Multiple Myeloma Team

Work program

Although the current induction therapy strategies guarantee an overall response rate of roughly 80%, a considerable proportion of patients with multiple myeloma (MM) exhibit sub-optimal responses or progress during therapy, representing a subgroup of high risk and poor prognosis.

The identification of new molecular markers for an appropriate risk stratification at diagnosis therefore remains a priority objective. Advances in molecular biology and genetics have allowed us to recognize the heterogeneity of the tumor component of MM, leading to the discovery of neoplastic subtypes with peculiar cytogenetic characteristics. In the past few years, the interest of the scientific community has long been aimed at understanding the role of immune and stromal cells that could influence the microenvironment and the behavior of tumor cells. However, to date, detailed data on the quantitative and functional composition of the MM microenvironment are not yet available.

Recently, thanks to the use of computational methods based on the study of gene expression profiles, the possibility of obtaining highly sensitive quantitative and qualitative information on the cellular composition of various tumor tissues has been demonstrated. This type of approach, known as CIBERSORTx ("Cell type Identification by Estimating Relative Subsets Of known RNA Transcripts"), represents a valid tool for implementing the genomic data already available in MM, investigating the biological contribution of specific cell subpopulations within the tumor microenvironment. This new research team is aimed at applying this cutting-edge bioinformatic technique of deconvolution on transcriptomic data to characterize different cellular components of the MM microenvironment, as well as to define their level of correlation with the clinical behavior of the disease. The results obtained will then be used to validate potential prognostic markers useful in early patient stratification. Furthermore, if validated, this approach could allow the identification of new molecular targets for future therapeutic strategies

Team Composition

Team Leader

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Team members

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Team Network

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Key funding

Ricerca Corrente 2022-Ministry of Health

Key publication

- **Daratumumab plus bortezomib or daratumumab plus lenalidomide as salvage therapy for patients with myeloma: initial follow-up of an Italian multicentre retrospective clinical experience by 'Rete Ematologica Pugliese'.**
  G. Mele, N. Cascavilla, N. Di Renzo, A. Guarini, P. Mazza, L. Melillo, V. Pavone, G. Tarantini, P. Curci, A. P. Falcone, C. Germano, A. Mele, G. Palazzo, G. Palumbo, G. Reddiconto, B. Rossini, G. Specchia, P. Musto & D. Pastore. Annals of Hematology, volume 101, pages1727–1739 (2022).
- **Primary, Bilateral and Diffuse Renal Non-Hodgkin's Lymphoma in a Young Woman Suffering from Turner Syndrome**.
  Rossini B, Skrypets T, Minoia C, Quinto AM, Zaccaria GM, Ferrari C, Maggialetti N, Mastrorosa A, Gatti P, Casiello M, Ciavarella S, Guarini A. J Pers Med. 2021 Jul 7;11(7):644. doi: 10.3390/jpm11070644.
- **Is whole body low dose CT still necessary in the era of ^{18}F-FDG PET/CT for the assessment of bone disease in multiple myeloma patients?**
  Maggialetti N, Ferrari C, Nappi AG, Quinto A, **Rossini B**, Zappia M, Minoia C, Guarini A, Brunese L, Rubini G.Hell J Nucl Med. 2020 Sep-Dec;23(3):264-271. doi: 10.1967/s002449912206. Epub 2020 Dec 14.PMID: 33306757 **Free article.**
- **Real world Italian experience of pomalidomide plus low-dose dexamethasone in the relapsed and refractory myeloma setting: extended follow-up of a retrospective multicenter study by the 'Rete Ematologica Pugliese E Basilicata'**.
  Mele G, Pastore D, Di Renzo N, Fragasso A, Guarini A, Mazza P, Musto P, Pavone V, Tarantini G, Curci P, Falcone AP, Mele A, Miccolis MR, Palazzo G, Palumbo G, Quinto AM, Reddiconto G, Rizzi R, Cascavilla N, Specchia G, Capalbo SF. Leuk Lymphoma. 2019 Dec;60(14):3565-3568. doi: 10.1080/10428194.2019.1636989. Epub 2019 Jul 9.