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Proteotyping bacteria and fungi by phylopeptidomics: pre-analytical factors review and potential

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Short abstract:

High-throughput identification of microorganisms is key for clinical diagnostics and microbiology in general. Mass spectrometry for proteotyping microorganisms has been shown efficient because rapid and low cost. Recent studies have demonstrated the discriminative power of proteotyping based on tandem mass spectrometry. As this technology can quickly identify the most probable taxonomical position of any microorganism, even if not yet previously characterized in terms of taxonomy, and discriminate closely related strains, its application on environmental isolates, new emergent threats, or large collections has been promoted. Here, I will introduce the phylopeptidomics methodology with striking examples, its potential to be multiplexed and thus applicable on thousands of samples, and review the pre-analytical factors required for its application. The potential and perspectives of this methodology will be also commented, as it apply even on mixtures of microorganisms and complex microbiota. The methodology is thus applicable on collections of more complex samples.