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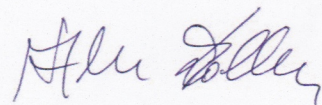
Igazolom, hogy

Bence Bátai (Hungarian Academy of Sciences-Semmelweis University Momentum Molecular Oncohematology Research Group, 1st Department of Pathology and Experimental Cancer Research, Semmelweis University, Budapest, Hungary)
EZH2 MUTATION SCREENING IN HUNGARIAN FOLLICULAR LYMPHOMA PATIENTS: PAVING THE WAY TO EPIGENETIC THERAPY címmel

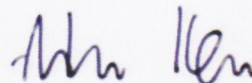
előadást tartott az Amerikai Magyar Orvosszövetség Magyarországi Tagozatának XIII. konferenciáján.

This is to certify that the above mentioned person gave a lecture at the 13th annual congress of the Hungarian Medical Association of America Hungary Chapter in Balatonfüred in 2019.

Balatonfüred, August 31, 2019



Ákos Koller, Prof.
President, HMAA-HC



András Khor, MD, PhD
President, HMAA



HMAA HC Summer Conference Balatonfüred
August 30 -31, 2019, State Hospital of Cardiology in Balatonfüred, Hungary
Science, culture and fun at HMAA conference on Lake Balaton.



***EZH2* Mutation Screening in Hungarian Follicular Lymphoma Patients: Paving the Way to Epigenetic Therapy**

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Keywords: *EZH2*; epigenetics; follicular lymphoma; molecular diagnostics; targeted therapy

Introduction: Mutations emerging in epigenetic regulators play a major role in the pathogenesis of follicular lymphoma. The *EZH2* histone methyltransferase harbouring gain-of-function mutations in 25% of the patients emerged as a promising therapeutic target. The *EZH2* inhibitor tazemetostat proved to be effective in a phase II clinical trial for the treatment of follicular lymphoma, demonstrating increased efficacy in patients harbouring *EZH2* mutations. To identify the patients most likely benefiting from an *EZH2* inhibitor therapy, we aimed to perform *EZH2* mutation analysis in a cohort of Hungarian follicular lymphoma patients.

Methods: We evaluated the *EZH2* mutation status of 321 patients with follicular lymphoma, by performing a digital droplet PCR (ddPCR) mutation analysis of the Y646, A682, and A692 hotspots in DNA samples from bone marrow or lymph node biopsy specimens. We also analyzed the association of *EZH2* mutation status and clinical data.

Results: Gain-of-function *EZH2* mutations were identified in 24.3% (78/321) of the patients. In most cases the mutation resulted in Y646N (35%, 28/81), Y646F (20%, 16/81), or Y646S (16%, 13/81) amino acid change. In contrast with previous studies suggesting a superior progression-free survival in *EZH2* mutant patients, we found no significant correlation between *EZH2* mutation status and survival data.

Conclusion: In this study, 24.3% of follicular lymphoma patients harboured *EZH2* mutations providing rationale for their recruitment into an *EZH2* inhibitor clinical trial in the future. We also optimized *EZH2* mutation testing using a highly sensitive ddPCR assay and included this test in the routine molecular diagnostic algorithm of follicular lymphoma.

Ethical Committee Approval: The study was approved by the Ethical Committee of the Hungarian Medical Research Council (ETT TUKEB) under the registration number: 14383-2/2017/EKU (2017-03-10).

Grants and financial support: The study was supported by the KH17-126718 grant of the Hungarian National Research, Development and Innovation Office (NKFIH) and the Momentum grant (LP-95021) of the Hungarian Academy of Sciences.

Acknowledgements: I would like to acknowledge clinicians taking part in our study for providing patient samples and clinical data.