BASTION

From Basic to Translational Research in Oncology

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Report on 20th Congress of the European Hematology Association,

Vienna, Austria, June 11-14, 2015

The annual Congress of the European Hematology Association is the most important European conference regarding latest advances in hematology. Visitors come to the Congress to meet others in the European hematology community, hear about the latest science in their own and adjacent fields, and discuss important developments in European hematology today. Clinicians and scientists meet and learn about each other's perspectives. This year we celebrated the Anniversary 20th meeting.

The educational sessions of EHA's Congress are rated top in the world. Mostly aimed at clinicians who wants to stay on top of the latest research in blood disorders diagnostics and treatment. Apart from this, the scientific program of the Congress includes oral presentations, scientific poster and e-poster sessions, and open meetings of Scientific Working Groups. Joint symposia are organized with national societies of hematology (like Japanese Society of Hematology). On the sidelines of the official Congress, satellite symposia are organized by various sponsors.

During this meeting I had a pleasure to present the results of our research project during e-poster session. Topic: Chronic myeloid leukemia – Biology.

Moreover, the Conference was for me a great chance to participate in many illustrious lectures, hear about most burning issues in hematology and to meet scientists working in a cognate fields .

Final Abstract Code: E1083

Title of the e-poster: "SELECTION OF RUNX1-MUTATED CLONE ASSOCIATED WITH RELAPSE AND BLAST CRISIS IN CHRONIC MYELOID LEUKEMIA PATIENT AFTER ALLO-HSCT AS REVEALED BY TARGETED ENRICHMENT AND DEEP SEQUENCING"

Authors: Iwona Solarska, Marcin M. Machnicki, Barbara Nasiłowska-Adamska, Barbara Pieńkowska-Grela, Ilona Seferyńska, Piotr Stawiński, Rafał Płoski and Tomasz Stokłosa

In summary:

We aimed at employing targeted deep-sequencing strategy to dissect the underlying genetic cause of clonal evolution and rapid progression to CML-BC in a patient who relapsed after allogeneic stem cell transplantation (alloHSCT), developed lymphoid CML-BCs and died within 18 month, in spite of having very good prognosis. We screened four sequential DNA samples: one from diagnosis and three samples from three consecutive BCs with targeted deep sequencing and we detected a nonsense R320 RUNX1 mutation in all 4 samples. Importantly, this mutation was already present in the diagnostic sample. It is important that In CML-BC RUNX1 mutations have been reported in few studies. We have shown that RUNX1 mutation may be already present in CML-CP at diagnosis and may potentially occur as a pre-leukemic event prior to t(9;22) translocation which confirms recent findings by Schmidt et al. in Leukemia (2014).*

It is worth to mention that during 20th Congress of the EHA, the Scientific Program Committee allocated the abstracts as follows: 8% Oral Presentation, 25% Paper Poster with presentation, 33% E-Poster, 22% Publication Only and 11% rejected.

Dr Iwona Solarska at the poster during poster session.