Large HLA disease association study with more than 50,000 controls shows protective effects for HLA-B*40:01 and C*03:04 in NPM1 mutated AML

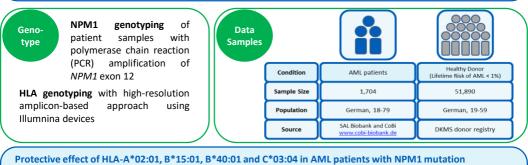


Elke Rücker-Braun^{1,2}, Bose Falk², Henning Baldauf², Carolin Massalski³, Gesine Schäfer⁴, Heidi Altmann¹, Jürgen Sauter⁵, Ute Solloch⁶, Vinzenz Lange⁷, Friedrich Stölzel¹, Christoph Röllig¹, Moritz J. Middeke¹, Malte von Bonin¹, Christian Thiede¹, Alexander H. Schmidt⁸, Martin Bornhäuser¹, Johannes Schetelig^{1,2}, Falk Heidenreich^{1,2}

1 Medical Clinic I, University Hospital Carl Gustav Carus, TU Dresden, Dresden, Germany, 2 Clinical Trials Unit, DKMS GmbH, Dresden, Germany, 3 Analysis, DKMS Life Science Lab GmbH, Dresden, Germany, 4 Research & Development, DKMS Life Science Lab GmbH, Dresden, Germany, 5 Scientific Projects, DKMS GmbH, Tübingen, Germany, 6 Scientific Projects, DKMS Life Science Lab GmbH, Dresden, Germany, 7 Management Team, DKMS Life Science Lab GmbH, Dresden, Germany, 8 Executive Department, DKMS GmbH, Tübingen, Germany

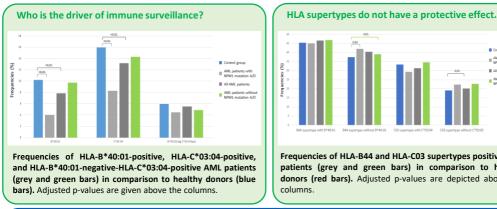
Background

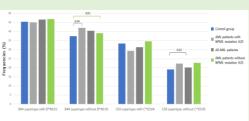
Mutations in the nucleophosmin 1 gene (NPM1) are common and recurrent molecular abnormalities in acute myeloid leukemia (AML). They are considered to be positive prognostic factors potentially due to immune responses mediated by NPM1 mutation (NPM1mut)-specific cytotoxic T cells and thereby suppressing NPM1mut-positive hematopoiesis. Here, in a large HLA association study we compared the distribution of HLA class I alleles at 2-fieldresolution between NPM1mut AML patients (n=471) and a control group of healthy individuals (n=51,890). HLA class I molecules of alleles which are underrepresented might present NPM1mut-derived neoepitopes more effectively and have the potential to elicit an anti-leukemic immune response.





Frequencies of the ten most frequent HLA-A, -B and -C alleles in AML patients with (grey bars) and without (green bars) NPM1 mutation A/D and in healthy donors (blue bars). Adjusted p-values are depicted above the columns.





Frequencies of HLA-B44 and HLA-C03 supertypes positive AML patients (grey and green bars) in comparison to healthy donors (red bars). Adjusted p-values are depicted above the

Conclusions

We found HLA-B*40:01 and HLA-C*03:04 underrepresented in NPM1 mutated AML suggesting that neoepitopes presented by these HLA alleles trigger T cell responses. NetMHCpan version 4.1 predicts that NPM1mut-derived immunopeptides bind strongly HLA-B*40:01 and weakly C*03:04. Relative linkage disequilibrium was shown for HLA-B*40:01 and HLA-C*03:04, but we could not identify a strong impact for either HLA-B*40:01 or HLA-C*03:04. Our findings suggest that further studies are warranted to confirm the presence and functionality of neo-epitope specific T-cells.

Next Step

Identification and isolation of HLA-B*40:01 and HLA-C*03:04 restricted NPM1mut-specific CD8+ T cell clones

