

ruled out through adsorption and elution with R1R1, Jk(b-) and Fy(b-) allogeneic RBCs. **Conclusion:** This study reported for the first time a rare case of anti-Cr^a in a Brazilian family. Due to the complexity of the Cromer system and the scarcity of anti-Cra and Cr(a-) RBCs, molecular analysis was essential for the conclusion of the case. Anti-Cr^a is rarely encountered and has already been related to moderate transfusion reaction but its clinical significance can be variable. Although no transfusions were required at this time, the family study was essential to find compatible donors.

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CLINICAL AND LABORATORIAL FACTORS ASSOCIATED WITH HEMOLYTIC DISEASE SECONDARY TO ABO INCOMPATIBILITY IN A BRAZILIAN COHORT OF 4,122 NEWBORNS

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Background: ABO incompatibility affects up to 15% of mother and fetus binomial. Hemolysis secondary to ABO incompatibility is an important differential diagnosis among newborns presenting with jaundice. Most studies evaluating risk factors for newborn hemolysis due to ABO incompatibility date from almost 40 years ago and literature lacks reports describing the laboratorial factors predictive of this disease after the advent of modern immunohematological reagents, which are more sensitive. **Goals:** To determine the clinical and laboratorial factors associated with the occurrence of overt hemolysis due to ABO incompatibility among Brazilian newborns. **Methods:** This was a nested case control study stemming from a cohort of 4,122 newborns of three different Brazilian hospitals. Mothers and newborns were ABO typed using conventional tube method and direct antiglobulin test (DAT) was also performed in tube using polyspecific anti human globulin. The occurrence of jaundice secondary to ABO incompatibility was retrieved from the medical files. Diverse clinical and laboratorial factors were associated with the endpoint (ABO incompatibility disease) using Chi-square test for categorical variables and t-test for continuous variables. Multivariable analysis was performed using logistic regression. A p-value less than 0.05 was considered significant. **Results:** Among the 4,122 newborns 44 had the diagnosis of hemolytic disease due to ABO incompatibility. The incidence of this complication was 7.9% considering only the situations in which there was ABO incompatibility between mother and fetus. Positive DAT, group O mother and group A newborn were significantly associated with the occurrence of clinical symptoms of hemolysis and this association was kept in multivariable model

($p < 0.001$ for the three variables). The presence of intra-uterine growth arrest, use of corticosteroids or antibiotics by the mother, type of birth (C-section or normal) and mother self-declared race were not associated with the occurrence of overt hemolysis secondary to ABO incompatibility. DAT presented 65.85% sensitivity, 96.28% specificity, 16.9% positive predictive value and 99.6% negative predictive value for the diagnosis of ABO incompatibility hemolysis. There were no cases of positive DAT in situations other than mother group O and newborns group A or B. The hemoglobin presented by the newborns right after birth was significantly lower when mothers were of group O and newborns were of group A ($p < 0.001$). **Discussion/conclusion:** Positive DAT, mother of group O and newborn of group A are independent factors associated with the occurrence of hemolysis due to ABO incompatibility of clinical relevance. With the improvement of the immunohematological reagents, positive DAT poses as an important diagnostic tool for the diagnosis of this complication, since the negative predictive value of the test is very high.

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COMPARAÇÃO DE PERFIL ANTIGÊNICO DOS SISTEMAS RH E KELL EM DOADORES X RECEPTORES NO MUNICÍPIO DO RIO DE JANEIRO DURANTE PERÍODO DE PANDEMIA COVID 19

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Introdução: Durante a pandemia de COVID-19 tivemos um aumento do consumo de hemocomponentes com redução do número de doações voluntárias, prejudicando a gestão de hemocomponentes. Pacientes em programas de hemotransfusão crônica ou com aloimunização necessitam de concentrados de hemácias com fenótipo idênticos para os sistemas Rh e antígeno K foram impactados pela menor disponibilidade de hemocomponentes seguindo essas premissas. **Objetivo:** Comparar a frequência dos antígenos E, e, C, c, K entre doadores e receptores de sangue em banco de sangue privado na cidade do Rio de Janeiro durante a pandemia de COVID-19, avaliar se o município possui perfil similar entre essas 2 populações e seu impacto para gestão de hemocomponentes. **Materiais e métodos:** Foram analisados resultados de identificação de antígenos E, e, C, c e K de doadores voluntários e de receptores com indicação de transfusão com protocolo de fenotipagem para sistema Rh e K no período de janeiro 2020 até junho 2021. Os doadores com tipagem O e A foram 100% fenotipados para os antígenos em questão. Os demais doadores foram fenotipados de acordo com a demanda do serviço de hemoterapia. Os receptores foram fenotipados conforme a indicação de aplicação do protocolo de fenotipagem. Número de indivíduos testados: Doadores 17.159 e Receptores 3.292. **Resultados:** Entre os doadores avaliados: 59% eram do sexo masculino, encontramos o

seguinte perfil antigênico antígeno D=88%, antígeno E=25%, antígeno e=98%, antígeno C=60%, antígeno c=83%, antígeno K=6%. Importante ressaltar que dentre os doadores D negativos o percentual de antígeno c e antígeno e negativos era de 0%. Entre receptores avaliados: 45% eram do sexo masculino, encontramos o seguinte perfil antigênico antígeno D=85%, antígeno E=23%, antígeno e=98%, antígeno C=64%, antígeno c=83%, antígeno K=6%. **Discussão:** Investigamos o perfil fenotípico de doadores comparativo ao de receptores com base no município do Rio tomando como base o período de pandemia de COVID-19. Avaliamos sexo, naturalidade e fenótipos de doadores e receptores. Realizamos um estudo preliminar com população de doadores no Brasil em 2018, sem comparação com receptores, e encontramos aproximadamente o mesmo resultado percentual de antigenemia deste estudo. Percebemos que a antigenemia dos receptores segue a mesma proporcionalidade que a dos doadores. **Conclusão:** Este estudo sugere que a população da cidade do Rio de Janeiro durante a pandemia de COVID-19 possui uma frequência de antígenos do sistema Rh e Kell semelhante entre doadores × receptores, e ao mesmo tempo semelhante ao nosso estudo realizado pré pandemia apenas com doadores da região sudeste e nordeste. Podemos então até o momento supor que a metrópole Rio de Janeiro possui população representativa do perfil antigênico brasileiro, com potencial para autossustentabilidade caso a cultura de doação de repetição fosse ampliada na população, reduzindo a dificuldade de atendimento principalmente para pacientes D negativos com antígenos raros como c ou e negativos. Estudos comparativos de todas as regiões do país podem auxiliar a compreensão mais fidedigna do perfil populacional a auxiliar nas estratégias de captação e retenção de doadores.

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COMPARISON OF PROPHYLACTIC GENOTYPIC MATCHING WITH PHENOTYPIC MATCHING FOR REDUCING THE RATE OF ALLOIMMUNIZATION AND HEMOLYTIC TRANSFUSION REACTIONS IN PATIENTS WITH SICKLE CELL DISEASE (SCD)

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Background: Patients with SCD are among one of transfused populations more often alloimmunized to red blood cell (RBC) antigens. Although transfusion services establish protocols of serologic matching and genotypic matching to reduce alloimmunization, there is still no consensus to the best practical approach although the obvious goal is to provide blood that will survive maximally. There are no studies comparing prophylactic genotypic matching to serologic matching. Based on this, our aim was to evaluate the effect prophylactic genotypic matching and serologic matching have on alloimmunization and hemolytic transfusion reactions in patients with SCD

receiving regular transfusions. **Methods:** A prospective study was conducted in 29 patients with SCD undergoing red cell transfusions in a period of 5 years. Fifteen patients were receiving prophylactic extended (ABO, Rh, K, Fy^a/Fy^b, S/s) serologic matching and 14 patients were transfused with RBC units genotypic matched for Rh, K, Fy^a/Fy^b, S/s, Di^a, Do^a/Do^b including Rh variants when possible. Serologic typing was performed by gel test (Biorad) and genotyping was performed by HEA, RHD and RHCE BeadChips (Immucor). **Results:** The patients received a range of 15-407 RBC units and the median age was 36. Of the 15 patients receiving prophylactic serologic matching, 6 developed alloantibodies (1 anti-D, 2 anti-e, 1 anti-S, 1 anti-Fy^a, -Do^a and 1 anti-C, -Di^a). Three of those patients were not having a good in vivo RBC survival at the time of antibody detection as assessed by a decrease in their hemoglobin levels and an increase in the frequency of transfusions. Molecular analyses showed that the 4 patients who developed Rh antibodies had RH variant alleles predicting partial antigens and the patients who developed anti-S and anti-Fy^a had discrepancies between the previous phenotype and genotype-derived phenotype. Of the 14 patients transfused with prophylactic genotypic matching RBC units, 2 were alloimmunized to Rh antigens (1 anti-D, 1 anti-e). Unexpected Rh antibodies found in these patients were not linked to expression of partial Rh phenotypes according to serological and molecular analyses but a result of altered Rh epitopes on transfused red cells. **Discussion and conclusion:** Our results showed that prophylactic genotypic matching is superior to phenotypic matching in patients with SCD especially if RH molecular matching is included, with the potential to decrease risk of transfusion reactions and to prevent alloimmunization.

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D CATEGORIA ENCONTRADO NA ROTINA DO LABORATÓRIO DE REFERÊNCIA EM IMUNO-HEMATOLOGIA DO GRUPO GSH

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Introdução: Até a década de 1930 os únicos antígenos significativos eram aqueles do sistema ABO. Em 1939 foram feitas duas descobertas significativas que incrementaram o cuidado na transfusão sanguínea e eventualmente resultaram na definição do mais extenso sistema do grupo sanguíneo, o sistema Rh, com atualmente 55 antígenos, sendo divididos em dois genes: RHD e RHCE. O antígeno RhD é considerado como um mosaico composto de 37 epítomos. Definindo-se, assim, as categorias do antígeno RhD parcial (DII, DIII, DIV, DV, DVI, DVII, DFR, DBT, RoHar) que são diferenciadas umas das outras de acordo com a presença ou ausência de um ou mais epítomos. A análise molecular das variantes do antígeno RhD mostrou que a perda da expressão de certos epítomos RhD está associada a

