



# **Genetic diversity of plasmodium falciparum in Mpongwe**

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# Objectives

1. To determine the genetic diversity of the *plasmodium falciparum* in Mpongwe.
2. To assess the multiplicity of infection in the study population



# Methods (1)

- Blood spot samples collected from microscope positive under five children were extracted for DNA by methanol fixation method, and stored at -20° C
- Block 2 of *msp-1*, and block 3 of *msp-2* and *Glurp*. were amplified by nested PCR, each amplification with conserved, or family-specific primer pair, being done separately.
- PCR products were electrophoresed on 1.5% ethidium bromide stained agarose gels
- DNA visualized by ultraviolet transillumination
- Fragments obtained were compared by size.



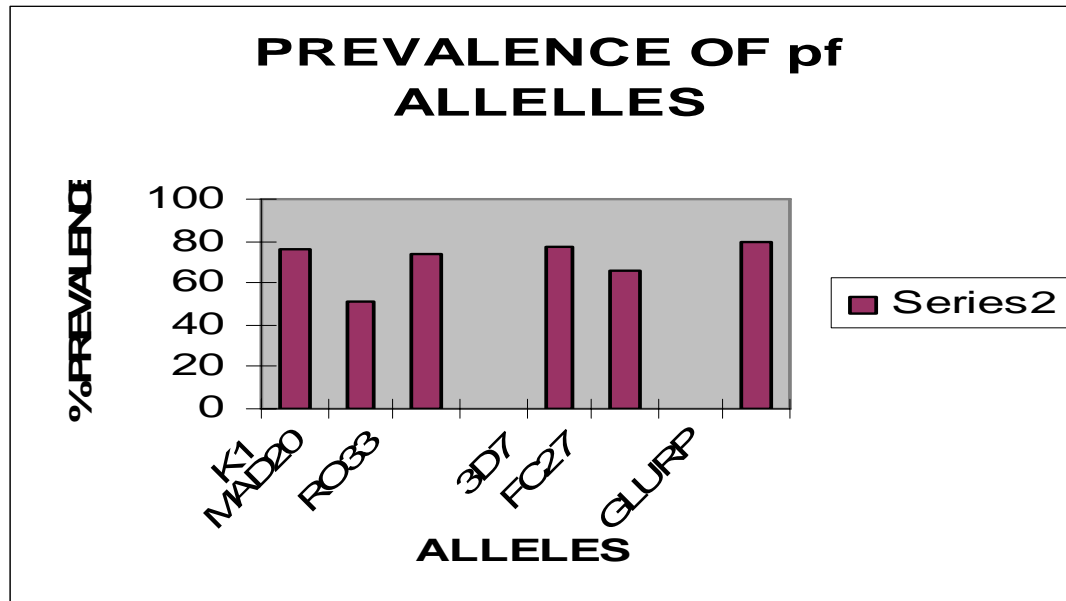
# Results (1)

- Among the 81 samples, at the *msp-1* locus Sixty-two (76.54%) harbored K1 parasites; 60 (74.04%) RO33 parasites and 41 representing 50.62% of the parasites were of the MAD 20 family.
- K1 family ranged from 190 to 300 bp; MAD20 alleles ranged from 200 to 280 bp; and the RO33 family had alleles ranging from 160 to 250 bp
- For the *msp-2* locus, 53 FC27 alleles ranged from 300 to 500 bp; and 63 3D7 alleles ranged from 350 to 500 bp. For *msp-2*, 53 (65.42%) of isolates contained FC27 parasites, and 63 (77.8%) 3D7 parasites.



# Results (2)

The prevalence of all analysed immunogenic alleles of *pf* was above 50%





## Results (3)

- And 79.01% (64 parasites) harbored GLURP parasites.
- The proportion of patients with mixed infections or samples having at least 2 strains of parasites was found to be 98.7%. Only one sample was observed to have just one strain of parasites.
- The average Multiplicity of infection in this population was 5.3, with some patients having as much as 10 parasite strains.
- MSP 1 and 2, and GLURP all showed polymorphism



# Discussion & Conclusions

- From the PCR analyses done it can be concluded that Mpongwe district has a highly genetically diverse population of *plasmodium falciparum* as seen from the extensive polymorphism mainly in the MSP1 and MSP2 antigens.
- It can be concluded also that malaria infections in this area are mainly characterized by mixed infections as evidenced by the high MOI (5.3)



# Future perspectives

- The study was conducted to provide preliminary data for the future malaria vaccine trials in the study population

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