

**INFECTIVITY AND GENETIC POLYMORPHISM OF  
ANOPHELES MACULATUS AND AN. VAGUS IN DIVERSE  
ENDEMICITY MALARIA AREAS IN THE KOKAP  
SUB-DISTRICT OF KULON PROGO**

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**ABSTRACT**

**BACKGROUND:** It is crucial to regularly monitor the infectivity and genetic polymorphism of Anopheles sp in endemic areas for early detection and accurate rapid response planning of indigenous malaria transmission. The Kokap Sub-District has the highest number of malaria cases in the Kulon Progo District. Its five villages showed diverse malaria endemicities. Anopheles maculatus was pointed out as the main vector and An. vagus as a suspect vector. The purpose of this investigation was to examine whether the populations of these two species were different with regard to infectivity and genetic polymorphism in villages that were high endemic (HEV) and low endemic (LEV).

**SUBJECT AND METHODS:** A cross-sectional observational study was performed in one HEV (Hargotirto) dan one LEV (Hargomulyo) on An. maculatus sp and An. vagus sp parous mosquitoes. The mosquitoes of both villages were collected simultaneously using the resting collection method, five times each, during October-December 2013. The collections were conducted in three houses by two collectors per house (one inside and one outside) in 50 minute intervals from 18.00PM to 06.00AM. Mosquitoes that meet the inclusion criteria were examined using the Multiplex-PCR method to detect the existence of Plasmodium and the Random Amplified Polymorphic DNA (RAPD) method to identify mosquito DNA polymorphism.

**RESULTS:** The PCR test results of DNA samples of An. maculatus (25 HEV and 7 LEV) and An. vagus (18 HEV and 20 LEV) of the two villages showed that only the HEV sample was Plasmodium sp positive with 28% An. maculatus and 17% An. vagus infectivities (OR=6.08; CI95%: 0.31-120.4; p=0.043). The RAPD-PCR test results of DNA samples of An. maculatus (5 per village) and An. vagus (5 per village) of the two villages showed identical degrees of DNA polymorphism.

**CONCLUSION:** The endemicity of the two villages was related to Anopheles sp infectivity. Although no Plasmodium sp positive anophelines were found in the LEV vector surveillance is nonetheless necessary considering the same levels of DNA polymorphism.

**Keywords:** Anopheles sp, infectivity, endemicity, genetic polymorphism