The distribution of the three target thalassemia genes through GIS visualization for thalassemia management Case study: Nakhon Chai Bu Rin area, Northeast of Thailand

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Abstract

Thalassemia is the most common genetic disorder which is one of major public health problems in Thailand. The Ministry of Public Health of Thailand supports the implementations of a prevention and control program throughout the country to avoid the birth of children with severe thalassemia diseases. Although a national program was inaugurated in 1994, it cannot yet fully achieve its objectives. The main reason is that general population still lacks of knowledge and awareness about the disease. This study aimed to apply Geographic Information System (GIS) to create information of the epidemiology of thalassemia for contributing to the deeper understanding of general public and also health personnel in Nakhon Chai Bu Rin area (Nakhon Ratchasima, Chaiyaphom, Buriram and Surin provinces), in the Northeast of Thailand. Quantum GIS software was the instrument that was used to present data distribution of three target thalassemia genes including α-thalassemia1 gene, β-thalassemia gene, and HbE gene leading to hemoglobin Bart's hydrops fetalis, Homozygous β-thalassemia and β-thalassemia/Hb E. As expected, HbE was the most prevalent abnormal hemoglobin in this area. A point feature on GIS visualization displayed the places where the gene occurs, thus, it enabled health personnel to determine locations of high prevalence areas and population at risk and then steps could be taken to plan of action for preventing the disease. Moreover, it also can help health personnel bring up interest and know-how about thalassemia to the community. However, the software of Quantum GIS is limited, it needed to develop the ability to retrieve data from routine for supporting health personnel to manage thalassemia workforces.