

Genetic Mutations Detected in Adult Patients Diagnosed With Chronic Myeloid Leukemia (CML): 24 Years of Experience in a Public Hospital in Guatemala



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INTRODUCTION

The development of TKIs in CML represents the success of molecular targeted therapy, since it has reduced the mortality in CML to almost equal that of the general population.(1,2) While TKI resistance and disease progression are multifactorial, genetic mutations play a vital role on these phenomena. (1,3) One study determined mutational status in CML and TKI resistance in various hospitals in Guatemala.(4) This study details long-term data on genetic mutations in CML in a public hospital in Guatemala.

AIM

To describe the genetic mutations detected in patients diagnosed with CML in the Hematology Unit in Hospital Roosevelt from 2002 to February 2026

METHOD

Descriptive, retrospective, cross-sectional, observational analysis from 2002 to February 2026. Data was retrieved from 318 patients diagnosed with CML in a public tertiary-level hospital in Guatemala from 2002 to February 2026. Results were obtained through a 30-gene myeloid panel using NGS or RT-PCR to determine variants in *BCR::ABL 1* and *ASXL 1* exon 13 in peripheral blood samples.

CONCLUSIONS

A genetic mutation was detected in 12.58% of adults with CML. The most frequent genetic mutations detected were *ASXL 1* in 25/66 and *ABL 1* in 24/66 of positive mutations. A larger study with a sociodemographic emphasis is required to determine more robust mutational tendencies in the Guatemalan population.

RESULTS

Table 1. Demographic characteristics of patients with CML, from 2002 o February 2026	
Median age (range) - years	46 (9 - 87)
Sex - no. (%)	
Female	157 (49.37%)
Male	161 (50.63%)
Cases per 5 years - no. (%)	
2002 - 2006	3 (0.94%)
2007 - 2011	28 (8.81%)
2012 - 2016	66 (20.75%)
2017 - 2021	93 (29.25%)
2022 - Feb 2026	128 (40.25%)
Total	318 (100%)

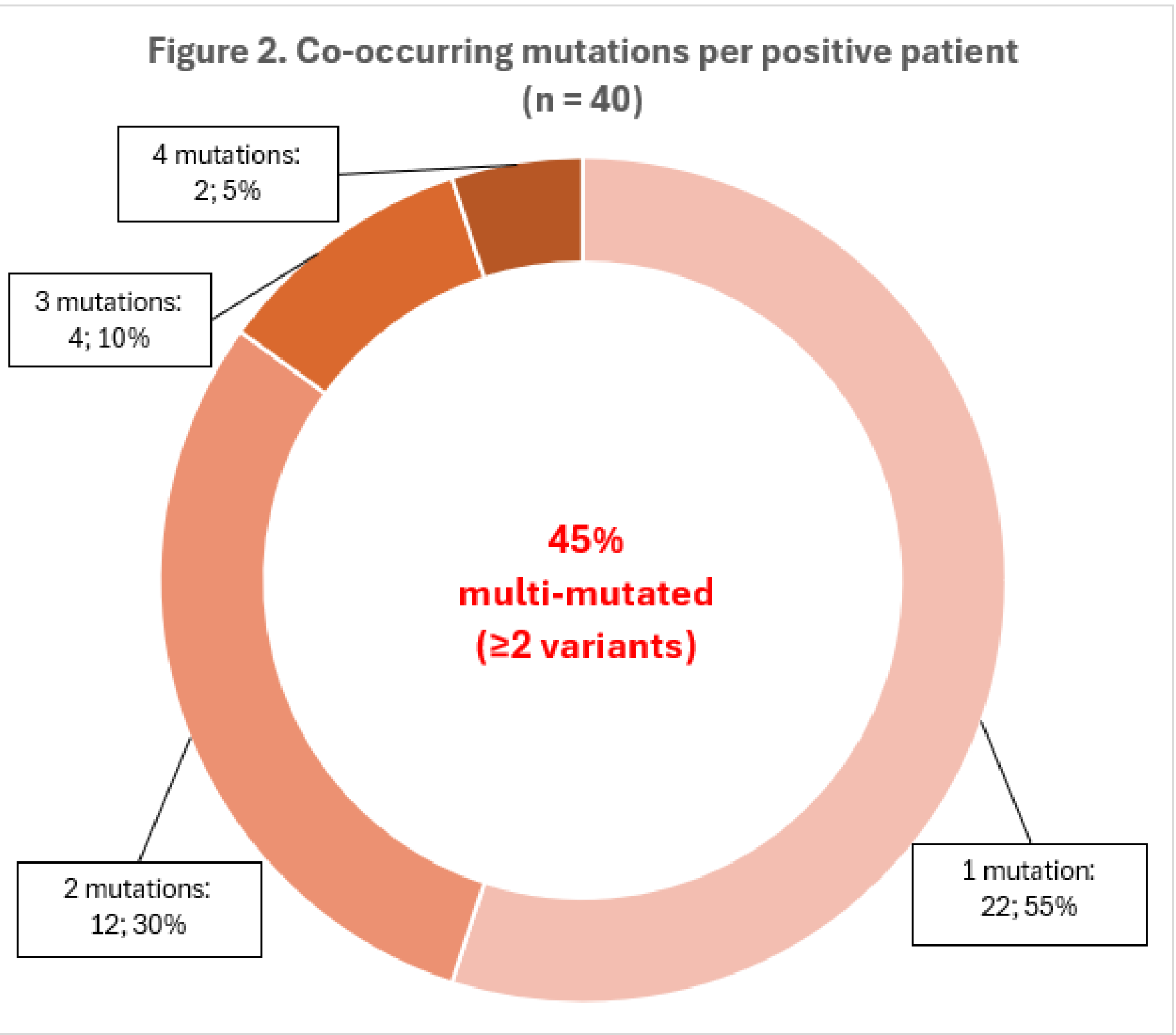
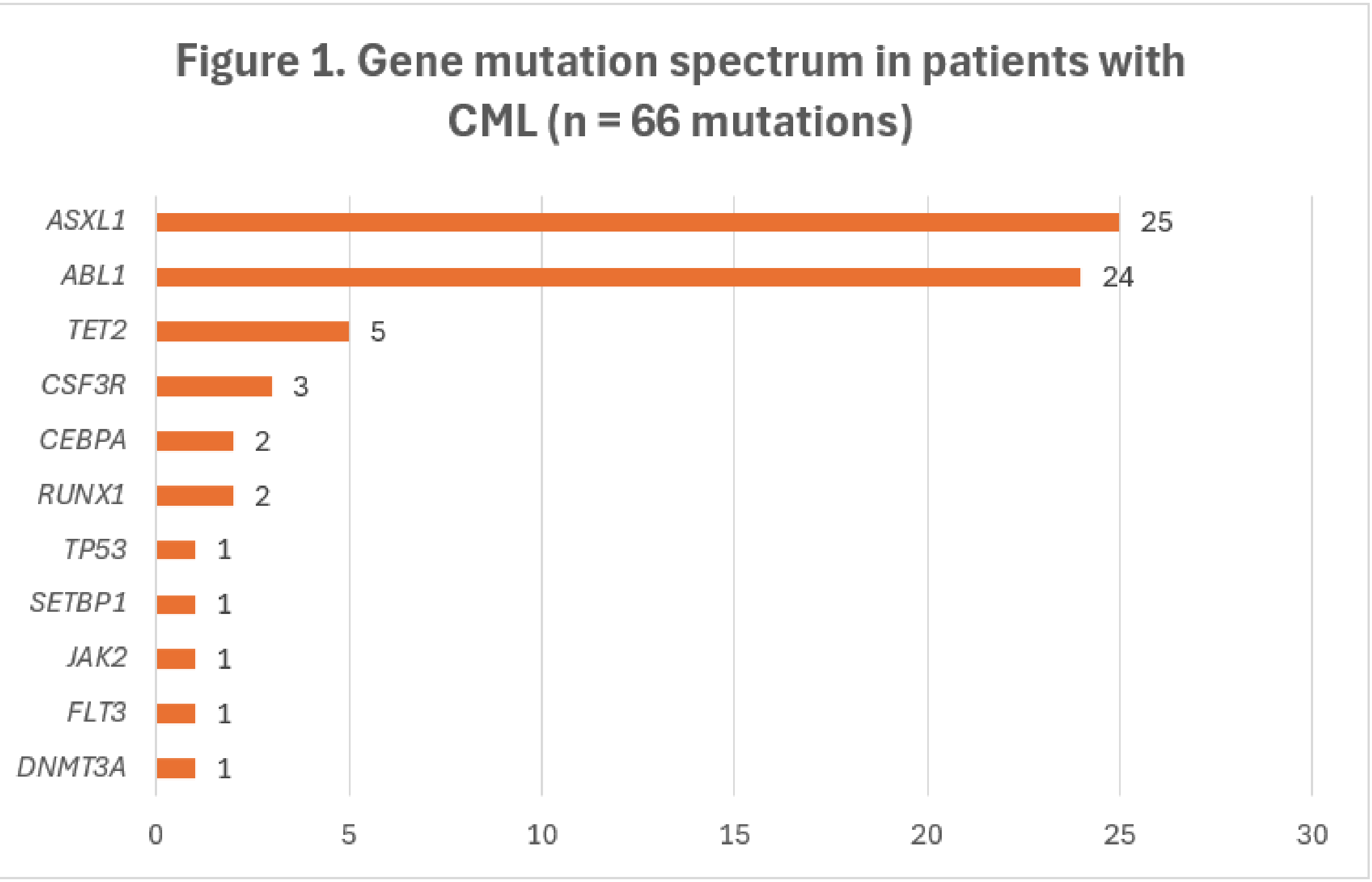
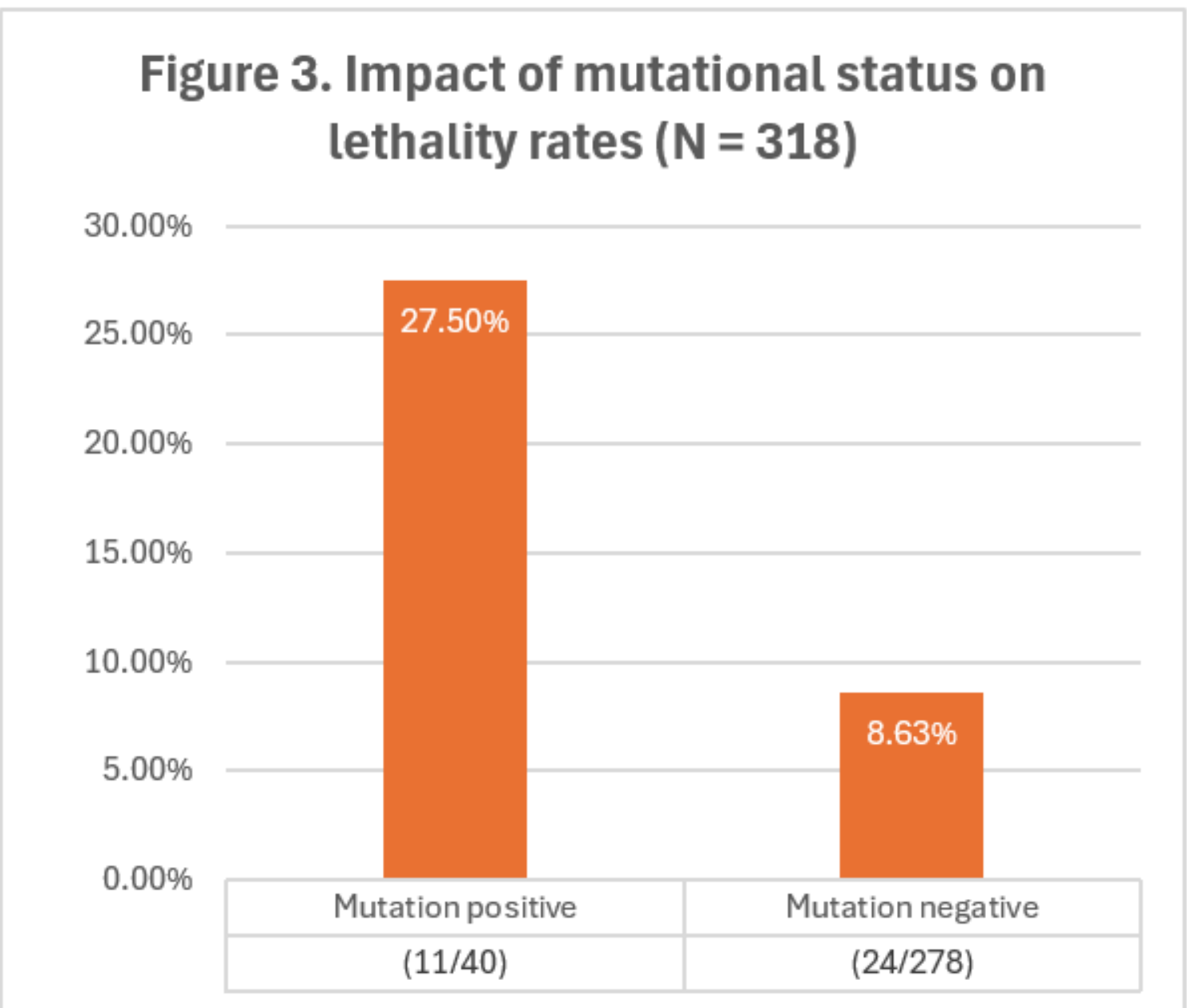


Table 2. TKI resistance and mutational status in patients wih CML			
TKI status	Mutation positive	Mutation negative	Total
TKI resistant	32 (24.43%)	99 (75.57%)	131 (41.19%)
TKI sensitive	8 (4.28%)	179 (95.72%)	187 (58.81%)
Total	40 (12.58%)	278 (87.42%)	318 (100%)

Note: Percentages reflect row proportions.

Table 3. Most prevalent protein expressions detected (n = 66)		
protein expression	no.	consequence
ASXL1		
p.Gly646Trpfs*12	05/66	frameshift
ABL1		
p.Thr315Ile	05/66	missense
p.Gly250Glu	04/66	missense
p.Glu255Lys	03/66	missense
p.Tyr253His	03/66	missense



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REFERENCES

- Yoshimaru R, Minami Y. Genetic Landscape of Chronic Myeloid Leukemia and a Novel Targeted Drug for Overcoming Resistance. Int J Mol Sci. 2023 Sep 7;24(18):13806. doi:10.3390/ijms241813806
- Jabbour E, Kantarjian H. Chronic myeloid leukemia: 2025 update on diagnosis, therapy, and monitoring. Am J Hematol. 2024 Nov 2;99(11):2191–212. doi:10.1002/ajh.27443
- Sun J, Hu R, Han M, Tan Y, Xie M, Gao S, et al. Mechanisms underlying therapeutic resistance of tyrosine kinase inhibitors in chronic myeloid leukemia. Int J Biol Sci. 2024;20(1):175–81. doi:10.7150/ijbs.86305
- Oliva A, Alvarado V, Fuentes-Merlos I, Castellanos M, Chopox L, Arrivillaga-Cano E, et al. CML-558 Genetic Alterations in Chronic Myeloid Leukemia Patients With Tyrosine Kinase Inhibitors Resistance From Guatemala Through Next-Generation Sequencing. Clin Lymphoma Myeloma Leuk. 2024 Sep;24:S375. doi:10.1016/S2152-2650(24)01320-X