

CIESM Congress Session : Genetic markers of biodiversity

Moderator : Anne Chenuil, IMBE, Aix-Marseille Univ., France

Moderator's Synthesis

Genetic markers of biodiversity are now extremely powerful and affordable. They potentially can contribute to

- i) the establishment of community species composition - a new possibility for multicellular organisms, metabarcoding being restricted to unicellular and planktonic cells until now,
- ii) phylogenetics reconstructions, and
- iii) intra-specific genetic structure description - an important contribution for the management of biodiversity, including connectivity assessment, reproductive mode, effective size estimations, and species delimitations.

The five communications illustrated the diversity of applications of genetic markers to biodiversity although they were mostly dealing with cryptic species: one case of species delimitations/ cryptic species on fish and one on sea urchins, one investigated the demographic history of an invasive alga, and two were on population differentiation in tuna and in jellyfish. Typical traps leading to inconsistencies using genetic tools without appropriate knowledge on population genetics processes were presented in the introduction and illustrated by certain presentations. For instance, the use of allozymes (ancient markers, old fashioned, yet still the best ones to answer many questions!) is often much more sound than the use of mitochondrial sequences. Not any genetic marker can answer every question. Now that technology is deeply revolutionizing this field, using suboptimal methods should be avoided but this will require training of mediterranean marine biologists.

