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RELATIONSHIP BETWEEN RBC PARAMETERS, HbA_2 LEVEL AND MOLECULAR FINDINGS IN ALPHA THALASSEMIA: HTAR EXPERIENCE

By

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ABSTRACT

Alpha thalassemia is a common recessively inherited blood disorder due to mutation or deletion of one or more alpha globin gene. Nowadays, the initial step for screening of alpha thalassemia is by determining the MCV and MCH values. Further investigation includes Hb analysis and confirmation test by molecular analysis. Among the popular molecular method commonly used today is the polymerase chain reaction (PCR). HTAR usually outsource its molecular tests for alpha thalassemia. However, only about 50% of the outsourced samples were positive for alpha thalassemia. Thus, to avoid performing molecular analysis unnecessarily, this study was proposed to find if there is any relationship between the RBC parameters, HbA_2 level and molecular findings for better screening of patients prior to request for molecular analysis. A total of 197 data which consisted of RBC parameters (TRBC, Hb, RDW, MCV, MCH, MCHC and Retic Count), HbA_2 level and molecular findings from HTAR patients diagnosed with alpha thalassemia in 2014. Independent t-test was conducted to evaluate whether the RBC parameters and HbA_2 level differed significantly for groups of positive or negative molecular findings. Out of the eight parameters tested, RDW, MCHC and rectic were found to be significantly different between groups of positive and negative molecular analysis. Then, the RDW, MCHC and Retic were then anaylzed using ROC Curve to determine the cut-off values for positive molecular findings, respectively. The cut-off values for MCHC and Retic could be determined while cut-off values for RDW could not be determined as the area under the curve was less than 0.5. The cut-off values for MCHC was equal or greater than 34.15 g/dL while the cut-off value for Retic was equal or greater than 2.1%.

Keywords: alpha thalassemia, alpha globin gene, multiplex PCR

CHAPTER 1
INTRODUCTION

1.1 BACKGROUND OF STUDY

Thalassemia is a type of genetic disorder characterized by quantitative defects in globin chain synthesis. It causes varying degrees of anemia which can range from significant to life threatening due to deficiency or absence of hemoglobin production (Bernini, 2001). According to Shivashankara et al. (2008), about 370000 newborns every year were affected severely with either homozygotes or compound heterozygotes of thalassaemia. Over 5% of the whole world populations are positive as carriers of hemoglobinopathies as reported by the World Health organization (2008). The people of Mediterranean, African, Middle Eastern, Indian, Chinese, or Southeast Asian origins are commonly associated with these conditions (Bernini, 2001). It is recognized as inherited hemoglobinopathy (Wee et al., 2008).

Thalassemia is also known as an autosomal recessive disorder and usually the thalassaemic syndromes inherited from both parents, father and mother whom are carriers of thalassaemia (Jameela et al., 2011). Clinical classification of thalassemia is based on the type of mutation or the deficient number of globin chains (Chen et al., 2015). There are two common types of thalassaemia which are alpha thalassaemia and beta thalassaemia (Wee et al., 2008).

According to Harteveld and Higgs (2010), alpha thalassemia is the most common recessively inherited hemoglobin disorder characterized by a microcytic hypochromic anemia with clinical phenotype varying from almost asymptomatic to lethal hemolytic anemia. It involves deletion of one or both alpha globin genes encoding the alpha globin chains. The gene cluster for alpha globin chain is located on chromosome 16. As for beta-thalassemia is associated with mutation in the beta globin gene at chromosome 11 (Antonio & Renzo, 2010).