Lack of resistance of Plasmodium falciparum to
dihydroartemisinin in Uganda based on parasitogolgical and
molecular assays

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Introduction

- Artemisinin-based combination therapy is now standard treatment for falciparum malaria. However, this regimen is threatened by resistance to artemisinins, manifest as delayed clearance of parasitemia after therapy, in southeast Asia.

- Artemisinin resistance in southeast Asia is associated with increased parasitemias in culture, compared to those in sensitive parasites, 72 hours after a 6 hour pulse with 700 nM dihydroartemisinin (DHA), and with propeller domain polymorphisms in the Plasmodium falciparum kelch (K13; PF3D7_1343700) gene.

- Given that artemether/lumefantrine has been adopted as standard therapy for malaria within the last decade in Uganda, we characterized artemisinin sensitivity in fresh P. falciparum isolates from Kampala using ex vivo ring-stage survival and IC50 assays. We also assessed the K13 gene for polymorphisms.

Methods

- Parasite isolate collection, filter papers (N=53)
- ex vivo IC50 assays (N = 15)
- gDNA from filter papers for K13, pfcr1 and pfmdr1 genotyping
- Long term cultures to test for recrudescence (N = 12)
- ex vivo ring-stage survival assays (N = 43)
- Parasite isolate collection, filter papers (N=53)

53 fresh P. falciparum isolates were collected from patients diagnosed with malaria from May-August 2014, at Mulago Hospital, Kampala.

- Parasite IC50’s to DHA were determined by a standard 72 h ex vivo microplate assay using HRP2 detection.

- Parasite susceptibility to DHA was assessed in the ex vivo ring-stage survival assay as described. Survival rates were expressed as the proportion of parasites in the 6 h, 700 nM DHA-pulsed cultures relative to DMSO controls, at the end of the 72 hour assay. Twelve cultures exposed to DHA were allowed to grow for 30 d to test for recrudescence.

- K13 propeller-encoding domains (codons 440-726) were dideoxy sequenced. Polymorphisms in pfcr1 and pfmdr1 were assessed with multiplex ligation detection reaction-fluorescent microsphere assays as previously described.

Results

- Fig. 2. Ring-stage survival assay.
  - Ring-stage survival was 0% in 40/43 cultures
  - Ring-stage survival ranged 0.7 - 1.9% in 3/43 cultures
  - No association with survival and SNPs in K13, pfcr1 or pfmdr1
  - Parasites reemerged from 10/12 long-term cultures after DHA pulse

- Fig. 3. Prevalences of wild-type, mixed, and mutant sequences at the indicated positions for all 53 isolates.
  - Wild Type
  - Mixed
  - Mutant

- Fig. 4. Ex vivo IC50 values for DHA from 15 isolates. The geometric mean IC50 value was 1.6 nM.
  - NH2 - P. falciparum sequences
  - BTB-POZ
  - S522C
  - A578S
  - 1 2 3 4 5 6 - COOH

- Fig. 5. Two kelch (K13) polymorphisms were detected from our samples. Numbered boxes indicate the six blades comprising the propeller domain of the kelch 13 protein.

Summary and Conclusions

K13 mutations were found in 2/53 parasite isolates from Kampala, but were not mutations associated with resistance in SE Asia.

RSA and IC50 data showed that parasites remain highly sensitive to DHA in vitro.

The results of this study, as well as findings from other studies, suggest that artemisinin resistance is not yet a problem in Uganda. The polymorphic nature of K13 in Africa and altered ACT partner drug sensitivity in Uganda indicate the continued need for surveillance of ACT efficacy in the region.