

Colourful relationships: Deciphering host and microbial origin of pigment profiles in Mediterranean sponge holobionts

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Many marine holobiont organisms, and in particular sponges, display colourful patterns with potential ecophysiological functions, such as photoprotection, visual awareness of toxicity/repellence, or even mimicry. Pigments may derive from host production, or from microbial origin, often involving photosynthetic taxa. Among the prokaryotic associates, Cyanobacteria seem to contribute most to the sponge colour sketch in certain species. Their presence, depending on the specific strains involved, may further entail symbiotic roles implicating compound exchange, nutrient and waste recycling. In this study we examined four Mediterranean sponge holobionts: *Petrosia ficiformis*, *Chondrosia reniformis*, *Chondrilla nucula* and *Crambe crambe*. These species were previously described to either host (*P. ficiformis*, *C. nucula*, *C. crambe*) or lack (*C. reniformis*) cyanobacteria, based on microscopy data. We analyzed sponge-associated cyanobacterial communities through 16S metabarcoding, and performed pigments profiling via HPLC and spectrophotometry, aiming to decipher the presence and origin (host or symbiotic) of the pigments with focus on the role of cyanobacterial populations. *C. nucula* and *C. crambe* revealed the highest relative abundance of cyanobacteria (~20% and ~10%), with respect to *P. ficiformis* and *C. reniformis* (<1%). Pigment patterns indicated that *C. nucula* had a clear symbiosis with cyanobacteria, whereas, *P. ficiformis* reported intact and partially degraded photosynthetic pigment forms. In *C. crambe* we identified host carotenoids, and cyanobacteria-belonged pigments. No carotenoid or chlorophylls were detected in *C. reniformis*. These data may suggest different roles of cyanobacteria in the target species, including strict symbiotic trophic associations for host nourishment, photoprotection or even cell farming (phagocytosis).