Mass spectrometry is becoming essential for identifying and characterizing the different forms of life present on Earth and their intimate, complex, functional mechanisms. We recently reviewed the different applications of mass spectrometry and proteomic approaches in the field of environmental microbiology ([1], [2], [3]). Profiling approaches by whole-cell MALDI-TOF mass spectrometry or specific biomarker searches are reliable, quick and cost-effective methods for screening for new microorganisms and assessing microbial diversity. Several examples will be given to illustrate the potential of mass spectrometry in environmental microbiology, with specific emphasis on marine proteogenomics. Proteogenomics consists of high-throughput identification and characterization of proteins by extra-large shotgun tandem mass spectrometry approaches and the integration of these data with genomic data ([4], [5]). We compared twelve Roseobacter exoproteomes and revealed the different adaptive strategies these marine bacteria have adopted ([6]). We also recorded large proteomic datasets in order to better annotate their genomes and proposed a re-annotation of the whole marine Roseobacter clade ([7]).

Furthermore, we defined specific biomarkers to screen for new Roseobacter isolates on the basis of genomic and proteomic data. Today, the analysis of environmental samples with the whole-cell MALDI-TOF mass spectrometry approach still represents a challenge due to the enormous microbial diversity existing on earth and the lack of a comprehensive database [8]. We defined widely distributed biomarkers for bacteria belonging to the Roseobacter clade. Figure 1 shows the highly divergent pattern of biomarkers for nine representative bacteria analyzed by MALDI-TOF mass spectrometry. These nine representatives were: Oceanicola batensis HTCC2597, Pelagibaca bermudensis HTCC2601, Roseobacter denitrificans OCH114, Phaeobacter gallaeciensis 2.10, Oceanibulbus indolifex HEL45, Roseobacter littoralis OCh149, Roseobacter sp. MED193, Roseovarius maritimus ISM and Dinoroseobacter shibae DFL12. We could predict by proteogenomics the exact masses of three relevant biomarkers: HU, L29 and L30 proteins for all the sequenced organisms from the clade. We screened a collection of 93 isolates from water sampled from Mediterranean Sea and grown on marine medium. The three biomarkers resulted in six possible m/z (monoprotonated and diprotonated ions) amongst a list of 103 theoretical values. From the systematic MALDI-TOF analysis of these 93 isolates, we could identify and document three new Roseobacter strains: a novel representative of the Phaeobacter genus, a member of the Thalassobacter genus and another Ruegeria strain (unpublished data). The later isolate originated from sea water sampling during a phytoplankton bloom. Due to its simplicity and effectiveness, this technique could be of immense value for monitoring bacteria.

**References**


**Fig. 1.** Whole-cell MALDI-TOF spectra of nine Roseobacter representatives. Spectra were acquired on a MALDI-TOF BiflexIV mass spectrometer (Bruker Daltonics). The m/z range where the HU, L29, L30, L32, and S17 proteins are detected as monoprotonated ions is shown.