Hemoblobin and Serum Ferritin level as Prognostic Factor in DLBCL

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Background: There are many factors used to predict outcomes in patients with malignant lymphomas. They have been demonstrated as meaningful prognostic factors in patients with DLBCL such as C-reactive protein (CRP), ferritin, β2-microglobulin (B2MG), Hemoglobin (Hb), absolute lymphocyte count (ALC) and albumin etc. However, some studies have shown that serum ferritin levels correlated with tumor mass and closely followed disease activity in patients with hematologic malignancies such as malignant lymphoma and acute leukemia. We studied the relationship between ferritin and Hb status for predicting more correct survival outcomes in patients with DLBCL treated with rituximab combined cyclophosphamide, adriamycin, vincristine and prednisone . **Methods:** A total of 234 patients who were newly diagnosed with DLBCL and received RCHOP at five hospitals in South Korea between January 2010 and August 2016 were enrolled retrospectively. Baseline CRP, ferritin, B2MG, Hb, ALC, albumin and factors of IPI were measured within 4 weeks before the first chemotherapy. The relationship between ferritin and Hb were divided into four groups; group 1 was defined low Hb (Hb < 10 g/dl) and high ferritin (≥ 300 ng/mL), group 2 was high Hb (Hb ≥ 10 g/dl) and high ferritin, group 3 was low Hb and low ferritin (< 300ng/mL) and group 4 was high Hb and low ferritin. Progression free survival and Overall survival were calculated with the use of the Kaplan-Meier thechnique. **Results:** In univariate analysis, the following factors showed significant higher 5 years overall survival rates : stage I/II disease ($p = 0.005$), ECOG 0-1 ($p < 0.001$), lower IPI ($p < 0.001$), Hb ≥ 10.0 g/dL ($p = 0.039$), lower ferritin ($p = 0.003$), and lower B2MG (< 3.5 mg/L) ($p = 0.024$). But some other factors did not show significant OS and PFS : extranodal involvement, ALC, and albumin. Especially, The 5-year OS according to the ferritin and Hb based group showed significant differences (41.8%, 63.2%, 74.2% and 78.9%, respectively, $p = 0.006$), (Figure 1). **Conclusions:** The survival outcomes showed significant differences according to levels of Hb and Ferritin. High level of ferritin and low level of Hb can be helpful to predict poor prognosis and to makes treatment planf

Assessment of a new genomic classification system in acute myeloid leukemia with a normal karyotype

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Aims: This study was performed to assess if recently recommended genomic classification is predictive in patients with normal-karyotype (NK) acute myeloid leukemia (AML).**Methods and results:** A total of 393 patients were included. Analysis of genetic mutations was performed using targeted resequencing with an Illumina Hiseq 2000. We identified driver mutations across 40 genes, with one or more driver mutations identified in 95.7% of patients. The molecular subclassification was as follows: 34.6% patients (n = 136) with AML with the NPM1 mutation, 10.7% (n = 42) with AML with mutated chromatin or RNA-splicing genes or both, 1.5% (n = 6) with AML with TP53 mutations, 13.5% (n = 53) with AML with biallelic CEBPA mutations, 2.0% (n = 8) with AML with IDH2-R172 mutations and no other class-defining lesion, 29.5% (n = 116) with AML with driver mutations but no detected class-defining lesion, 4.3% (n = 17) with AML with no detected driver mutation, and 3.8% (n = 15) patients with AML who met the criteria for ≥ 2 genomic subgroups. The ranges of complete remission (CR) rates in other subgroups were observed to be 75.9?97.2%; however, the CR rate in the subgroup with AML with mutated chromatin or RNA-splicing genes or both was 61.9%. The 5-year overall survival and relapse rate of subgroup in AML with mutated chromatin, RNA-splicing genes, or both was 11.6% (95% CI = 1.4?21.8%) and 71.4% (95% CI = 45.7?86.5%), respectively. **Conclusion:** This study suggests that the recently recommended genomic classification is an appropriate and replicable categorization system in the NK AML population. The subgroup of AML with mutated chromatin, RNA-splicing genes, or both showed extremely poor survival in NK-AML, so a novel approach is needed to improve their prognosis. **Key words:** genomic classification, AML, normal karyotype, next generation sequencing, prognosis