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Sommario/riassunto	<p>Modern molecular -omics tools (metagenomics, metaproteomics etc.) have greatly contributed to the rapid advancement of our understanding of microbial diversity and function in the world's oceans. These tools are now increasingly applied to host-associated environments to describe the symbiotic microbiome and obtain a holistic view of marine host-microbial interactions. Whilst all eukaryotic hosts are likely to benefit from their microbial associates, marine sessile eukaryotes, including macroalgae, seagrasses and various invertebrates (sponges, acidiants, corals, hydroids etc), rely in particular on the function of their microbiome. For example, marine sessile eukaryotes are under constant grazing, colonization and fouling pressure from the millions of micro- and macroorganisms in the surrounding seawater. Host-associated microorganisms have been shown to produce secondary metabolites as defense molecules against unwanted colonization or pathogens, thus having an important function in host health and survival. Similarly microbial symbionts of sessile eukaryotes are often essential players in local nutrient cycling thus benefiting both the host and the surrounding ecosystem. Various research fields have contributed to generating knowledge of host-associated systems, including microbiology, biotechnology, molecular biology, ecology, evolution and biotechnology. Through a focus on model marine sessile host systems we believe that new insight into the interactions between host and microbial symbionts will be obtained and</p>

important areas of future research will be identified. This research topic includes original research, review and opinion articles that bring together the knowledge from different aspects of biology and highlight advances in our understanding of the diversity and function of the microbiomes on marine sessile hosts.
