The protein and genomes and its implication as malaria parasites drugs

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Malaria is a major cause of human morbidity and mortality. Malaria is a hematoproteozoon parasitic infection transmitted by certain species of anopheles mosquitos’ four species of plasmodium commonly infect humans, but one, Plasmodium falciparum, accounts for the majority of instances of morbidity and mortality. There has been a resurgence of interest in malaria in recent years as the immensity of the burden it imposes on poor countries in the tropics has become apparent, and as efforts at control have foundered after the failure of the global eradication campaign in the 1960s. Control has traditionally relied on two arms: control of the anopheles mosquito vector through removal of breeding sites, use of insecticides, and prevention of contact with humans (via the use of screens and bed nets, particularly ones that are impregnated with insecticides); and effective case management. Case management has relied largely on antimalarial (mainly chloroquine, and more recently sulfadoxine-pyrimethamine [SP]), which are inexpensive and widely available and are eliminated slowly from the body. Together with antipyretics, antimalarial are among the most commonly used medications in tropical areas of the world. Misuse is widespread. In many parts of the tropics, the majority of the population has detectable concentrations of chloroquine in the blood. Resistance is the most likely explanation for a doubling of malaria-attributable child mortality in eastern and southern Africa, we have developed a dynamic range which will facilitate greater understanding of the biology of these parasites.

Biography

Mohammed Hassan: has completed his bachelor degree from faculty of medicine, University of Gezeria, Sudan 2014 at the age of 23, He is work as a doctor in Wedmadani Educational hospital, Ministry of Health, Sudan, He interesting in the malaria in tropical area research, Now he doing his specialty in medicine.

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