Dr. Rosaria Orlandi - CURRICULUM VITAE

Educational Background

2003-2004
Master in Bioinformatics, University of Torino - Fondazione per le Biotecnologie
1997-1998
School of Management of Technology, University of Milan
1992-95
School of Applied Genetics (Cytogenetics and Molecular Genetics), University of Milan
1977-1981
Ph.D. Degree in Biology, University of Milan

Professional Experience

1991-to date
Dirigente Sanitario Biologo
Department of Experimental Oncology, Fondazione IRCCS Istituto Nazionale dei Tumori (INT), Milan, Italy
1989-1991
Research Associate
Division of Experimental Oncology, Istituto Nazionale Tumori (INT), Milan, Italy
1987-1988
Post-Doctoratal Fellowship
Laboratory of Dr G. Winter, Medical Research Council, Cambridge (UK)
1982-1986
Post-Doctoratal Fellowship
Division of Experimental Oncology, INT, Milan, Italy
1979-1981
Student Apprenticeship
Institute of Biochemistry, Faculty of Biology, University of Milan

Scientific Research

Development of murine and engineered monoclonal antibodies (MAbs) for cancer immunodiagnosis and immunotherapy

- development of the cloning strategy for immunoglobulin variable domains by polymerase chain reaction (Orlandi et al., PNAS 1989);
- production and characterization of murine and chimaeric MAbs;
- generation of immunoconjugates using MAbs and toxins and analysis of their activity *in vitro* and *in vivo.*

Structural and functional analysis of molecular targets of therapeutic MAbs

- biochemical analysis of glycoproteins and glycolipids identified by Mabs and differentially expressed on tumor cells;
- studies on expression of proto-oncogenes and oncogenes in cellular models;
- epitope mapping of complex epitopes on $p185^{HER2}$ oncoprotein
- studies on cellular function and involvement in cancer progression of the novel human gene Sel1L**.**

Development of Peptide Phage Display in HER2 models

- Selection of phage-displayed peptide libraries using anti HER2 MAbs for identification of tumor-antigen mimics (Orlandi et al., Europ Journal of Immunol 1994)
- Engineering of a phage-displayed peptide with specific binding to HER2 receptor for targeted gene transduction of mammalian cells (Urbanelli et al., J.Mol.Biol.2001)

Cancer Biomarker Discovery

- Identification by Mass Spectrometry of complement component C3adesArg and a C-terminal–truncated form as candidate breast cancer serum biomarkers Identified (Li et al, Clinical Chemistry 2005)

- Identification of hepcidin and ferritin ligh chain blood levels as potential diagnostic marker for breast cancer (Orlandi et al. Ann Oncol. 2013) and studies on iron-related molecules in cancer plasma and tissues (Ciniselli et al., 2016; Pizzamiglio et al., 2017) .
- Discovery of potential early diagnosis biomarkers analysis in plasma samples of breast cancer patients (AIRC 5x Mille "Tumor-Microenvironment related changes as new tools for early detection and assessment of high-risk disease" (Giussani et al., Cancers (Basel) 2021)
- Profiling of plasma cytokines and blood immune cells in breast cancer patients for pathological complete response prediction (FP7 IMMUNOCAN. Miceli et al., Clinical Breast Cancer, 2022).

Functional genomics

- Studies on expression profile of Extra Cellular Matrix (ECM) genes and identification of ECM signatures in breast cancer (Bergamaschi et al, J Pathol. 2008; Triulzi at al. PlosOne 2013; Triulzi et al, Clinical Cancer Res 2014, Sangaletti et al., 2016 Cell Rep; Giussani et al., J Cell Physiol. 2018, Mercatelli et al., J Biophotonics. 2020).
- Comparative analysis of gene and miRNA expression of breast cancer from Chinese and Italian patients (Huang et al, Cancer Medicine, 2015; Dugo et al., Breast 2018)

Application of breath analysis to cancer detection

- Studies on human breath analysis for identification of volatile signatures in breast cancer (Martinez-Lozano Sinues, J. of Breath Research, 2015).
- Generation of statistical bioinformatics pipelines for analysis of Mass Spectrometry data in clinical context, using spectra data (Cristoni et al, Rapid Commun Mass Spectrom. 2009) and matrix data (Martinez-Lozano Sinues, J. of Breath Research, 2015)

Technological Development in Clinical Breath Analysis

- Development of technology and instruments for collection and storage of human breath samples for clinical purposes (**PCT/IB2019/056152**).
- Development of dedicated artificial intelligence- based computational tools for breathomics data and for oncology clinical practice (under construction).