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Most patients in Cambodia with treatment failure post atovaquoneproguanil lack *cytb* mutations in Y268 locus by Sanger sequencing



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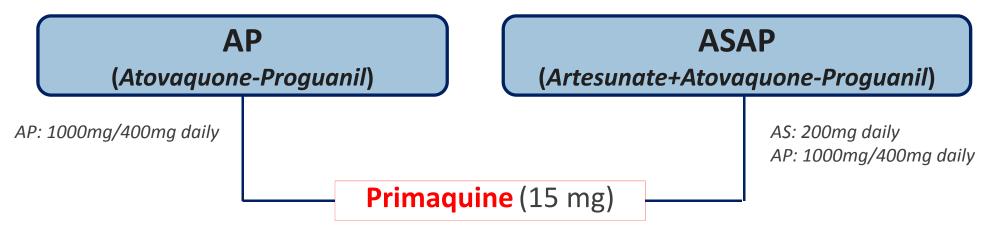
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The investigators have adhered to the policies for protection of human subjects as prescribed in AR 70–25.

Limited data on drug resistance to malarone in Cambodia

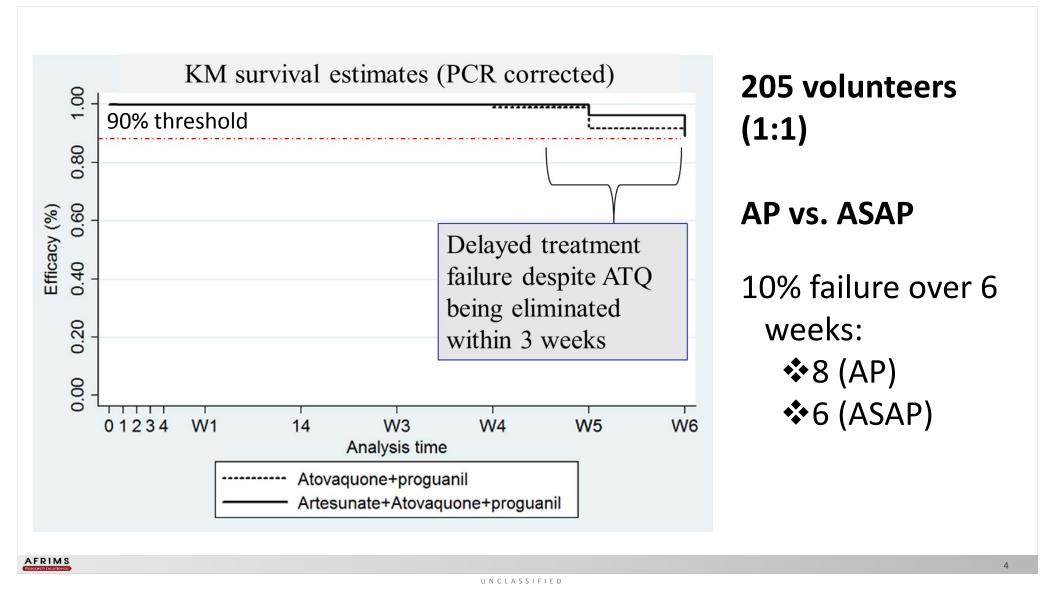
TES in volunteers with uncomplicated *P. falciparum* or mixed *P. falciparum/P. vivax* infection



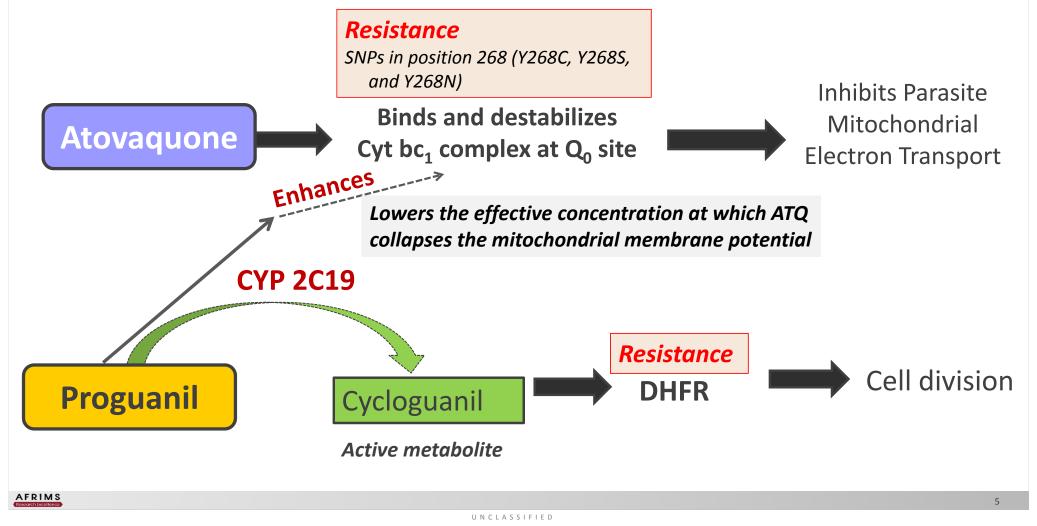
Weekly follow-up and malaria smears/PCR correction until 42 days (6 weeks)

Analyzed atovoquone and cycloguanil markers of resistance

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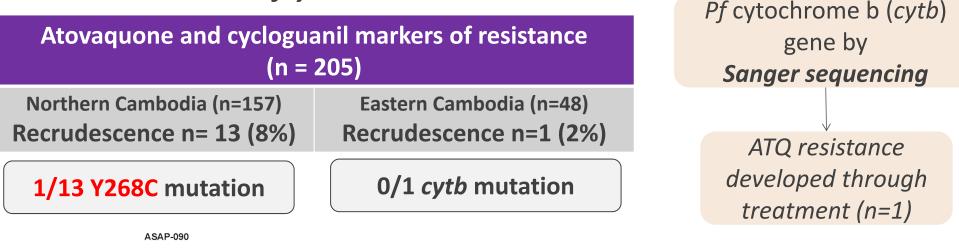


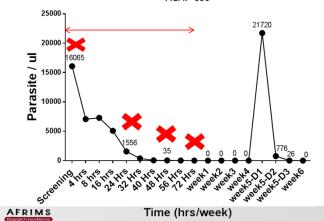




Cause of treatment failure (n=14)

1 volunteer with *Pfcytb* mutation on DR





Amplicon deep sequencing targeting *cytb* confirmed the presence of the Y268C mutation in 99.8% of the sequence reads at recrudescence, but did not detect the mutation at D0, or 24, 48, 72 hours into treatment, despite ~1.3 million read depth, even at a minor allele frequency down to 0.25%

UNCLASSIFIED

Conclusions

- □ The vast majority of treatment failures (13/14) could not be explained by atovaquone resistance in *Pfcytb*
- □ *De novo* mutation through treatment with AP was infrequent (0.5%) consistent with prior estimates
- "Monotherapy" with AP should be avoided in Cambodia (high resistance to cycloguanil, short half-life of proguanil, and variability in ATQ exposures leaves leaves ATQ unprotected during treatment with AP)
- ✓ AP remains a reasonable rescue drug choice given its PCR-adjusted ACPR of approximately 90% but should not be used as a first-line agent on its own
- There may be a role for AP use in combination with other antimalarials, such as ACTs. This approach could become a viable option against MDR parasites in Cambodia but clinical efficacy studies are needed to identify safe and effective drug combinations with AP.



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