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CLOUD METABOLOMICS - RESPONSE TO COLD SHOCK IN BACTERIA ORIGINATING FROM CLOUDS

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The presence of microorganisms in the atmosphere was demonstrated a long time ago. Only recently the detection of metabolic activity in clouds (Sattler et al., 2001) raised questions about their implication in the physico-chemical processes occurring in these environments. The first results revealed that microorganisms are contributing to the transformation of organic compounds in cloud water (Vaitilingom et al., 2013); they also could be responsible for the formation of ice crystals (Attard et al., 2012; Joly et al., 2013), which leads to precipitations (Lohmann & Feichter, 2005). However, these environments are harsh for microorganisms: low temperatures, high UV radiations and oxidants, freeze-thaw cycles, lack of nutrients and highly dynamic conditions. Hence, it is thought that bacteria living in clouds have specific adaptations for surviving and successfully disseminating by air means. In this context, we aim at documenting those potential physiological particularities through -omics approaches, for complementing previous results.

In this study we investigated the response of *Pseudomonas syringae*, a species commonly found alive in clouds (Vaitilingom et al., 2012), to temperature downshifts. After extraction of polar (and slightly non-polar) compounds, we analyzed metabolic profile of cells exposed to low temperature through LC/MS and NMR using Metabolic Profiler® facility. Multivariate statistical tools highlighted numerous elements (116 ions and 216 buckets) for relevant contribution. From this, we identified biomarkers involved in cold stress metabolism, such as trehalose, glutathione and amino acids.

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