MDS Symposium (Valencia, May 2017)

Taking place only every second year, the MDS International Symposium happened this time in Valencia. During four days, the conference gathered about 1100 physicians and researchers to discuss the newest discoveries in experimental research as well as the most promising therapies within the field of myelodysplastic syndromes (MDS).

One of the main focuses during the conference was the use of New Generation Sequencing technique. DNA sequencing has become more and more important during the past years within the field of hematology. However, MDS is one of the groups of diseases where this technique has developed the most. This year in Valencia many studies presented sequencing data for different MDS cohorts worldwide. Other work aimed to show the role of mutation analysis in predicting response to specific treatments. Presented data also discussed the association between occurrence of particular mutations and bone marrow failure syndromes such as Aplastic Anemi or Paroxysmal Nocturne Hemoglobinuria.

A very appreciated talk was the one given by David Steensma from Dana Farber Cancer Institute, Boston, on clonal hematopoiesis. The recent advances in DNA sequencing now allow us to identify somatic mutations in individuals otherwise asymptomatic without any other clinical or morphological sign of hematologic malignancy. When a mutation is found over a threshold of 2%, this condition is termed CHIP (Clonal Hematopoiesis of Indeterminate Potential). About 10% of individuals older than 70 years have CHIP, and in this group, the estimated rate of progression to MDS or any other hematological malignancy is 0,5 to 1% per year.

The most commonly found mutation in these individuals are *DNMT3A* and *TET2.* Further, the number and the size of the clone carrying such mutation seem to be predictive of the risk of progression. Interestingly, CHIP has been shown to be associated with a higher risk of cardiovascular diseases. This risk is estimated to be as high as other well established risk factors such as smoking or high cholesterol values. The underlying mechanisms for this association remain unclear.

Overall, one of the major project presented this year was the one headed by Elli Papaemmanuil on behalf of the International Working Group of MDS. This work aims at establishing a new prognostic score for MDS which would involve clinical and laboratory data, cytogenetic parameters and presence of genetic mutations. For this purpose, DNA from nearly 7000 MDS patients from several countries around the world

will be sequenced on a common platform at Memorial Sloan Kettering Cancer Center, USA.

With a cohort of more than 1000 MDS patients, Sweden will be the biggest contributor in terms of patient material for this exciting international project. I was therefore honored to be presenting the Swedish part of this project via a poster in Valencia. Besides the cohort size, the strength of the Swedish contribution is the population-based setting with patient material collected from the whole country (33 different sites, varying from smaller clinics to bigger university hospitals). Another valuable advantage is the variety, and the quality of the numerous available clinical data in the Swedish registers.

To summarize, this year's MDS conference was very enriching and provided an ideal opportunity to get the latest updates within the field. It also gave me a good starting point for future collaborations.

Finally, I would like to thank The Swedish Blood Cancer Fund (Blodcancerfonden) for offering me a travel grant, and with this, giving me the opportunity to attend the 2017 MDS Symposium in Valencia.

Best regards,

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