performed by HEA BeadChip (Immucor, Warren, NJ). Because of the discrepant serology and HEA for Lu*a* and Lu*b* phenotypes, Sanger sequencing of *BCAM* and *KLF1* was also performed. **Results:** The patient RBCs typed Lu(a–b–) and HEA predicted a Lu(a+b+) phenotype. Genomic sequencing of *BCAM* showed the patient was heterozygous c.230G/A consistent with *LU*A/LU*B* genotype and revealed the common polymorphism c.586G/A (rs28399654) that does not impact the expression of Lutheran antigens. In *KLF1* the novel c.954G>T in exon 3 encoding p.Trp318Cys was found. The change c.954G>C encoding the same amino acid change was previously reported associated with the In(Lu) phenotype and this allele has been assigned *KLF*BGM62* by ISBT. **Conclusion:** Recognizing In(Lu) patients is important to provide better classification of KLF1 variants affecting Lutheran antigens expression and allow for phenotype prediction from genotype, accurate typing, and better transfusion management of related challenging transfusion scenarios.

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ASSISTENTIAL DIAGNOSIS OF RED CELL TRANSFUSIONS WITH ANTIGEN MATCHING IN PATIENTS WITH HEMOGLOBINOPATHIES AS A BASIS FOR THE DEVELOPMENT OF A COMPUTER SYSTEM ENABLING THE MANAGEMENT OF RARE BLOOD

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Background: The advancement of personalized medicine and the use of precise matching to a patient with specific antigen profile, particularly for chronically transfused populations, such as those with sickle cell disease and thalassemia, has increased the request for rare blood. **Aims:** The objective of this study is to present data aimed at diagnosing patients and donors with rare blood types as a basis for the development of a computer system enabling risk management related to rare blood. **Methods:** A cross-sectional study analyzing data from 3,647 patients with hemoglobinopathies at the Rio de Janeiro Blood Center, Brazil, was conducted as a partial diagnosis to identify patients with rare phenotypes. The institution's rare donor registry was also accessed to assess blood availability for these patients. **Results:** The absence of multiple common antigens and other rare phenotypes such as Kp (b-), Jk(a-b-), Lu(b-), K+k-, U-, Js(b)-, Hy-, Uvar Jo(a-) were identified in these patients. Rare phenotypes resulting from RH variants in sickle cell patients were also identified, such as DAR, DIIIa, DAU5, hrB-. In twenty (32.3%) patients, 28 antibodies were identified. The mean red blood cell transfusion was 14 units. One hundred sixteen donors with phenotypic profiles corresponding to these patients were identified. However, we found that there are more patients with rare phenotypes than blood donors and that the number of compatible donors is insufficient to meet the transfusion need of the patients. **Summary/ conclusions:** Based on the assistential diagnosis of compatible transfusions conducted in these patients with hemoglobinopathies, which demonstrates the shortage of donors with rare phenotypes for performing transfusions with precise matching, we propose a modeling for the development of a computer system that allows for better identification and monitoring of patients and donors with rare phenotypes, preventing associated complications, and enhancing blood transfusion processes in the most optimized way that best suits the reality of blood centers.

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ALOIMUNIZAÇÂO ERITROCITÁRIA APÓS TRANFUSÂO DE CONCENTRADO DE HEMÁCEAS EM PACIENTES ATENDIDOS NOS HOSPITAIS EM BELO HORIZONTE – MINAS GERAIS

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Objetivos: Descrever os anticorpos identificados na aloimunização eritrocitária em pacientes que receberam transfusão de concentrado de hemácias (CH) em Belo Horizonte. Adicionalmente, busca-se analisar a relação entre a aloimunização e variáveis como sexo, idade e número de transfusões de CH recebidas. **Material e métodos:** : Foram avaliados os pacientes atendidos nos diversos hospitais de Belo Horizonte, pela Vita Hemoterapia, que receberam transfusões de CH e que desenvolveram aloimunização. Os dados foram coletados, a partir dos registros do sistema informatizado e NotiVisa, referentes a sexo e idade do paciente, número de transfusões recebidas antes da aloimunização e o tipo de anticorpo identificado, através da técnica de gel centrifugação. A análise estatística foi conduzida para avaliar a prevalência de aloimunização e sua associação com as variáveis estudadas. **Resultados:** : Entre o período de dezembro de 2022 a dezembro de 2023, foram identificados 73 pacientes que desenvolveram aloimunização após receberem transfusão de CH. Em relação a população analisada, foram identificados 31 (42,4%) pacientes do sexo masculino e 42 (57,5%) do sexo feminino, com média de idade de 63,5 anos. Ao analisarmos o número de CH transfundidos previamente à aloimunização, identificamos que 51 (69,9%) pacientes