SEAWEED DISTRIBUTION IN CALVI BAY: FROM 35 YEARS OF TEMPORAL CHANGES TOWARDS R MODELLING OF DISTRIBUTION MAPS.

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http://www.stareso.ulg.ac.be/projets-collaborations/stare-capped/

Introduction
1. Seaweeds often display high biodiversity and important roles in coastal habitats, from surface to over 80 meters; their community specific composition and status are natural integrating witnesses of environmental conditions (Fig. 1).

2. Calvi Bay (Corsica, France) is a reference site in the Western Mediterranean Sea, qualified as pristine. The oceanographic research station STARESO and Liège University initiated seaweed surveys in 1979 and 1991 along 24 historical transects (Fig. 2) [1,2].

Objectives
Reassess seaweeds community status in Calvi Bay, extend the geographic and depth ranges of their monitoring, developing R tools associated to a compilation of all distribution data to allow an improved synthesis, vision and statistics, from average profiles at bay scale to remarkable sub-areas.

Methodology
In 2013-2015, new records of macroalgae communities specific composition and cover rate were estimated in scuba-diving, subsurface Calvi or apnea observation, both at historical transects locations (0-15 m), as along additional ones (shallow horizontal 0-3m, deeper 0-40 m) (Fig. 2) [3,4]. In 2016, imagery from a ROV (Remotely Operated Vehicle) campaign were exploited to evaluate the complementary potential of such approach in usual sites, as assess macroalgae cover in less investigate habitats or areas [6]. Overall, Macroalgae communities are estimated within 96 transects and categorized into 89 biological units (+ 80 species + 9 turf communities).

Results
1. Evolution of surface communities (0-3m) allowed the quantification of water masses quality through the CARLIT index, synthesising ecological status (Fig. 3): reduction from “very good” (0.75) in 1979 to “good” (0.65) in 1991, then recovering to “very good” (0.81) in 2014 [4,5].

2. Macroalgal distribution depth profiles of all algae are compiled with R codes to produce some synthesis of their distribution (max depth, min depth, depth of max coverage, graphs of average fitted, or detailed profiles (Fig. 4). Cystoseira brachycarpa constitutes widespread seaweeds fields over rocky habitats between the surface and 30 m. After a regression in some sites during the 80-90’s, the reconstitution of their populations confirms an improvement of local environmental conditions. South of STARESO station, was present from 0.5 to 10 m in early 80’s, absent in early 1990’s, and observed back from 1 to 9 m since 2014 (cover rates > 70%, 240 ind./m², 5 kg/m² fresh biomass). Depth distribution range is not completely recovered in the whole Bay (0.5 - 3.5). In some sites, the massive presence of filamentous algae (up to 95%, Fig. 1) can induce local degradations of native communities [3,4].

Conclusions
Large amount of information is being compiled concerning macroalgae in Calvi Bay. R tools are developed to facilitate analysis and visualisation of spatial-temporal patterns. 2013-2016 surveys confirmed the high general biodiversity of Calvi bay, underlined improvement of its ecological status between 1991 and 2014, precised the depth distribution range, cover rate ranges and optimal depth of many macroalgae. It also allowed identification of species not yet referenced in the bay (i.e. Cystoseira forniculaca). Yet the proximity between filamentous algae maximum cover rate and main sewage outlet together with the surrounding particular accumulation visible on ROV imagery do stress the importance of sustaining on-going efforts in wastewater treatments to protect biodiversity and ecosystem pristine functions.

Highlights
1) Important Macroalgae distribution dataset in Calvi bay
2) Very good global ecological status and high biodiversity confirmed from macroalgae.
3) Adapted distribution modelling and mapping are required to improve understanding of macroalgae roles and reactions to environmental and anthropic pressures in that ecosystem.

http://www.phytoysystems.ulg.ac.be/en/groups/eukaryotic-phylogenomics
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References: