Poster Presentations

PP-01

Anti-HNA-3a Antibodies: A Cause of Unexpected Positive Flow Crossmatches in Kidney Transplantation

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Objectives: Crossmatch-(XM) testing is the established method for donor-specific anti-human leukocyte antigen (HLA) donor specific antibodies (DSA) detection prior to kidney transplantation. However, a positive T/B-flow-XM-(T/B-FXM) can occur in the absence of HLA-DSA, highlighting the role of other histocompatibility systems. Recent, guidelines have included human-neutrophil-antigens antibodies 3-a (anti-HNA-3a) testing for cases with unexplained positive XM. The aim of this study was to investigate the frequency of anti-HNA-3a in kidney transplant candidates-(KTC) and to present three T/B-FXM (+) cases due to circulating anti-HNA-3a.

Materials and Methods: Anti-HNA-3a were measured in 509 KTC using the LabScreen Multi-kit (One-Lambda). A positive result was determined by a normalized background value-(NBG)≥10 and MFI>1000. HNA typing was performed using PCR-SSP.

Results: A total of 8 patients (1.57%), 7 of whom were women, exhibited positive anti-HNA-3a with an average MFI: 6512 and NBG: 54. All women had a history of pregnancy and/or blood transfusions. During the study period, three anti-HNA-3a positive patients were selected for XM with deceased donors (DD), according to the DD-allocation rank.

Patient 1: 62-year-old woman, cPRA: 63%,MFI-anti-HNA-3a: 13682, XM with 3-DDs.

Patient 2: 40-year-old woman, cPRA: 0%, MFI-anti-HNA-3a: 15420, XM with 5-DDs.

Patient 3: 49-year-old woman, cPRA: 0%, MFI-anti-HNA-3a: 4245, XM with 1-DD.

All candidates exhibited unexplained T/B-FXM (+) in the absence of HLA-DSA or autoantibodies, resulting in their exclusion from transplantation. HNA typing revealed that the three patients were homozygous for HNA-3b and all donors expressed HNA-3a, confirming that the positive T/B-FXM was caused by the anti-HNA-3a.

Conclusion: Anti-HNA-3a can lead to positive FXM in allo-sensitized HNA-3b homozygous patients, given that most donors express HNA-3a. Although the clinical significance of anti-HNA-3a has not been fully elucidated, their screening is important for immunological risk assessment and timely therapeutic intervention.

PP-02

High-Resolution Characterization of KIR Genes Polymorphism in Healthy Individuals From the Bulgarian Population

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Objectives: Killer-cell immunoglobulin-like receptor *(KIR)* gene content has been widely studied in health and disease. In recent years KIR allele-level diversity has been described across human populations and the results of these studies highlight the population-specific nature of KIR diversity. Considering this, in the present study we aimed to analyze for the first time the allele polymorphism of nine *KIR* genes defined by a high-resolution method in the Bulgarian population.

Materials and Methods: In the present *KIR* gene polymorphism was investigated in 155 healthy, unrelated individuals from the Bulgarian population by applying next-generation-sequencing (NGS). Nine *KIR* genes (KIR2DL1,KIR2DL2,KIR2DL3,KIR2DL4,KIR3DL1,KIR3DS1,KIR3DL2,KIR3DL3, and KIR2DS2) were typed by NGS methods using the commercially available kits of GenDx, NGSgo, and then analyzed by NGSengine software (v. 2.29.0).

Results: In Bulgarians, the allele frequency distribution of *KIR* genes was found to be comparable to that observed in other European populations. The highest degree of polymorphism was observed for the *KIR3DL3* gene with 23 observed common alleles. On the contrary, the *KIR3DS1* gene was found to have the lowest degree of polymorphism with only two observed alleles in Bulgarians: KIR3DS1*01301 (31.6%) and KIR3DS1*049N (0.7%). The obtained results from the Ewens-Watterson test of neutrality suggest selection events that maintain the genetic variation in the population. Pairwise linkage disequilibrium (LD) for the 10 KIR loci was also estimated where some instances of strong LD among specific sets of KIR alleles were observed.

Conclusion: This is the first study investigating KIR allelic polymorphism at high resolution in a Southeast European population. This data will contribute to a better understanding of the genetic heterogeneity of this region and can be also may be applicable in clinical practice.