МЕДИЦИНСКИ УНИВЕРСИТЕТ - ВАРНА
„Проф. д-р Параскев Стоянов“
Ул.“Марин Дринов“ 55, Варна 9002, България
Тел. : 052/ 65 00 57, Факс: 052/ 65 00 19
e-mail: uni@mu-varna.bg, www.mu-varna.bg

MEDICAL UNIVERSITY - VARNA
“Prof. Dr. Paraskev Stoyanov”
55, Marin Drinov Str., 9002 Varna, Bulgaria
Tel.: +359 52/ 65 00 57, Fax: + 359 52/ 65 00 19
e-mail: uni@mu-varna.bg, www.mu-varna.bg

Fund “Nauka” Project № 21008 Resume – Competition-Based Session 2021:

“Molecular-genetic analysis of newly diagnosed patients with acute myelogenous leukemia”

Project leader: Assoc. prof. Trifon Georgiev Chervenkov, MD, PhD

Acute myelogenous leukemia (AML) is a neoplastic condition affecting myeloid progenitor cells. This is the most common type of leukemia among adults with a frequency of 4.2 in 100000. AML is characterized by immense genetic heterogeneity, various evolution, and prognoses. Thus, current guidelines include the identification of the genetic basis of every single case as part of the initial diagnostic evaluation. This aims at maximal precision and personalization of the therapeutic approach. Molecular-genetic markers have diagnostic, prognostic, and predictive value, so other than conventional cytogenetic analysis (CCA), a molecular-genetic assay is also needed. The latter completes CCA by adding information about detailed changes beyond the scope of cytogenetics.

The project team aims to study the effectiveness and informativeness of Multiplex ligation-dependent probe amplification (MLPA) that dates back from 2002 and is based on the well-known polymerase chain reaction. Incorporating MLPA along with CCA in the initial assessment of an AML case would enrich the knowledge and improve prognostication and personalized approaches for these patients. As the method is still relatively new, there is a limited number of publications about its implementation. The project team’s experience would improve the understanding of its routine clinical usage both locally and internationally.

61 newly diagnosed patients – 29 women and 32 men (median age 62 years) and 21 healthy control individuals of similar age and sex distribution were included. Peripheral venous blood was used as a source of DNA.

The study showed that MLPA could be a helpful part of the initial genetic assessment along with CCA. Molecular-genetic data was discovered for more than half (55.7%) of the patients in the study:

- 22 (36.1%) had a single gene AML-associated variant in one or more of the genes: *NPM1, IDH2, DNMT3A, FLT3*
- 18 (29.5%) had a chromosomal rearrangement in chromosomes 1, 4, 5, 6, 7, 11, 14, 17, 21.

Also, MLPA aided in the classification and stratification of 42.6% of the patients, overcoming well-known limitations of CCA. A comparison of the X060 kit the project team used with other kits used in other similar studies showed that it introduces no less information regarding chromosomal and single-gene findings. This characterizes it as an advantageous

source of information for the particular contingency of patients. The project team thinks that MLPA would be especially helpful in countries with limited national health benefits program. Since Bulgaria is a good example of such conditions, the project team finds the method applicable at least until health policies guarantee better provision of advanced diagnostic services for these patients.