

ORAL PRESENTATION

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“Omic” landscapes of breast cancer - the end of the beginning

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Breast cancer is the most common malignancy and the second cause of cancer mortality in women. Despite tremendous progress, with 80% overall survival at 10 years, the outcomes of the disease are extremely heterogeneous and it is very hard to predict prognosis and response to therapy. This clinical behaviour reflects the underlying heterogeneity of breast cancers and the characterization of these at the molecular level is the first step towards truly individualized cancer management. We have now profiled over 2000 breast cancers with linked clinical outcome data at the genomic, transcriptomic and epigenomic level. This constitutes the largest “omic” dataset ever gathered in human cancer and the molecular landscapes obtained provide unique insights into the biology and clinical behaviour of breast cancer. Our laboratory is now exploring the potential translation of this knowledge into better prognostic and predictive markers, and in parallel is studying its functional significance at the cellular and organism level with the aim of unravelling the mechanisms of mammary gland malignant transformation.

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