# SYNTHETIC BIOLOGY STRATEGIES FOR THE HETEROLOGOUS PRODUCTION OF MYCOSPORINE-LIKE AMINO ACIDS FROM MARINE MICROBIOME

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**Abstract**

In recent decades, growing awareness of the health risks associated with ultraviolet radiation (UVA: 320–400 nm; UVB: 280–320 nm) has driven a significant rise in the global production and use of sun protection products (1). Furthermore, the chemicals present in skincare products can lead to side effects, highlighting the growing demand for bio-based sunscreen ingredients (2). Oceans encompass a vast array of habitats and environmental conditions that support immense microbial biodiversity. Many marine organisms have developed mechanisms to protect themselves from the harmful effects of UV radiation by producing UV-absorbing compounds, including scytonemins (unique to cyanobacteria), mycosporines, mycosporine-like amino acids (MAAs), carotenoids, and melanin (3). This variety of compounds holds significant promise for cosmeceutical and cosmetic applications due to their photoprotective, anti-aging, antimicrobial, antioxidant, and moisturizing properties (4). The access to the large marine reservoir of molecules is limited by the relatively low amount of microorganismw that we are able to cultivate, which is a fraction of the marine microbiome. In this study, metagenomics is used as a powerful tool to unveil MAA biosynthetic enzymes of curated marine microbiomes on MGnify. Several clusters of MAAs were predicted using AntiSMASH and the genes were synthetized and cloned. The heterologous expression of MAAs clusters in *E. coli*, revealed the production of different MAAs, detected by LC-MS/MS analysis. This strategy demonstrated the possibility of functional accessing marine microbiome via metagenomes and could be the starting point for the production of different type of MAAs though microbial cell factory.

**Keywords:** Marine microbiome, metagenome, UV, absorbing compounds, mycosporine, heterologous expression

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