Background Malaria rapid diagnostic tests (RDTs) play a significant role in malaria case management and case investigations. Variability or absence of antigens targeted by PfHRP2-based RDTs have been reported worldwide. However, little data is available concerning genetic variability within Sudanese *Plasmodium falciparum* isolates while variable sensitivity of PfHRP2 based RDTs has been observed. The objective was to find out the possible effect of PfHRP2 gene variation and suspected deletion on the performance of PfHRP2-based RDTs.

Methods Seventy-seven *P. falciparum* isolates were selected from three geographical regions of Sudan. Malaria HRP2-RDTs and Giemsa-stained blood films data were included for analysis. The *pfhrp2* exon 2 fragments were amplified to study genetic variation and suspected deletion. Chi-square test was used for testing significance of results.

Results Forty percent (31/77) of *P. falciparum* isolates showed amplification for PfHRP2 (which revealed five alleles of different sizes), whereas 60% of isolates were PfHRP2 PCR-negative. There is a concordance of positive and negative rates on PfHRP2 RDT and gene amplification results of (35%) and (33%) respectively. Eighty-seven percent (78%) of RDTs positive isolates were PfHRP2 negative (p-value=0.001), while 4 out of 31 *pfhrp2* positive isolates gave false negative results in RDT detection. Twenty out of 47 RDTs positive isolates were PfHRP2 negative (p-value=0.001). *Plasmodium falciparum* HRP2-RDTs showed higher sensitivity than microscopy in malaria detection (p-value=0.007).

**Conclusions** The study provided baseline data on genetic variation and suspected deletion in PfHRP2 and its potential effect on RDT performance.

PA-015 GENE VARIATION AND SUSPECTED PLASMODIUM
FALCIPARUM HISTIDINE-RICH PROTEIN 2 GENE
DELETION AND ITS IMPACT ON SENSITIVITY OF
MALARIA RAPID DIAGNOSTIC TESTS IN SUDAN

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