Author’s response to reviews

Title: Hierarchical Cluster Analysis of Immunophenotype Classify AML Patients with NPM1 Gene Mutation into Two Groups with Distinct Prognosis

Authors:

Chien-Yuan Chen (chienyuanchen@ntu.edu.tw)
Wen-Chien Chou (wchou@ntu.edu.tw)
Woei Tsay (woei12@gamil.com)
Jih-Luh Tang (tangjh@ntu.edu.tw)
Shang-Yi Huang (sy551225@ms7.hinet.net)
Ming Yao (yaoming@ntu.edu.tw)
Hwei-Fang Tien (tienhf@ntu.edu.tw)

Version: 2 Date: 13 August 2012

Author’s response to reviews: see over
Dear Editor-in-Chief,

We had made a correction about the editorial comment.

1) Consent - Please state in the Methods section whether written informed consent for participation in the study was obtained from participants or, where participants are children, a parent or guardian.

Ans: page 6. We add “The informed consent for participation in the study was obtained from all the participants.”

2) Please expand the methods section as to briefly describe each procedure.

Mononuclear cells obtained from bone marrow aspirates were isolated by Ficoll-Hypaque gradient centrifugation and cryopreserved. Genomic DNAs were extracted and amplified by Illustra GenomiPhi V2 DNA amplification kit as described by the manufacturer (GE Healthcare). The primer design was according to the previous study [7, 11, 19-21]. Analysis of the gene mutations of CEBPA [7], NPM1 [11], MLL-ITD [19], WT1 [20], FLT3-ITD, FLT3-TKD, JAK2, PTPN11, NRAS, and KRAS [21] was performed by polymerase chain reaction and direct sequencing. Abnormal sequencing results were confirmed by at least two repeated analyses.

In future correspondence regarding this manuscript please contact me using the following address:

Correspondence: Chien-Yuan Chen MD.
Department of Internal Medicine, National Taiwan University Hospital
No. 7, Chung-Shan South Road, Taipei 100, Taiwan
Email: chienyuanchen@ntu.edu.tw
Tel: 886-2-23123456-63531, Fax: 886-2-23123456-63531

With best regards

Sincerely yours,

Chien-Yuan Chen