Artefacts of MALDI sample preparation investigated by high-resolution Scanning Microprobe MALDI Imaging mass spectrometry (SMALDI-MS)

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MALDI dried droplet preparations using 2,5-dihydroxybenzoic acid as a matrix were investigated by scanning microprobe matrix-assisted laser desorption/ionization mass spectrometry (SMALDI MS). Mass spectrometric images of lateral distributions of sample components and impurities were obtained with a lateral resolution of 1 μm. Results show the crystallization behavior of the matrix as a function of various physico-chemical parameters as well as inhomogeneous separation of components on various scales between millimeters and sub-micrometers. Segregation was found to be a sample-wide, crystal-wide and sub-crystalline, general phenomenon. Effective parameters in this context are hydrophobicity, polarity, and mobility, among others. Peptide ion signals were observed from inside the matrix crystals, while carbohydrate signals and alkali ion signals were observed predominantely from outside the larger matrix crystals.

The described investigations shed some light on processes that cause well-known problems of quantification and sample suppression in MALDI MS. They also help to optimize matrix preparation for high-resolution MALDI imaging of biological samples.

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