



PFHRP2/3 GENE DELETIONS AND ANTIMALARIAL RESISTANCE GENES IN PLASMODIUM FALCIPARUM MALARIA PATIENTS IN SINDH, PAKISTAN

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Introduction

- Pakistan's location at the intersection of South Asia, Central Asia, and the Middle East makes it a vital U.S. partner for regional security and economic corridors.
- A heavy malaria burden demands vigilant surveillance to ensure accurate diagnosis and treatment.
- Deletions in the pfhrp2 and pfhrp3 genes of Plasmodium falciparum cause false-negative rapid diagnostic test (RDT) results.
- We aimed determine the frequency of pfhrp2 and pfhrp3 gene deletions and screen for genetic mutations associated with antimalarial drug resistance.



Picture1: Collaborative logistics meeting was conducted with teams from NAMRU-EAC, Aga Khan, and partner sites to prepare for study implementation

Picture courtesy of M. Asim Beg, MBBS, PhD, FRCP (Edin), Professor, Aga Khan University, Karachi, Pakistan
Picture taken by: Zainab Rafeeq, Technologist, Aga Khan University, Karachi, Pakistan

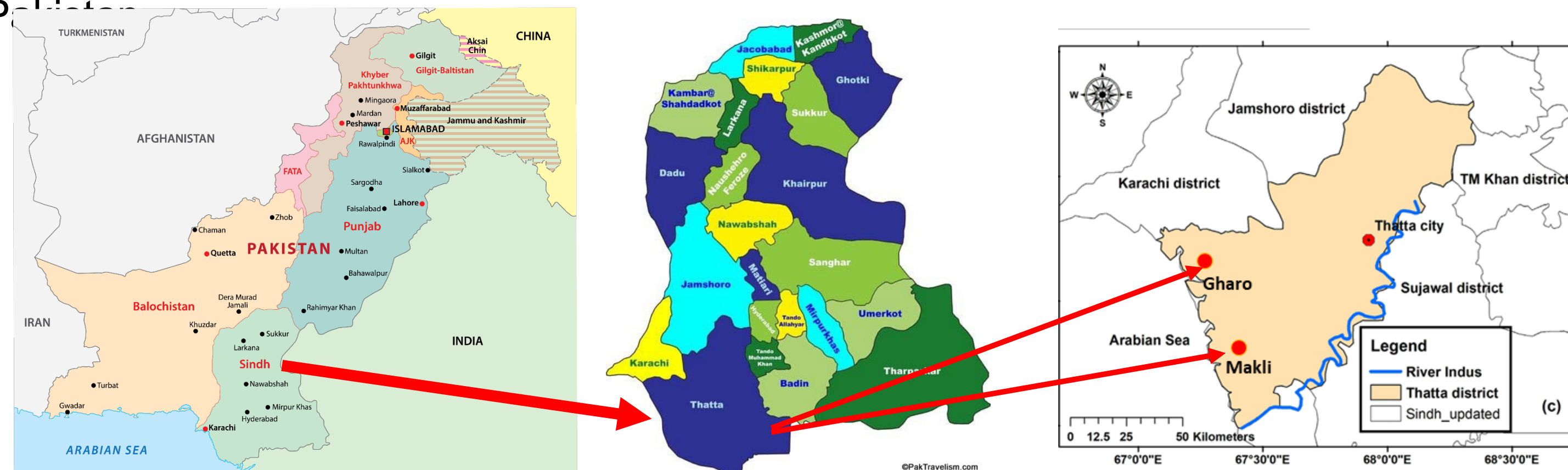
Objectives

- Determine the percentage of P. falciparum parasites lacking pfhrp2 or pfhrp3 genes in malaria patients.
- Determine the percentage of chloroquine, sulphadoxine-pyrimethamine, atovaquone - proguanil and artemisinin drug-resistance mutations in P. falciparum parasites.

Study Design & Methodology

Study Sites:

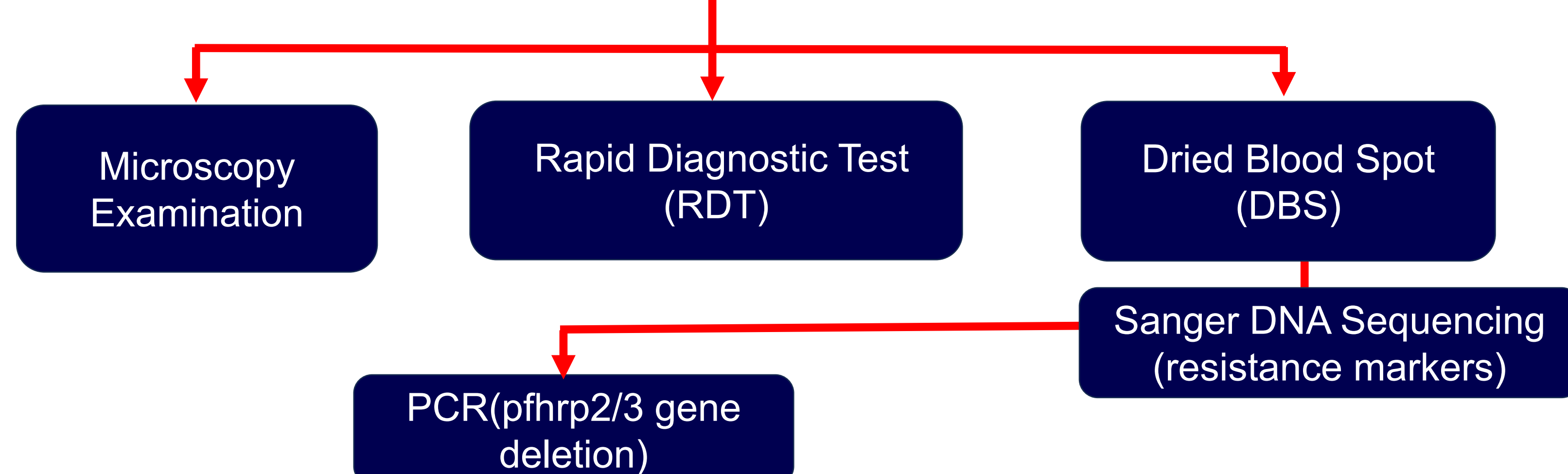
Malaria control program Basic Health Units (BHU) in Makli and Gharo, Sindh Province in Pakistan



Map of Sindh province, Pakistan, retrieved from worldatlas.com

Samples Collection and Testing

FINGER PRICK BLOOD SAMPLE (n= 343)



Results

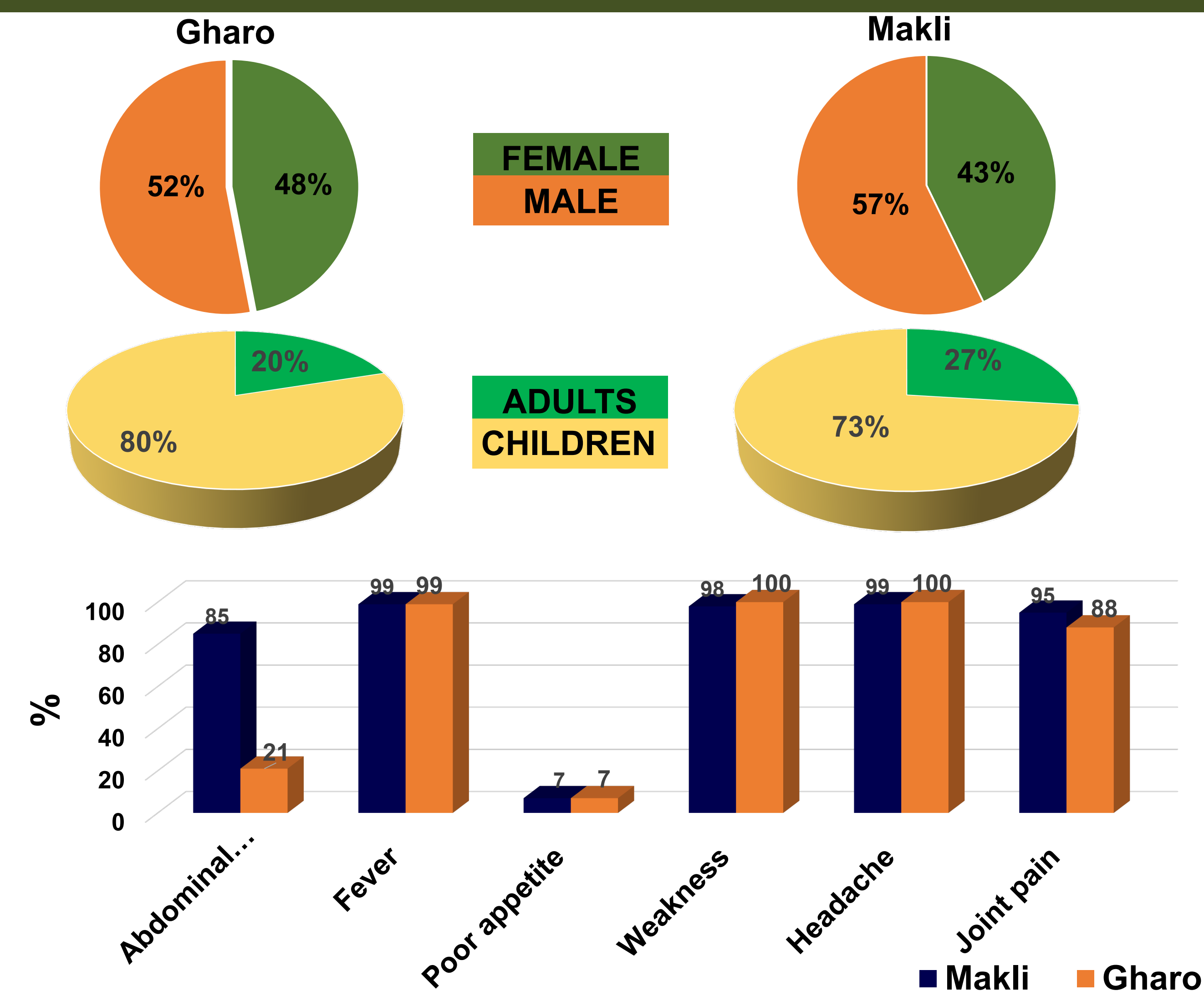
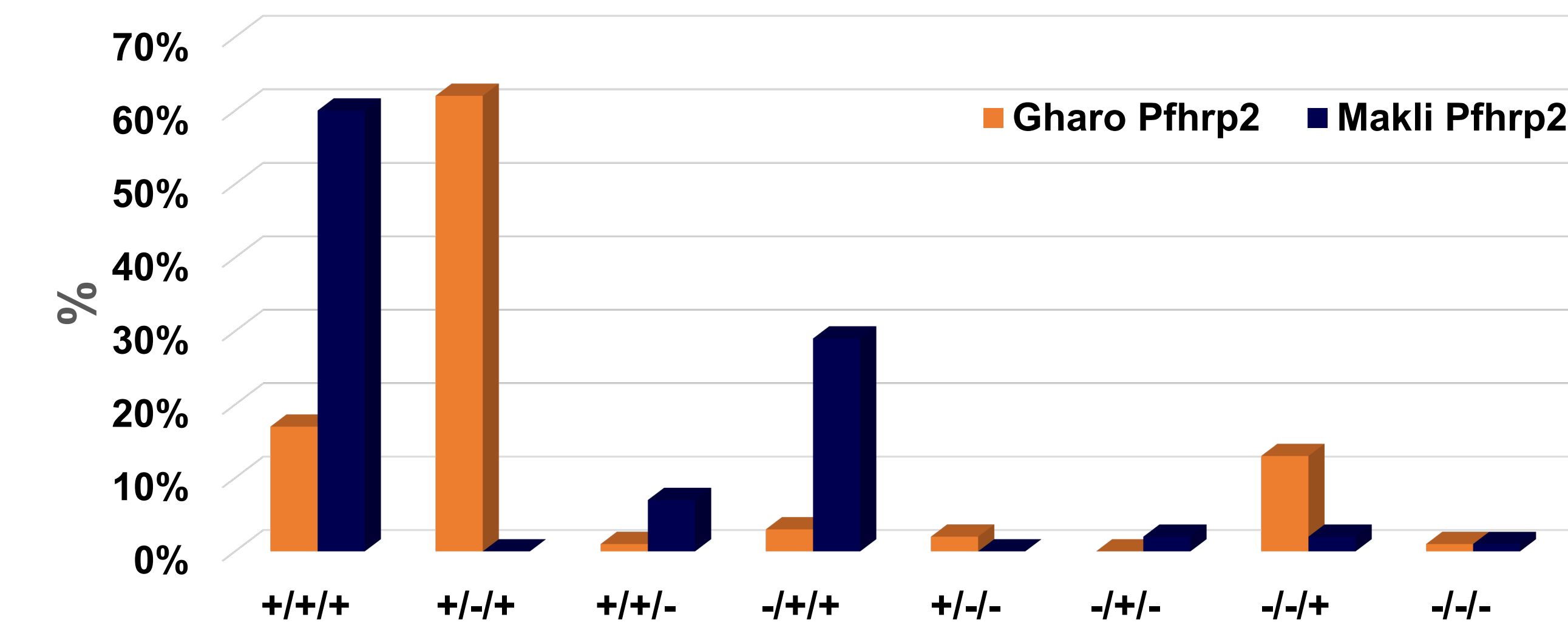


Figure 1: Demographic and clinical characteristics of enrollees from Makli and Gharo, Thatta District, Sindh Province, Pakistan



MAL7P1.230 (upstream)/ Pfhrp2 exon 1-2/ MAL7P1.228 (downstream)

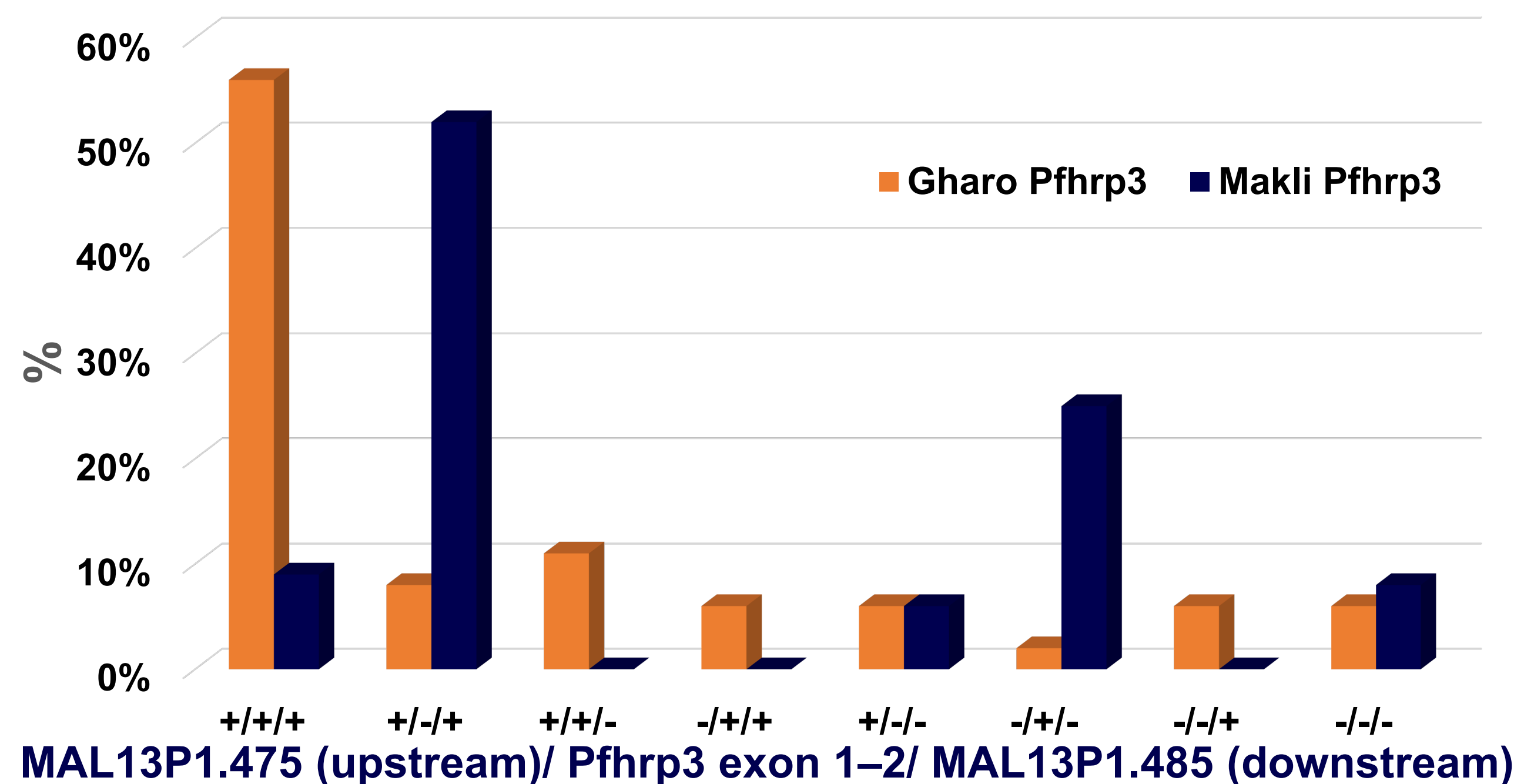


Figure 2: Deletion pattern of Pfhrp2/Pfhrp3 and their flanking genes in Gharo (n=160) and Makli (n=183)

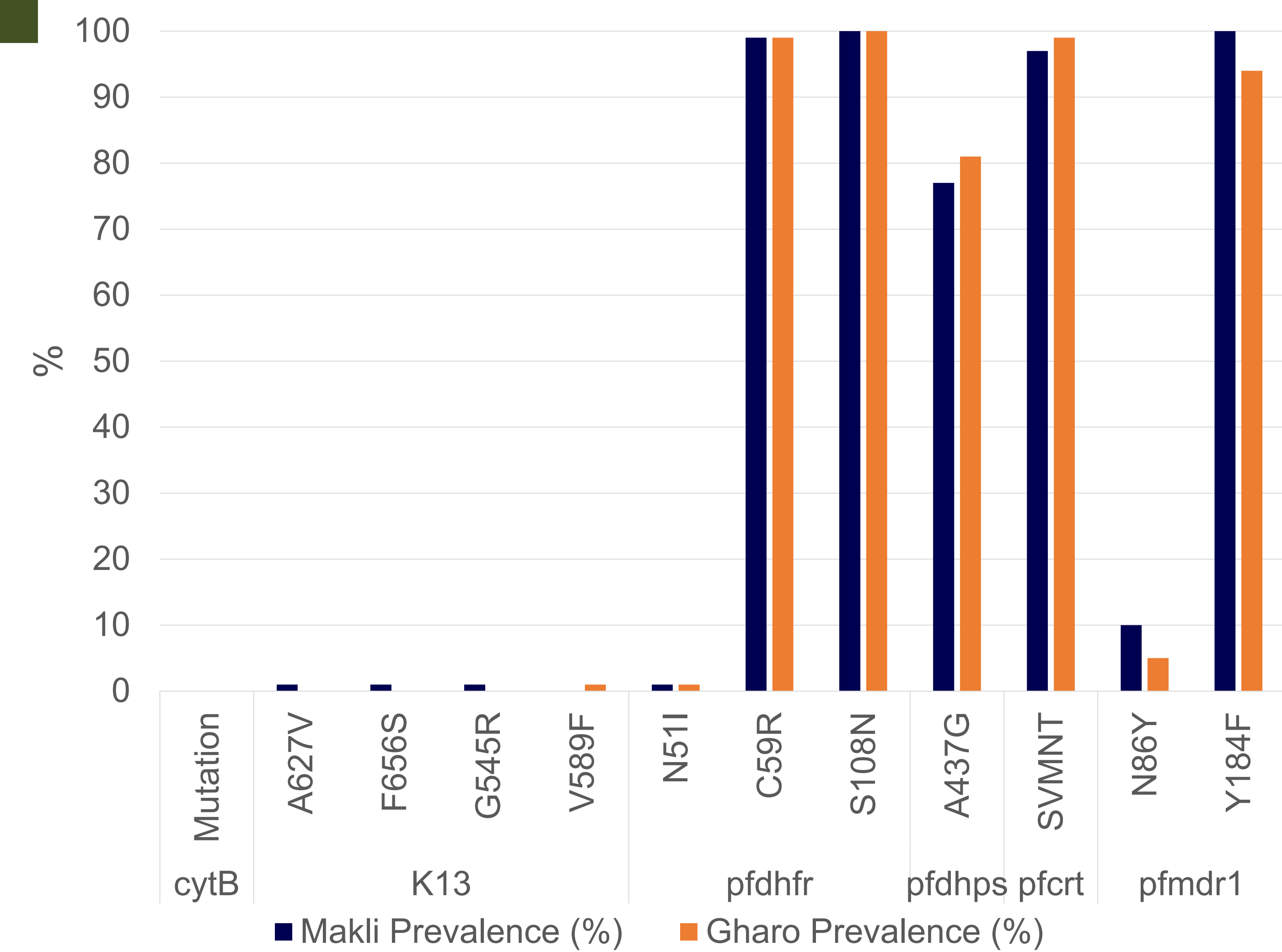


Figure 3: Mutations Prevalence Detected in Makli and Gharo.

Conclusions

- The observed prevalence of pfhrp2/pfhrp3 gene deletions exceeding 5% may warrant further evaluation of rapid diagnostic testing performance and could indicate a need to review national clinical testing protocols.
- Our analysis revealed significant levels of resistance to traditional therapies, chloroquine and sulfadoxine-pyrimethamine. Conversely, artemisinin and atovaquone appear to remain effective.
- The prevalence of these key resistance markers is remarkably similar between the Makli and Gharo, suggesting widespread and homogenous drug pressure in the region.
- Genetic variations observed within the pfmdr1 indicate sustained drug-induced selective pressure. Continuous molecular monitoring is essential to guide national malaria control strategies and secure the operational readiness of diagnostic and therapeutic interventions, especially in geographically strategic areas of U.S. military priority, such as Pakistan.

Partners/Collaborators



THE AGA KHAN UNIVERSITY