

Personal information

Date and place of birth: 13/10/1981, Sant'Angelo Lodigiano, Italy. Citizenship: Italian
Work Address: Department of Oncology and Hemato-Oncology, University of Milan, via Francesco Sforza 35-20122 Milan, Italy. Phone: +39 02 55033328 Email: marta.lionetti@unimi.it

Education and training

November 2009-February 2013: PhD in Experimental Hematology, University of Milan, Italy.
January 2006-November 2009: CEE Specialization Course in Medical Genetics, University of Milan. Final grade: 70/70 e lode.
November 2003-July 2005: Second level degree in Medical Biotechnology, University of Milano Bicocca. Final grade: 110/110 e lode.
October 2000-November 2003: First level degree in Biotechnology, University of Milano Bicocca. Final grade: 110/110 e lode.

Research experience

April 2017–onwards: University of Milan research fellowship: “Biological and functional implications of deregulated long non-coding RNAs in multiple myeloma”– Institution: Fondazione Policlinico, Milan. Focus: setup of NSG library preparation by hybrid capture-based enrichment and targeted resequencing on Illumina MiSeq instrument. Mutational analysis of a MM-gene panel in patients at different clinical stages of plasma cell dyscrasia.

October 2012–March 2017: University of Milan research fellowship: “The role of non-coding RNA in multiple myeloma”– Institution: Fondazione Policlinico, Milan. Focus: analysis of microRNA expression in multiple myeloma (MM) and plasma cell leukemia (PCL); miRNA functional characterization through manipulation of cell lines. Setup of high-throughput amplicon sequencing in the lab on Roche Genome Sequencer Junior instrument. Gene mutation analysis by high-throughput sequencing in MM and chronic lymphocytic leukemia (CLL), by managing the work of a small team of two PhD students.

February 2011–September 2012: Fondazione Italiana Ricerca sul Cancro (FIRC) research fellowship: “The role of non-coding RNA in multiple myeloma”– Institution: Fondazione Policlinico, Milan. Focus: analysis of miRNA expression in MM and PCL; miRNA functional characterization through manipulation of cell lines.

January–December 2010: Fondazione Matarelli research fellowship: “Genomic approach for risk stratification of multiple myeloma patients”– Institution: Fondazione Policlinico, Milan. Focus: analysis of miRNA expression in MM and PCL; miRNA functional characterization through manipulation of cell lines.

January–December 2009: research fellowship: “Physiopathology of bone disease and bone marrow environment in multiple myeloma: genomic approach for the identification of molecular pathways and targets”– Institution: Fondazione Policlinico, Milan. Focus: Analysis of gene and miRNA expression profiling in CLL and MM.

March–December 2008: research fellowship: “Global gene-expression profiling of multiple myeloma: insights into the bio-clinical diversity of the disease”– Institution: Fondazione Policlinico, Milan. Focus: Analysis of gene and miRNA expression profiling in CLL and MM.

March 2007–February 2008: research fellowship: “Monitoring of disease in patients with hematologic malignancies: analysis in quantitative ‘real time’ PCR of specific genetic lesions”– Institution: Fondazione Policlinico, Milan. Focus: Mutation analysis of immunoglobulin heavy chain variable (IGHV) genes; analysis of gene expression profiling in MM.

March 2006-February 2007: research fellowship: “Global gene-expression profiling of multiple myeloma: insights into the bio-clinical diversity of the disease”– Institution: Fondazione Policlinico, Milan. Focus: IGHV genes mutation analysis; analysis of gene expression profiling in MM.

Technical skills and competences

-Genomic DNA, total RNA and protein extraction, purification and quantification. -Nucleic acid separation on agarose gel. -Western blotting. -PCR, reverse transcription, RT-PCR, RT microRNA PCR. -Automatic sequencing of PCR fragments through Big Dye Terminator chemistry (ABI PRISM 310). -Quantitative real time-PCR and RT-PCR through TaqMan chemistry (ABI PRISM 7700, StepOne and 7900HT).

-Basic techniques for the analysis of gene and miRNA expression profiling through hybridization on Affymetrix chips (HG-U133A and Gene 1.0st, and miRNA array 3.0, respectively), from total RNA extraction to data acquisition and processing through specific bioinformatic approaches.

-Cell cultures in sterility. -Transfection through electroporation and lipidic systems. -Cell viability assays. -Amplification of plasmidic DNA in competent cells and extraction. -Luciferase assay in adherent cells.

-High-throughput amplicon targeted resequencing by means of Roche 454 technology on the Genome Sequencer Junior instrument.

- NSG library prep for Illumina targeted resequencing by hybrid capture-based enrichment.
- Sequence analysis, i.e. variant calling, annotation, scoring and interpretation.

Informatics' competences: use of bioinformatic tools such as BLAST, PrimerBLAST, PrimerExpress, ClustalW, Mutation Taster. Use of the main biologic and biomedic online databases about genomics, transcriptomics and proteomics. Use of statistic softwares, including MedCalc and SPSS.

Publications

47 total publications.

H-index: 22 (Web of Science; Scopus).

Marta Lisnitskiy