

## Prevalence and genotype-phenotype correlation study of *ASXL1* variants c.1773C>G(Tyr591Ter) and c.1282C>Tp.(Gln428Ter) in a Sri Lankan Myeloproliferative Neoplasm cohort

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Molecular insights into *ASXL1* gene variants are valuable for the diagnosis and prognosis of myeloproliferative neoplasms (MPNs). Their prevalence varies across ethnicities, with limited data available for South Asian populations. This study investigated two Asian-specific *ASXL1* variants—c.1773C>G (p.Tyr591Ter) and c.1282C>T (p.Gln428Ter)—and assessed genotype–phenotype correlations in a Sri Lankan MPN cohort. Fifty patients from a tertiary care hospital in North Colombo were recruited following ethical approval (EC-24-150). Variant selection was based on Genome Aggregation and VarSome databases. Detection was performed using Tetra-primer ARMS-PCR, with a modified touchdown PCR protocol for the c.1282C>T variant. Results were validated through Sanger sequencing and analyzed using IBM SPSS Statistics 19. Of the cohort (PV: 82%, ET: 10%, PMF: 8%; male:female ratio 2.3:1; mean age 56 years), the c.1773C>G variant was identified in 12% (n=6, all heterozygous) and was present across all MPN subtypes. The c.1282C>T variant was not detected in any patient. ARMS-PCR results were consistent with Sanger sequencing. No statistically significant genotype–phenotype correlations were observed, though trends included lower hemoglobin and higher platelet counts in variant-positive patients. This is the first report of the c.1773C>G variant in Sri Lankan MPNs. The absence of the c.1282C>T variant may reflect its rarity or post-treatment clonal loss. The development and validation of cost-effective ARMS-PCR protocols for *ASXL1* variant screening represent a significant step toward personalized MPN management in South Asia. Larger studies are warranted to confirm these findings.

**Keywords:** *Sri Lankan Myeloproliferative Neoplasms, ASXL1c.1773C>G(Tyr591Ter), ASXL1c.1282C>T(Gln428Ter), Tetra-primer ARMS-PCR, Touchdown-PCR*