Title: Upregulation of miR-29a and genomic DNA hypermethylation in normal karyotype AML showing DNMT3A mutation

Randazzo V[1], Agueli C[1], Salemi D[1], Valenti D[1], Mirto M[2], Marfia A[1], Bica MG[1], Cannella S[1], Fabbiano F[1], La Rosa C[2], Caradonna F[2], Santoro A[1].

[1] Laboratorio di Diagnostica Integrata Oncoematologica e Manipolazione Cellulare (Divisione di Ematologia con UTMO) Ospedali Riuniti Villa Sofia Cervello - Palermo – Italia.

[2] Dipartimento di Scienze e Tecnologie Biologiche Chimiche e Farmaceutiche (Sezione di Biologia Cellulare) Università di Palermo – Italia.

Acute Myeloid Leukaemia (AML) is frequently associated to normal karyotype and *DNMT3A* mutations (R882). Since we previously demonstrated distinctive miRNA expression in some AML groups, we study 384 miRNA in 9 selected DNMT3A-mutated NK-AML patients. Comparing these data with our previous results obtained in 31 DNMT3A-unmutated AML, we focused on a significant up-regulation of miR-155, miR-29a, miR-196b and miR-25. We investigated expression of these miRNAs in additional 24 DNMT3A-mutated AML patients and we confirm the up-regulation of miR-155, miR-29a and miR-196b; in particular, we judged very interesting the over expression of miR-29a since is known to directly target *DNMT3A*, *TET1* and *TDG* mRNAs. Evaluating the expression levels of these targets in 17 AML DNMT3A-mutated patients, we revealed a no significant differences in expression of *DNMT3A* and *TDG* but a significant down-regulation of *TET1*.

These data suggest that miR-29a acts as DNA methylation-regulator: in presence of *DNMT3A* activating mutations and *TET1* down-regulation it may probably cause a perturbation of DNA methylation. In fact, analyzing the methylation of the bone marrow genomic DNA from 3 DNMT3A-mutated and 3 DNMT3A-unmutated cases by Methylation Sensitive Arbitrarily Primed-PCR, we found a genomic hypermethylation of DNMT3A-mutated cells compared to the unmutated ones.

How *DNMT3A* mutations contribute to leukemogenesis is not yet well characterized. Uncovering how *DNMT3A* mutations affect DNA methylation and epigenetic regulation of gene expression may have important implications in treatment selection because DNA hypomethylating agents are increasingly used in AML therapies, and response to these drugs may be affected by DNMT3A changed function.

Biography

Dr. Maria Mirto is completing her master studies in Health Biology at University of Palermo (Italy). She worked and is working with a joint work group dedicated to Epigenetic studies in Acute Myeloid Leukemia consisting of *Cellular biology and Genetics Lab* of Department STEBICEF (University of Palermo) and *Oncohematologic Integrated Diagnostic Lab* (United Hospitals "Villa Sofia Cervello" Palermo) – Italy. These teams have several publications in topic. These presented results are part of her degree thesis.