#31: Genome-wide association analysis identifies genetic loci associated with resistance to multiple antimalarials in *Plasmodium falciparum* from China-Myanmar border

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Drug resistance has been one of the greatest challenges for malaria control, and the recent emergence of resistance in *Plasmodium falciparum* to artemisinin family drugs is concerning. To identify genetic markers potentially associated with antimalarial drug resistance, we performed genome-wide association analysis to assess the associations of single nucleotide polymorphisms (SNPs) from a high-density SNP array with in vitro sensitives to 10 commonly used antimalarial drugs in 94 parasite isolates from the China-Myanmar border area, where artemisinins have the longest history of deployment. Among the numerous SNPs identified to be associated with reduced in vitro drug sensitivities, a SNP located in the autophagy-related protein 18 (ATG18, PF3D7_1012900) was associated with decreased IC50 values to dihydroartemisinin, artemether and piperaquine, which have all been used extensively in this region. Being an artemisinin-interacting protein and a putative phosphatidylinositol-3-phosphate binding protein, the identification of ATG18 suggests a potential involvement of autophagy in artemisinin resistance.