de registros médicos de prontuários físicos e eletrônicos de 2003 a 2024. **Resultados:** Avaliamos um total de 66 pacientes, 30 tinham o diagnóstico de MF primária, 24 de MF PF, 8 de MF pós PV e 3 de MF pós TE. Do total, 53% eram do sexo feminino, 43,9% se declaravam brancos, com mediana de idade ao diagnóstico de 63 anos. No período avaliado, 48% dos pacientes faleceram, com uma média de tempo entre o diagnóstico e óbito de 61,5 meses (48,5 meses no grupo de MFP e 20 meses na MF secundária os), 4 progrediram para leucemia aguda e dois realizaram transplante de medula óssea. Treze pacientes (19,69%) apresentaram trombose venosa em algum momento do acompanhamento, dos quais 10 possuíam mutação em JAK2. Das mutações canônicas, JAK2 V617F foi encontrada em 62,12% dos casos. Vinte e sete pacientes realizaram sequenciamento genético (NGS), com identificação de variantes patogênicas em 16, sendo a ASXL1 (56,2%) a mais prevalente. Ao diagnóstico, 40,9% apresentaram sintomas constitucionais, sendo a perda ponderal o mais comum (37,8%) e 59,09% possuíam esplenomegalia. Na biópsia de medula óssea, 27,2% possuíam grau de fibrose MF3. Dos pacientes com MFP, 43,3% possuíam alto risco pelo IPSS. Dez pacientes fizeram uso de Ruxolitinib, enquanto 65,15% dos pacientes utilizaram Hidroxiureia. Vinte pacientes (30,3%) apresentaram alguma infecção relatada em prontuário durante o acompanhamento, sendo 2 (10%) casos de Herpes Zoster, todos em usuários de Ruxolitinib. **Discussão:** Entre os pacientes com diagnóstico de MF, a maioria possuía o diagnóstico de MFP. O grupo de MF secundária mostrou pior prognóstico, em relação a sobrevida a partir do momento de transformação para MF. O NGS ainda é pouco disponível na realidade da saúde pública brasileira, e os dados disponíveis foram possíveis em decorrência de estudos clínicos de colaboração. É perceptível o impacto na qualidade de vida dos pacientes, com elevada carga de sintomas. Ainda é escasso o acesso à terapia com inibidores de JAK2 no Brasil. **Conclusão:** Apesar de haver dados na literatura internacional acerca de MF, entender o comportamento da doença e seu impacto na nossa população é de suma importância para melhor manejo e cuidado dos pacientes brasileiros.

https://doi.org/10.1016/j.htct.2024.09.811

COMPARISON OF BCR-ABL (P210) GENE FUSION TRANSCRIPT DETECTION: A STUDY WITH THE BRAZILIAN AMAZON POPULATION

MB Oliveira [a], ATM Tavares [a], KVM Queiroz [b], JAA Castro [c], KADS Barile [c,d], AS Khayat [a], CEM Amaral [c,d]

[a] *Universidade Federal do Pará (UFPA), Belém, Brazil*
[b] *Universidade da Amazônia (UNAMA), Ananindeua, Brazil*
[c] *Fundação Centro de Hemoterapia e Hematologia do Pará (HEMOPA), Belém, Brazil*
[d] *Centro Universitário Metropolitano da Amazônia (UNIFAMAZ), Belém, Brazil*

Objective: Chronic Myeloid Leukemia (CML) is a myeloproliferative neoplasm characterized by the proliferation of myeloid lineage progenitor cells, increasing the circulating cells of the granulocytic lineage. The aim of this study is to evaluate the status of the BCR-ABL gene fusion transcript (P210) in cases of CML in patients from the Brazilian Amazon in relation to frequency and association with known prognostic laboratory data. **Materials and methods:** The research was approved by the ethics committee number 20528519.8.0000.5550 and included a total of 161 patients detectable for one of the BCR-ABL gene transcripts between 2015 and 2024. Clinical data (leukocyte count, blast count, platelets, and hemoglobin levels) and epidemiological data (sex and age) were collected from secondary data from the LABMASTER database system of the HEMOPA Foundation. For the analysis of fusion transcripts, c-DNA was obtained to detect the presence of molecular biomarkers by Real-Time PCR (RT-qPCR) using specific Taqman probes on the Rotor Gene equipment. Descriptive statistics were used for qualitative variables, determining absolute and percentage frequencies of the qualitative variables. For quantitative variables, median values and standard deviation were calculated according to the variables under study. The Kruskal-Wallis test was used to test the association of the presence of one of the P210 transcripts (B2A2, B3A2, and/or Both) with the clinical data, adopting a p-value ≤ 0.05 as significant. Statistical analyses were performed using SPSS software version 29.0. **Results:** Regarding the BCR-ABL gene, 39% (63/161) presented the B2A2 transcript, 30% (50/161) presented B3A2, and 31% (48/161) presented Both. Of the patients, 57% (92/161) were male and 43% (69/161) were female, with a median age of 44.5 years. In terms of white cell count, patients had a median of 164,200/mm^3; regarding blast count, the median was 6,816/mm^3; for platelet count, the median was 401,250/mm^3; and for hemoglobin levels, the median was 11 g/dL. The Kruskal-Wallis test revealed no statistical difference between the types of P210 gene fusion transcripts and the analyzed clinical laboratory data. **Discussion:** Studies conducted by other researchers on CML and the BCR-ABL gene found a higher prevalence in male patients, which is consistent with the findings of this study. However, the median age of patients is about 10 years lower than reported in the literature. Studies in Latin American (Argentina, Colombia and Ecuador) presented the B2A2 transcript as the most frequent, which corroborates the findings of this study, while in European countries (Bulgaria, Italy, and Serbia), the B3A2 transcript was the most prevalent. These differences can be explained by different ethnicities, but deeper studies are needed to understand the impact of genetic ancestry and the presence of the fusion transcript. **Conclusion:** In the present study, the B2A2 transcript was observed as the most prevalent in patients with CML and this type of transcript had a higher median leukocyte compared to the other groups, and patients with the B3A2 transcript had a higher median platelet compared to the others. However, no significant difference was found between the groups. The transcript impacts the disease development process, so it is worthwhile to study the P210 pathways and find new treatment strategies.

https://doi.org/10.1016/j.htct.2024.09.812