Acute Myeloid Leukemia (AML) is a heterogeneous malignancy characterized by clonal expansion of abnormal myeloid progenitor cells in the bone marrow and peripheral blood. The genomic classification in AML involves the analysis of genetic mutations and alterations within leukemic cells. One of the key genomic classifications is based on recurrent cytogenic abnormalities, such as translocation and inversions.

In the trial, about 1540 patients were enrolled in prospective trials of intensive therapy, combining driver mutations in 111 cancer genes with cytogenetics and clinical data. The purpose of the trial is to get a comprehensive study of leukemia genes, acknowledging the landscape of AML in older patients that may be underrepresented. The process began by obtaining samples from patients participating in three prospective multicenter clinical trials of German-Austrian AML study groups. Then, the Bayesian Dirichlet process was used to establish classification rules that partitioned the participants into subgroups, minimizing the overlap between categories. The importance of the Dirichlet process is that it defines an infinite prior distribution for the number and proportions of clusters in the mixture model. In addition, the advancements in next-generation sequencing technologies have facilitated the identification of recurrent molecular mutations in AML. The mutations in genes like FLT3, NPM1, and CEBPA have been incorporated into prognostic models, allowing more precise risk stratification. For instance, the FLT3-ITD mutation had led to the development of FLT3. The results showed that about 5234 driver mutations have been identified with the involvement of 76 genes or regions in 1540 patients. Furthermore, point mutations accounted for 73% of all drivers and were often enriched in patients with Acute Myeloid Leukemia classified as intermediate risk.

In conclusion, the integration of gene expression profiling has enhanced the genomic classification of AML. Additionally, genomic classification not only aids in risk stratification but also plays a pivotal role in predicting treatment response and guiding therapeutic decisions. Emerging therapies are also being developed to specifically target molecular vulnerabilities. And of course, genomic classification in AML significantly improved the understanding of the disease, providing valuable prognosis, treatment, and developments.

Citations:

Papaemmanuil, Elli. et al. Genomic Classification and Prognosis in Acute Myeloid Leukemia. Nature; https://doi.org/10.1056/NEJMoa1516192 (2016).

Dohner, H., Weisdorf, D.J., & Bloomfield, C.D. Acute Myeloid Leukemia. New England of Medicine, 377 (6), 541-552. Nature; https://doi.org/10.1056/NEJMra1406184 (2017).