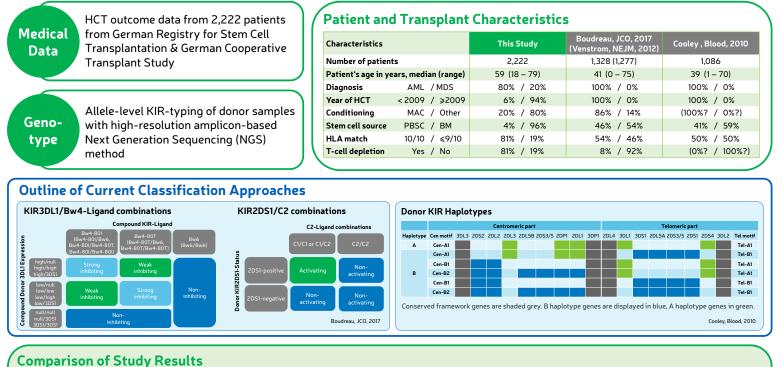
Donor KIR-Haplotype B Content does not Impact on Outcome after Unrelated Hematopoietic Stem Cell Transplantation in a Large Cohort of Patients with Acute Myeloid Leukemia or Myelodysplastic Syndrome

Schetelig J^{1,2}, Baldauf H¹, Massalski C³, Frank S⁴, Sauter J¹, Stelljes M⁵, Ayuk FA⁶, Gerbitz A⁷, Bethge W⁸, Bug G⁹, Klein S¹⁰, Wendler S¹, Heidenreich F¹, Lange V³, de Wreede L¹¹, Fürst D^{12,13}, Kobbe G¹⁴, Ottinger H¹⁵, Beelen D¹⁵, Mytilineos J¹², Schmidt A¹, Bornhäuser M²

1DKMS, Dresden & Tuebingen, ²University Hospital Carl Gustav Carus, Dresden, 3DKMS Life Science Lab, Dresden, 4German Register for Stem Cell Transplantation, Ulm, ⁵ University Hospital Rünster, 6UKE (University Hospital Eppendorf) University Medical Center, Hamburg, 7Medical Department, Division of Hematology, Oncology and Tumor Immunology, Charitè Berlin, 8University Hospital Tübingen, 9University Hospital Frankfurt, 10University Hospital Mannheim, ¹¹University Medical Center, Department of Biomedical Data Sciences, Leiden, The Netherlands, ¹²Institute for Clinical Transfusion Medicine and Immunogenetics Ulm, German Red Cross Blood Transfusion Service, Baden-Wuerttemberg – Hessen and University Hospital Ulm, ¹³Institute of Transfusion Medicine, University of Ouisburg – Essen

Background

Relapse and subsequent death are the major reasons for failure of allogeneic hematopoietic cell transplantation. Natural Killer (NK) cells might contribute to Graft versus Leukemia (GvL) effects. Their degranulation depends on the net effect of activating versus inhibiting signals. Killer cell immunoglobulin-like receptor (KIR) genes are encoded on Chromosome 19 and are inherited independently from the major histocompatibility complex (MHC). KIR genotype information has been associated with transplant outcomes in the framework of a Receptor-Ligand model aiming at maximization of activation and minimization of inhibition (KIR2DS1 & KIR3DL1; Venstrom, NEJM, 2012 & Boudreau, JCO, 2017) and by grouping donors according to presence or absence of haplotype B motifs which contain more activating KIRs (Cooley, Blood, 2010). Here the results of the largest confirmatory study, published so far, are reported.



HR 1.00 0.89 1.29 HR 1.00 1.05 1.08 N 1,357 782 83 Cen-A/A 1,047 1.00 Cen-A/B 207 1.134 0.053 Cen-A/B 207 1.34 0.053 Probability of Relapse bability of Relapse Probability of Relapse Probability of Relaps 0.4 0 0.4 This Study This Study 0.3 0.3 0.2 . . Years since HCT Years since HCT Years since HC Years since HCT HR 0.71 1.00 1.17 2DS1 positive with C1/C1 or C1/C2 2DS1 positive with C1/C1 or C1/C2 Probability of Relapse m, NEJM, 201 Probability of Relapse Cooley , Blood, 2010 Probability of Relapse Probability of Relapse 0.4 0 0.4 0.3 0.2 Years since HCT Years since HCT Years since HCT Years since HCT

Multivariate analysis of relapse incidence by means of Cox regression models adjusted for patient age, donor age, disease risk, performance status, HLA-/CMV- and sex-match, conditioning regimen, T-cell depletion and graft type. Almost identical distributions of 3DL1 strong/weak/non-inhibiting and 2DS1 activating/non activating donor-recipient constellations and donor KIR B-haplotypes were found in this study compared to the studies from Boudreau et al., Venstrom et al. and Cooley et al.. However, the characteristic pattern of relapse incidence published was not observed. This was also true for the subgroup analyses in patients with or without myeloablative conditioning, with HLA-compatible donors, with AML or MDS, with or without ATG, or with or without total body irradiation.

Conclusions

The donor-KIR-gene based classification using information on 2DS1/3DL1 KIRs to predict risk of relapse could not be replicated in a large cohort of patients with AML/MDS. Also, the impact of donor KIR haplotype on the risk of relapse could not be replicated. Striking differences between the transplant procedures of the original and the contemporary cohort may explain the conflicting results. NK alloreactivity cannot be predicted universally.

Next Steps

- ⇒ Explore more genotype information
- \Rightarrow Create 'Data Warehouse' to speed up research
- ⇔Engage in further collaborations

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