ACUTE MYELOID LEUKAEMIA

Background

Deciphering the cytogenetic and molecular lesions underlying the pathogenesis of AML provided, apart from greater insights into disease biology, also useful information predicting the likelihood of achieving and maintaining remission following conventional chemotherapy, leading to the development of risk-stratified treatment approaches. Using novel genomics technologies, such as next generation sequencing (NGS) techniques, major progress has been made in further unravelling the heterogeneity of the disease. On average, AML harbours a median of 13 mutations, with in excess of 200 genes being recurrent mutation targets. However, translating this knowledge into clinical practice is lagging. Concerted efforts from basic, translational, and clinical hematologists will be required to make major advances in the forthcoming years. New drugs targeting leukemic drivers or a multitude of deregulated pathways are awaiting clinical application. New immunotherapy approaches, such as vaccination, CAR T cells, natural killer (NK) cells, bispecific T-cell engagers, novel mono-clonal antibodies, and immunoconjugates, hold great promise.

Mission

- Annual scientific meeting at EHA
- To institute a platform for translational research
- Provide a forum to bridge gaps between basic scientists and clinicians treating patients with AML
- Consideration of the implications of high throughput sequencing technologies and minimal residual disease assessment to clinical trial design

Chairs

David Grimwade: King’s College London, david.grimwade@genetics.kcl.ac.uk
Gert Ossenkoppele: VU University Medical Center, g.ossenkoppele@vumc.nl
Executive Committee

Hubert Serve:  *Goethe University Frankfurt, serve@em.uni-frankfurt.de*
Francesco Lo Coco:  *University Tor Vergata, lccfnc00@uniroma2.it*

Members of Working Group

Jan Cornelissen  j.cornelissen@erasmusmc.nl
Ruud Delwel  h.delwel@erasmusmc.nl
Konstanze Döhner  Konstanze.Doehner@uniklinik-ulm.de
Hervé Dombret  herve.dombret@mac.com
Estelle Duprez  Estelle.Duprez@inserm.fr
Claudia Haferlach  claudia.haferlach@mll.com
Robert Hills  hillsrk@cf.ac.uk
Gunnar Juliusson  Gunnar.Juliusson@med.lu.se
Paresh Vyas  paresh.vyas@imm.ox.ac.uk

Annual Activity

The AML Scientific Working Group was formed in 2013 and arranged scientific meetings in 2013 and 2014 and a further scientific session at EHA19 entitled “AML from leukemogenesis to treatment” which proved to be a very well attended (>400 participants) and lively interactive session. It opened with a presentation from Prof Stefan Frohling (Department of Translational Oncology, NCT Heidelberg, German Cancer Research Center (DKFZ), Heidelberg, Germany) entitled “Therapeutic targeting of AML with aberrant homeobox gene expression" in which he covered two topics: 1. AML driven by CDX2 (a non-clustered homeobox gene) as well as 2. new approaches at targeting MLL-rearranged leukemias, e.g. by inhibition of CDK6. Stefan showed the data providing the rationale for evaluation of palbociclib in this group of patients and the clinical trial that he leads is now open for recruitment in a number of European centres. Prof Clara Bloomfield (The Ohio State University Comprehensive Cancer Center, Columbus, OH, USA) provided an update on: “What’s new in the WHO classification of AML?” It is expected that the WHO2016 will be published before the summer
of 2016. This refined classification will take into account an extended range of molecularly and genetically defined subtypes of AML, which will be included in the first instance as provisional disease entities.

Over the course of the last year, members of the AML SWG have discussed the preparation of an update to the ELN AML guidelines (Blood, 2010), to be developed in collaboration with ELN. The group had productive meetings in September and December 2015. The AML recommendations are now nearly finalised and will be published in the course of this year after publication of WHO2016 classification.

In collaboration with some relevant ELN Working Parties (MRD, AML, Diagnostics, NGS) we have organized in 2015 a few meetings in which we discussed the value of minimal residual disease detection in AML. In February 2016 a major meeting attended by leading AML MRD experts from Europe and USA covering flow cytometric, molecular, NGS and clinical MRD was very productive. This will probably result in a manuscript containing recommendations on harmonization of methods to apply MRD detection in clinical trials for AML. The SWG decided not to organize a separate AML SWG meeting because this would be redundant due to the 2-yearly AML meeting organized by ESH that is excellent.