



# Population-adjusted cut-off: A new approach for enhancing the diagnostic efficacy of hematological discrimination formulae for screening $\beta$ -Thalassemia trait

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## ABSTRACT

Screening for  $\beta$ -thalassemia trait ( $\beta$ TT) is crucial for preventing  $\beta$ -thalassemia major in offspring. Although hematological discrimination formulae (HDF), developed using complete blood count parameters, are cost-effective tools for screening  $\beta$ TT, their performance varies across different populations. This study evaluated the performance of 32 HDF for screening  $\beta$ TT in the Sri Lankan population. Data were retrieved from laboratory databases and categorized into confirmed  $\beta$ TT and non- $\beta$ TT groups based on high-performance liquid chromatography results. The  $\beta$ TT screening performance of the HDF was assessed using accuracy measurements, the receiver operating characteristic (ROC) curve, and Youden's index (YI). Furthermore, a population-adjusted cut-off was determined using the Index of Union (IU) method to optimize the predictive accuracy of HDF in screening  $\beta$ TT. Bordbar demonstrated excellent predictive performance in males (AUC = 0.908; YI = 0.815), while Shine & Lal, Kerman-I, Nishad, Sehgal, Bordbar, and Roth demonstrated high discriminative ability in females (AUC > 0.833; YI > 0.666). Applying a population-adjusted cut-off improved the  $\beta$ TT screening potential of Shine & Lal, Kerman-I, Nishad, Bordbar, and Roth in males (AUC > 0.911; YI > 0.822) and enhanced the performance of Kerman-II in females (AUC > 0.861; YI > 0.722). Notably, Shine & Lal (AUC = 0.937; YI > 0.873) and Nishad (AUC = 0.897; YI > 0.794) demonstrated the best performance for males and females, respectively, when a population-adjusted cut-off was applied for screening  $\beta$ TT. In conclusion, determining a population-adjusted cut-off is a new initiative to enhance the  $\beta$ TT screening performance of HDF across different populations.

## 1. Introduction

$\beta$ -thalassemia is a heterogeneous group of genetic disorders causing a substantial number of morbidity and mortality, as well as a financial burden worldwide [1].  $\beta$ -thalassemia, a genetic disorder characterized by a mutation in the  $\beta$ -globin gene, is classified into  $\beta$ -thalassemia major,  $\beta$ -thalassemia intermedia, and  $\beta$ -thalassemia trait ( $\beta$ TT) based on their clinical and laboratory findings [2,3]. Approximately 60,000 children are estimated to be born with  $\beta$ -thalassemia, with an additional 1.5 % of the global population being carriers annually [4,5].  $\beta$ -thalassemia is the primary type of thalassemia in Sri Lanka, affecting 2.5 % of all three major ethnic groups [6]. Screening  $\beta$ TT and identifying its heterozygous

variant hemoglobin (Hb) is crucial for preventing and controlling  $\beta$ -thalassemia major in offspring [7]. The  $\beta$ TT is suspected when observing the near-normal Hb level, slightly elevated red blood cell (RBC) count, and microcytic hypochromic cells in the evaluation of routine RBC indices and blood picture, but confirmation of  $\beta$ TT is performed by quantifying HbA<sub>2</sub> in high-performance liquid chromatography (HPLC) or capillary zone electrophoresis [8,9]. Besides, reverse transcriptase polymerase chain reaction (RT-PCR) or DNA sequencing is employed to detect specific mutations in  $\beta$ TT [10–12]. However, the availability and accessibility of these techniques are restricted to resource-limited countries due to high costs [13,14].

Over the past few decades, several hematological discrimination

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