e compatibilidade transfusional. A análise de interações gênicas por meio da STRING evidenciou conexões funcionais e estruturais entre sistemas sanguíneos distintos, envolvendo processos de glicosilação e integridade de membrana. Os resultados reforçam o potencial de análises in silico para orientar pesquisas futuras, otimizar diagnósticos, prevenir reações transfusionais e compreender variações fenotípicas em diferentes populações.

https://doi.org/10.1016/j.htct.2025.105624

ID – 2443

ASSESSMENT OF THE CLINICAL SIGNIFICANCE OF COMMON RH VARIANTS IN TRANSFUSED SICKLE CELL DISEASE PATIENTS

TD dos Santos, LL Castilho

Hemocentro Unicamp, Campinas, SP, Brazil

Introduction: Variants in the RH genes—arising from single nucleotide variants (SNVs), small insertions or deletions, or hybrid gene rearrangements—can alter antigen expression, leading to weak, partial, or altered Rh phenotypes. Such variants may not be reliably detected by routine serologic methods, particularly in transfused patients or in populations with high genetic diversity such as the patients with SCD. Clinically, the presence of RH variants has significant implications but the full clinical impact of alloimmunization associated with RH variants in these patients remains unclear as not all patients with RH variants form alloantibodies and not all alloantibodies are implicated in hemolytic transfusion reactions. **Objectives:** We aimed to assess the risk of alloimmunization and the clinical significance of the produced antibodies in transfused patients with SCD carrying the most common RHD and RHCE variants. **Material and methods:** We selected 37 patients with the most common RHD and RHCE variants found in this population, who were receiving chronic or episodic transfusions and had a history of ≥15 RBC transfusions. (4 with RHD*DAU0, 6 with RHD*weak partial D 4.0, 2 with RHD*DIIIa, 4 with RHD*DAR, 4 with RHCE*ceAR 3 with RHCE*ce48C, 3 with RHCE*ceEK, 2 with RHCE*ceMO, 4 with RHCE*ce733G and 5 with RHCE*ce48C,733G. All patients were being transfused with Rh and K matched RBC units. RH genotyping was performed on all patients using the RHD and RHCE BeadChips array (Werfen) and Sanger sequencing. Antibody screening and identification with autologous control were conducted using the gel test. Direct antiglobulin test (DAT), adsorption with autologous RBCs, and crossmatching with allogeneic partial e-antigen from donors carrying the same alleles were also performed when possible. To assess the clinical relevance of the alloantibodies produced we compared the patient's total Hb or HbA and HbS percentages at time of antibody detection with pretransfusion values and clinical suspicion of anemia and hemolysis. **Results:** Among the 37 SCD patients with RH variant alleles, 16 developed Rh alloantibodies. Among them, 5 developed anti-D (3 with RHD*DAR, 1 with RHD*DIIIa and 1 with RHD*partial weak D 4.0) and 11 developed anti-e (3 with RHCE*ceAR, 2 with RHCE*ceEK, 1 with RHCE*ceMO 2 with RHCE*ce733G and 3 with RHCE*ce48C, 733G). . Four patients developed autoantibodies (2 anti-D (RHD*DAU0) and 2 anti-e (RHCE*ce48C). When we assessed the clinical effect of the alloantibodies produced, we observed a decrease in the Hb levels at time of antibody detection in 10 patients (3 with RHD*DAR, 1 with RHD*DIIIa, 3 with RHCE*ceAR, 2 with RHCE*ceEK, 1 with RHCE*ceMO). No clinical suspicion of anemia was observed in the patients who developed alloantibodies associated with RHD*weak partial D 4.0, RHCE*ce733G and RHCE*ce48C,733G and they did not experience or report signs and symptoms of a transfusion reaction. **Discussion and conclusion:** Our findings demonstrate that the specific RH variants an individual inherits may have varying clinical effects. Some variants are associated with the production of autoantibodies, while others lead to the formation of alloantibodies with or without clinical significance. This is particularly important for transfusion recommendations in SCD patients, given the scarcity of RBC units with RH variants for allele-matched transfusions. To our knowledge, this is the first study to demonstrate the clinical significance of the most common RH variants found in SCD patients.

https://doi.org/10.1016/j.htct.2025.105625

ID - 302

AVALIAÇÃO IMUNO-HEMATOLÓGICA DE VARIANTES RHD EM AMOSTRAS COM AGLUTINAÇÃO FRACA: EXPERIÊNCIA DE UM SERVIÇO PRIVADO NO INTERIOR PAULISTA

MP Carlin, ICG Branco, MDJ Rodrigues, JDJ Santos, TFC da Silva, AND Andrade, JS Carrascosa, CHR Kruzich, CADA Kruzich, CA Joussef

Hospital Unimed Piracicaba, Piracicaba, SP, Brasil

Introdução: O antígeno RhD é altamente polimórfico e de grande relevância clínica na prática transfusional. A hemaglutinação fraca pode ocultar variantes capazes de induzir aloimunização em pacientes transfundidos ou gestantes. **Objetivos:** Estimar a prevalência de variantes RhD na população atendida, comparar a reatividade dos reagentes utilizados na rotina e propor protocolo de triagem imunohematológica que dispense genotipagem. **Material e métodos:** Estudo observacional e transversal realizado na Agência Transfusional do Hospital Unimed Piracicaba entre abril e agosto de 2024. Foram incluídos pacientes com solicitação transfusional e gestantes. A tipagem RhD foi realizada por método convencional em tubo, com dois reagentes monoclonais (Anti-D IgM e Anti-D Blend IgG+IgM). Amostras com discrepância entre os reagentes, aglutinação fraca (< 2+) ou positividade na pesquisa de D fraco foram genotipadas por PCR multiplex. **Resultados:** Foram realizadas 2.283 tipagens RhD. Destas, 270 (11,8 %) apresentaram resultado RhD negativo, enquanto 2.013 (88,2 %) foram classificadas como RhD positivas. Não houve discrepância entre os reagentes monoclonais. Três casos (0,13% do total RhD positivos)