The impact of **DNMT3A/FLT3-ITD/NPM1** on patients with acute myeloid leukemia after allogeneic hematopoietic stem cell transplantation

**Long Su**

Department of Hematology, the First Hospital, Jilin University, Changchun, China

*Correspondence to: Long Su, Department of Hematology, the First Hospital of Jilin University, Changchun 130021, China. Tel: +86-0431-88782157; Fax: +86-0431-88782688; E-mail: sulongjdyy@163.com

**Key words:** acute myeloid leukemia, genetic mutations, **DNMT3A**, **FLT3-ITD**, **NPM1**

**To the editor:**
Recently, Ardestani and colleagues published their excellent findings in this journal [1]. They found that **DNMT3A** mutations alone do not affect the clinical outcomes of acute myeloid leukemia (AML) patients undergoing allogeneic hematopoietic stem cell transplantation (allo-HSCT), but when accompanied by **FLT3-ITD** mutations, the overall survival (OS) was significantly reduced and the relapse rate increased. **NPM1** mutations had no impact on both relapse-free survival (RFS) and OS, but there was a significant difference between AML patients with and without **NPM1** mutations for relapse [1].

Integrative genomic analysis of **de novo** AML identified a subset of AML patients in which **DNMT3A**, **FLT3**, and **NPM1** mutations coexist at a higher frequency than would be expected for a chance occurrence [2]. Our unpublished data also showed that a close association could be observed among **DNMT3A**, **FLT3**, and **NPM1** mutations in patients with AML by factor analysis ($P < 0.05$) based on 357 **de novo** AML patients analyzed by next-generation sequencing. Previous study demonstrated that younger (<60 years) patients with **DNMT3A/FLT3/NPM1** mutations had a significantly shorter event-free survival (EFS) ($P = 0.047$) and a tendency towards shorter OS ($P = 0.095$) compared to those in the other mutation groups [3]. Adverse impact of **DNMT3A** mutations is more pronounced than that of **FLT3-ITD** among patients with **NPM1** mutations [3]. Accordingly, how do **DNMT3A/FLT3-ITD/NPM1** triple mutations influence the prognoses of AML patients underwent allo-HSCT in this study? What about the impact of **DNMT3A** or **FLT3-ITD** on **NPM1** mutated AML patients? Recent studies reported that variant allele frequency of **NPM1** and **FLT3-ITD** genes were closely related to the long-term outcomes in patients with AML [4-5]. I wonder to know if there is information available for variant allele frequency in this subsets of patients in order to re-analyze the impact of **NPM1** and **FLT3-ITD** on the prognoses of patients post allo-HSCT.

**Conflict of Interest:**
The authors of this paper have no conflicts of interest, including specific financial interests, relationships, and/or affiliations relevant to the subject matter or materials included.
References: