Mass spectrometry-based proteomic investigation of novel therapeutic strategies for triple negative breast cancer

Sveva GERMINI - *Istituto Superiore di sanità*

Latest developments in mass spectrometry (MS) give a crucial contribution to the investigation of proteins involved in human health and disease, thanks to dramatically improved sensitivity and scan speed, which enhance proteome coverage depth and accurate quantification in high-throughput proteomic analyses. The innovative MS data-independent acquisition (DIA) mode achieves higher reproducibility and proteomic depth than the conventional data-dependent acquisition (DDA) one.

Moreover, emerging deep neural networks based algorithms make it feasible to unravel the inherent DIA data complexity even without any spectral library. We have applied an advanced combination of state-of-the-art MS techniques and data analysis tools to investigate a drug repurposing therapeutic strategy for triple negative breast cancer (TNBC), an aggressive tumour lacking efficient treatments so far. We have analysed the effect on TNBC cells' proteome caused by the anti-diabetic agent metformin and/or the phosphatidylcholine-specific phospholipase C-inhibitor D609: our data show key biological pathways modulation, shedding light on the possible drug mechanism of action.