From this broad definition authors focused on case studies: echolocation (Parker et al 2013) or repetitive adaptations of marine mammals (Foote et al 2015). However, cases of “repetitive similarities” should be defined in a better way.

We so far: i) proposed neologisms that can apply to any biological level: allo-convergent, iso-convergent and retro-convergent evolution. This is important since, in the case of iso-convergent evolution, one can suspect that the underlying molecular mechanism(s) could be similar (Stern and Orgozozo 2008). Such cases could then be used as meta-models (Kopp 2009) to decipher biological mechanisms at genetic, epigenetic, transcriptional or any biological level, ii) initiated the development of the LEIA database to store reported cases of convergent evolutions at the phenotypic level and sort out cases of iso-convergence, iii) developed a road map to study these cases at different biological levels, and illustrate the case studies of ovi-/vivi- parity transitions in mammals or in amniotes