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Molecular surveillance of putative drug resistance markers of antifolate and artemisinin among imported *Plasmodium falciparum* in Qatar

Devendra Bansal^{a*}, Praveen K. Bharti^b, Anushree Acharya^a, Mohamed H Abdelraheem^c, Priyanka Patel^b, Ashraf Elmalik^d, Salem Abosalah^d, Fahmi Y. Khan^e, Mohamed ElKhalifa^f, Hargobinder Kaur^g, Elmoubasher Farag^h, Nilanju P Sarmahⁱ, Pradyumna K. Mohapatraⁱ, Rakesh Sehgal^g, Jagadish Mahantaⁱ and Ali A. Sultan^a

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ABSTRACT

Malaria remains a significant public health challenge and is of global importance. Imported malaria is a growing problem in non-endemic areas throughout the world and also in Qatar due to a massive influx of migrants from endemic countries. Antimalarial drug resistance is an important deterrent in our fight against malaria today. Molecular markers mirror intrinsic antimalarial drug resistance and their changes precede clinical resistance. Thus, in the present study, molecular markers of sulphadoxine-pyrimethamine (*Pf dhfr* and *Pf dhps*) and artemisinin (*Pf ATPase6* and *Pf k13*) were sequenced to determine the drug resistance genotypes among 118 imported *P. falciparum* isolates in Qatar, between 2013 and 2016. All the isolates had mutant *Pf dhfr* alleles, with either double mutant (51I/108N) (59.3%) or triple mutant (51I, 59R and 108N) (30.6%) genotypes. I164L substitution was not found in this study. In case of *Pf dhps*, majority of the samples were carriers of either single (S436A/ A437G/ K540E) mutant (47.2%) or double (S436A/K540E, A437G/K540E, K540E/A581G) mutant (39.8%). A single novel point mutation (431V) was observed in the samples originated from Nigeria and Ghana. Polymorphisms in *Pf ATPase6* were absent and only one non-synonymous mutation in *Pf k13* was found at codon G453A from a sample of Kenyan origin. High levels of sulphadoxine-pyrimethamine resistance in the present study provide potential information about the spread of antimalarial drug resistance and will be beneficial for the treatment of imported malaria cases in Qatar.

KEYWORDS



Imported malaria; molecular drug resistance; sulphadoxine-pyrimethamine; artemisinin combination therapy; Qatar

Introduction


More than a century ago after its discovery, and more than six decades of efforts to control it, malaria remains a serious health problem in most tropical and subtropical countries. The World Health Organization (WHO) estimates that 3.3 billion people are at risk of malaria infection, 219 million clinical cases and 435,000 deaths globally in 2017 [1]. Qatar has been free from local malaria transmission since 1970 [2], however, an influx of migrant workers from malaria-endemic countries, representing a major threat for re-introduction of local drug resistance malaria transmission [3–6]. In addition to the flow of imported cases, the receptivity and risk of malaria reintroduction are evident by the presence of the mosquito vectors, *Anopheles stephensi* and *An.*

multicolor [4,7,8]. This situation is similar to that in other countries of the Arabic Peninsula [9]. Currently, according to the national guidelines, artemisinin-based combination therapies (ACT) and artesunate/doxycycline or quinine/clindamycin is recommended for uncomplicated and complicated/severe *P. falciparum* malaria, respectively. However, chloroquine (CQ) followed by primaquine is the first-line regimen for the treatment of *P. vivax* malaria in Qatar. Moreover, mixed infections are usually treated as *P. falciparum* malaria.

Resistance to the antifolate sulphadoxine-pyrimethamine (SP) has been found to be associated with key point mutations in the dihydrofolate reductase (*dhfr*) and dihydropteroate synthase (*dhps*) genes. The level of resistance to SP has been shown to

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increase with the accumulation of mutations at codons 16, 51, 59, 108 and 164 as the *Pfdhfr* inhibit its activity, and the parasite becomes resistant to pyrimethamine. While mutations at codons 436, 437, 540, 580 and 613 of *Pfdhps* reduce the substrate binding capacity and confer resistance to sulphadoxine [10,11].

The exact mechanism of action of ACTs is still a matter of debate but, recent emergence of *P. falciparum* artemisinin (ART) resistance in southeast Asia threatens the global efforts to control malaria. Hitherto, several studies provide compelling evidence that ACTs act by selectively inhibiting sarcoplasmic/endoplasmic reticulum Ca^{++} -ATPase ortholog in *P. falciparum* (*PfATPase6*) protein, believed to be the primary target (at codon S769N) for ART, but is not yet fully confirmed [12–15]. In recent years, mutations in the propeller region of a kelch protein (K13) were associated with ART-resistant isolates [16,17], which was further confirmed by in vitro and ex vivo studies [18].

Monitoring drug resistance and pattern of mutations is essential for early detection and subsequent preventions of the spread of drug resistance. Hence, there is a need for monitoring antimalarial drug resistance in Qatar for prompt management of imported *P. falciparum* malaria, as majority of immigrant workers come from malaria-endemic countries, namely India, Pakistan and Sudan [3,4,6]. Therefore, the present study was conducted to determine the prevalence of point mutations involved in antimalarial resistance genes *Pfdhfr*, *Pfdhps* (SP) and *PfATPase6*, *K13* (ART) among imported *P. falciparum* isolates in Qatar. The study's findings will generate a new understanding of the disease as well as baseline information on antimalarial drug resistance among imported *P. falciparum* in Qatar.

Materials and methods

Study area, sample collection and ethical approval

The present study was carried out in Doha, Qatar, during January 2013–September 2016. Details of the study's population characteristics have previously been described [19]. The venous blood samples from 583 symptomatic patients attending the Hamad General Hospital (HMC), Doha, Qatar were collected in sterile vacutainer and screened for malaria parasites by microscopy, and species identification was confirmed by species-specific nested PCR [20]. Socio-demographics information including age, gender, nationality, treatment and clinica was collated using a structured questionnaire and from patient's medical records. The ethical clearance for patient's participants and sample collections was obtained from

Hamad Medical Corporation and Weill Cornell Medicine-Qatar Institutional Review Board (Protocol no. – 14–00097).

DNA extraction, nested PCR and sanger sequencing

The genomic DNA of *P. falciparum* was extracted using QIAamp DNA blood mini kit as per the manufacturer's instructions (Qiagen, CA, USA).

Alleles of the *Pfdhfr*, *Pfdhps* genes (for SP resistance) and *K-13* propeller, *PfATPase6* (for ART resistance) were determined using nested PCR followed by sanger sequencing, as previously described protocols with some minor modifications [21]. Primers for primary and nested PCR, and PCR cycling conditions are listed in the supplementary material [21]. The spanning codons 51–164 of *Pfdhfr* gene, codons 425–640 of *Pfdhps* gene codons 653–797 of *PfATPase6* and codon 427–702 of *K-13 propeller* were amplified by PCR. In brief, primary PCR was performed with 2 μL extracted genomic DNA (5ng/ μL), 12.5 μL of 2X Master mix (Applied Biosystems, CA, USA), 1 μM each primer and the mixture was made up to 25 μL volume with nuclease-free water (Ambion, CA, USA). The PCR products were purified using MinElute PCR Purification Kit according to the manufacturer's instructions (Qiagen, CA, USA). Purified products were sequenced using the Sanger method (Genewiz INC, NJ, USA) with respected-nested primers. Obtained DNA sequences were edited manually in BioEdit9 and aligned using ClustalW10. Multiple Sequence Alignment (MSA) was performed to see intraspecific variation if any, among the sequences. The presence or absence of mutations was assessed by comparing each sequence to the *P. falciparum* 3D7 reference strain for *dhps* (PF3D7_0810800), *dhfr* (PF3D7_0417200), *ATPase6* (PF3D7_0106300) and *andk13* (PF3D7_1343700). In order to determine the association between SNPs (present in *Pfdhfr* and *Pfdhps*) in the population, both inter and intragenic linkage disequilibrium (LD) tests were performed using the Haploview Software [22].

Statistical analysis

Statistical analyses were performed using IBM SPSS version 22.0 (Armonk, NY: IBM Corp). Frequencies of alleles and genotypes among parasite groups were compared using the χ^2 test. The *P* values <0.05 were considered statistically significant. Unadjusted odds ratios (ORs) of mutant alleles among different parasite origins along with their 95% confidence intervals (CI) were calculated using Univariate logistic regression model.

Results

A total of 583 patients were examined by microscopy followed by PCR for malaria between January 2013 and October 2016 in Hamad General Hospital and Al-Khor Hospital, 448 (76.8%) were found to be positive for malaria parasites. The majority were infected with *P. vivax* (n = 318 [71%]), followed by *P. falciparum* (n = 118 [26.3%]) and mixed *P. falciparum* and *P. vivax* (n = 12 [2.7%]) were less frequent.

The majority of malaria patients were male, with a mean age of 33 years (95% CI 30.0–35.0). The vast majority of *P. falciparum* cases originated from East Africa (60%, n = 71) followed by the Indian subcontinent (20.3%, n = 24), West and Central Africa (17.8%, n = 21) and less frequently from Oman or Yemen and Saudi Arabia (1.7%, n = 2) (Figure 1). The origin of the majority of patients of *P. vivax* was from the Indian-subcontinent (81.8%) followed by East Africa (10.7%) and different parts in Africa (6%).

Prevalence of *pfdhfr* alleles and genotypes

Out of 118 *P. falciparum* isolates, 108 (91.5%) were successfully amplified, sequenced and analyzed for *Pfdhfr* gene. All the isolates were mutant either single, double, triple and/or quadruple. Most of the sequenced isolates showed a mutation at codons N51I (89.8%), C59R (36.1%) and S108N (94.4%). However, no mutation was seen at codon I164L (Table 1). In addition, four novel mutations were detected at codons 185, 178, 183 and 181.

Out of 108 samples genotyped, a large proportion (59.3%) of the isolates carried the double mutants genotype, while the triple mutant genotypes were detected in 30.6% isolates. However, the prevalence of quadruple mutant genotypes was only 1.9% (Figure 2). The frequency of triple mutation was high in West and Central Africa, and quadruple mutation was found only in the East Africa isolates (Figure 2)

Table 1. Frequency (%) and number (n) of the *Pfdhfr* and *Pfdhps* mutations.

	Mutant alleles	n = 108 (%)
<i>Pfdhfr</i>	51I	97 (89.8)
	59R	39 (36.1)
	108N	102 (94.4)
	178S	1 (0.9)
	181N	1 (0.9)
	183H	3 (2.8)
	185A	1 (0.9)
<i>Pfdhps</i>	431V	6 (5.6)
	436A	11 (10.2)
	437G	57 (52.8)
	540E	71 (65.7)
	581G	29 (26.9)
	613S	1 (0.9)

Based on the geographical location, eight genotypes were detected (ACICSILYT, ACNCNILYT, ACICNILYT, ACNRNILYT, ACIRNILYT, ACICNISYT, ACIRNILYA and ACIRNILHT) in 67 East Africa isolates. A majority of the samples (65.7%) harbored the double mutants ACICNILYT followed by triple mutants ACIRNILYT (20.9%) and single mutant ACICSILYT (4.5%) genotype. While among the isolates from the Indian subcontinents, seven different genotypes (ACNCNILYT, ACICSILYT, ACNCNILYT, ACNRNILYT, ACICNILYT, ACNCNILHT and ACIRNILYT) were found. Of these, 30%, 25% and 5% harbored double mutant genotypes (ACNRNILYT, ACICNILYT and ACNCNILHT), respectively. The triple mutant genotype ACIRNILYT were detected in 20%. The single mutant genotypes (ACNCNILYT, ACICSILYT and ACNCNILYT) were carried by 10%, 5% and 5% isolates, respectively. However, in West and Central Africa, we observed only four genotypes (ACICSILYT, ACICNILYT, ACIRNILYT and ACICNILHT) and most of the isolates (62%) carried triple mutant (ACIRNILYT) followed by double mutant (ACICNILYT) (28.6%) genotypes (Table 2). Further analysis revealed that triple mutants were significantly higher in

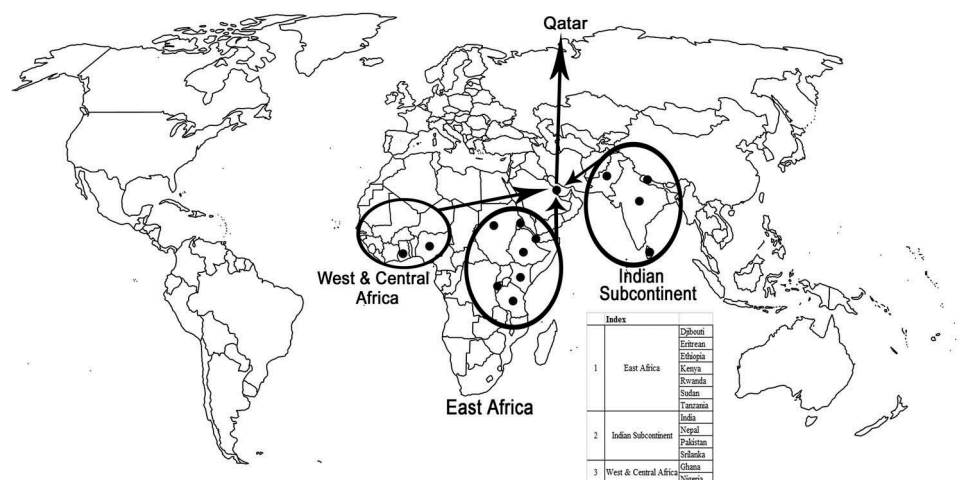


Figure 1. A map showing the countries of origin of the patients from whom *Plasmodium falciparum* samples were collected in Doha, Qatar.

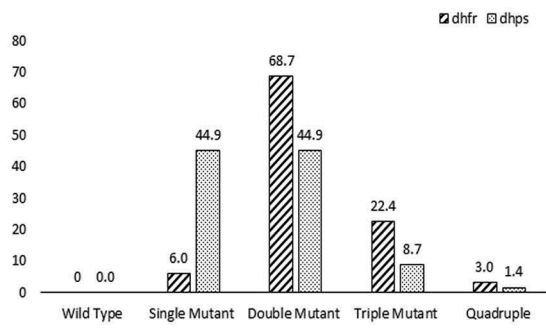


Figure 2A : Allelic Pattern in East Africa

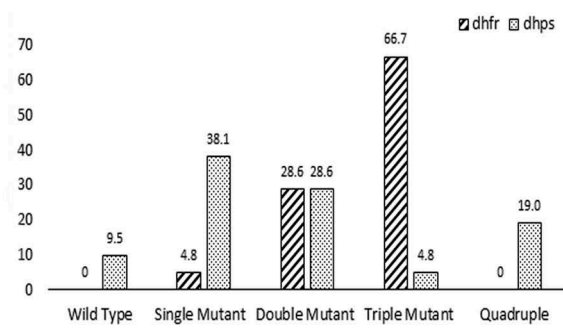


Figure 2B: Allelic Pattern in West & Central Africa

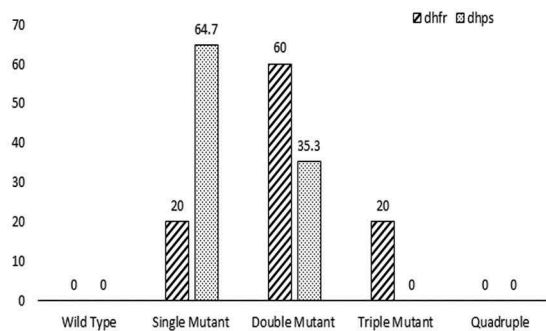


Figure 2C : Allelic Pattern in Indian Subcontinent

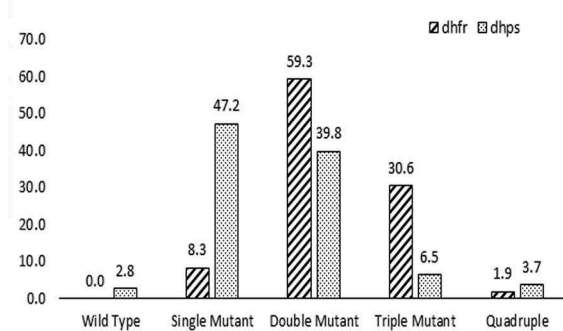


Figure 2D :Allelic Pattern In Overall

Figure 2. Mutation rates in *P. falciparum* genes (*Pfdhfr*, *Pfdhps*) that confer SP resistance from the isolates collected from East Africa, West and Central Africa and Indian subcontinent.

West and Central Africa as compared to East Africa and Indian subcontinents ($p=0.001$).

Table 2. The frequency distribution of genotypes for *Pfdhfr* and *Pfdhps* haplotypes among different nationalities.

Genotypes	<i>Pfdhfr</i>		
	East Africa n = 67 (%)	Indian subconti- nents n = 20 (%)	West and Central Africa n = 21 (%)
ACICSILYT	3 (4.5)	1 (5)	1 (4.7)
ACNCNILYT	1 (1.5)	2 (10)	0
ACICNILYT	44 (65.7)	5 (25)	6 (28.6)
ACNRNILYT	2 (3)	6 (30)	0
ACIRNILYT	14 (20.9)	4 (20)	13 (62)
ACICNISYT	1 (1.5)	0	0
ACIRNILYA	1 (1.5)	0	0
ACIRNILHT	1 (1.5)	0	0
ACNCSILYT	0	1 (5)	0
ACNCNILHT	0	1 (5)	0
ACICNILHT	0	0	1 (4.7)

Genotypes	<i>Pfdhps</i>		
	East Africa n = 69 (%)	Indian subcontinents n = 17 (%)	West and Central Africa n = 21 (%)
AAKAA	1 (1.4)	0	0
SGKAA	6 (8.7)	8 (47.1)	8 (38.1)
SAEAA	24 (34.8)	2 (11.8)	0
AAEAA	1 (1.4)	0	0
SGEAA	18 (26.1)	3 (17.6)	0
SGEGA	6 (8.7)	0	1 (4.8)
SAEGA	12 (17.4)	3 (17.6)	1 (4.8)
SAKGA	0	1 (5.9)	0
VAGKGA	0	0	3 (14.3)
VAGKGS	0	0	1 (4.8)
VAAKAA	0	0	2 (9.5)
AGKAA	0	0	2 (9.5)
AAKGA	0	0	1 (4.8)

Prevalence of *pfdhps* alleles and genotypes

Sequencing of the *Pfdhps* gene was successful for 108 (91.5%) isolates and overall 2.8% harbored wild type alleles only, while the single mutant (S436A/A437G/ K540E) allele was observed in 47.2%, double mutant (S436A/K540E, A437G/K540E, K540E/A581G) alleles in 39.8%, triple mutant (A437G/K540E/A581G) allele in 6.5%, quadruple in 2.8% and 0.9% had quintuple (431V/S436A/A437G/A581G/613S) mutant alleles (Figure 2). No triple or quadruple mutation was observed in the Indian subcontinent. A majority of quadruple mutant genotypes was observed from West and Central Africa origin. Furthermore, mutations at 540E, 437G and 581G were frequent, occurring at a prevalence of 65.7%, 52.8% and 26.9%, respectively. Moreover, we found a single novel point mutation (431V) in six (5.6%) isolates, of these five were from Nigeria and one from Ghana (Table 1). The mutation frequencies of the double mutant alleles (540E/581G) were detected in 14.8% isolates (437G/540E) in 19.4%, 1.8% for both (436A/437G) and (431V/436A) and only 0.9% for both (436A/540E) and (436A/581G). The triple mutant alleles (437G, 540E, 581G), quadruple mutant alleles (431V, 436A, 437G, 581G) and quintuple mutant alleles (431V, 436A, 437G, 581G, 613S) were detected in 6.5%, 2.8% and 0.9% of isolates, respectively. Interestingly, significant quadruple mutants were observed in West and Central Africa as

compared to East Africa and Indian subcontinents ($p=0.001$).

Furthermore, the sulphadoxine (wild type) *Pfdhps* genotype is **SAKAA** positioning 436, 437, 540, 581 and 613. In comparison to the wild type genotype (**SAKAA**), seven genotypes (**AAKAA**, **SGKAA**, **SAEAA**, **AAEAA**, **SGEAA**, **SGEGA** and **SAEGA**) were detected in 69 successfully sequenced samples from East Africa. The prevalence of **SAEAA** genotype was higher (34.8%) followed by **SGEAA** (26.1%), **SAEGA** (17.4%), **SGKAA** and **SGEGA** (8.7% of each) genotype. In the Indian subcontinents, of the 17 successfully sequenced isolates, five genotypes (**SGKAA**, **SAEAA**, **SAKGA**, **SGEAA** and **SAEGA**) were detected. Higher prevalence of single mutant **SGKAA** (47.1%) was noted followed by **SAEGA** and **SGEAA** (17.6% of each) and 11.8% **SAEAA** genotype. In the case of West and Central Africa, eight genotypes (**SGKAA**, **VAGKGA**, **VAGKGS**, **VAAKAA**, **AGKAA**, **AAKGA**, **SGEGA** and **SAEGA**) were detected in 21 successfully sequenced isolates. The single mutant genotype (**SGKAA**) was more prevalent and observed in 38.1% of the isolates, 14.3% had **VAGKGA**, 9.5% of each had **AGKAA** and **VAAKAA**. Additionally, only single mutant genotype (**SGKAA**) was observed in GCC isolate (Table 2).

Polymorphisms of *pfatpase6* and *pfk13* genes

A total of 113 and 110 *P. falciparum* samples were successfully genotyped for *PfATPase6* and propeller region of *Pfk13* genes, respectively. All isolates carried the wild type *PfATPase6* gene. Furthermore, in *Pfk13*, the frequency of mutations associated with ART resistance reported in Southeast Asia was not observed. However, only one non-synonymous mutation at codon G453A was identified in isolate imported from a sample of Kenyan origin.

The Pair-wise LD estimation to assess the selection of *P. falciparum* resistant markers revealed a total of 37 possible pairs of SNPs with fine statistically significance intragenic and intragenic associations were found between different geographic regions from a possible 154 points (Figure 3).

Discussion

Globally, emergence and spread of antimalarial drug resistance of *P. falciparum* malaria is an important deterrent in our fight against malaria. Recent reports of tolerance/resistance to artemisinin derivatives and spread of drug-resistant strains is a major concern, in particular, the long-term effectiveness of artemisinin-combination therapy (ACT) in Southeast Asia, Indian subcontinents and Africa [23]. Antimalarial drug resistance data is not available in Qatar and it has been well established that human migration can interact

with natural features to establish drug resistance in new areas. Thus, there is a need to monitor antimalarial drug resistance in the migrant population and also in native Qatari visiting endemic regions to stall the potential spread of this deadly infection in Qatar. Recently, we determined the current extent of chloroquine resistance among imported *P. falciparum* malaria and found a high prevalence of CQ resistance patterns [19]. In the present study, the genetic polymorphism in the antimalarial drugs resistance genes (*Pfdhfr*, *Pfdhps*, *PfATPase6* and *Pfk13*) was investigated among imported *P. falciparum* isolates in Qatar.

Resistance to SP was first reported from the Thai-Cambodian border in the 1960s [24] and has spread to several parts of Southeast Asia, South America and Africa [25–27]. Resistance is likely to progress geographically and in intensity at a rising rate, becoming fixed in the population if proper and timely measures are not taken to interrupt it.

In this study, all the isolates were found mutated and had at least one of 51I, 59R and 108N of *Pfdhfr* alleles, while no mutation was seen at codon 164L. Overall, the double mutant genotype (51I/108N) and triple mutant genotype (51I, 59R, 108N) were found to be more prevalent among the imported cases, which are in agreement with well-established SP resistance found in Africa and Southeast Asia [28,29]. Moreover, the double mutant genotype (51I/108N) was predominant from East African isolates than other areas because the majority of the isolates were from Sudan origin. The double mutation was prevalent in Sudan in 2007 [30] and still maintains the double mutant genotype with an emerging triple mutation [31]. Triple mutants (51I, 59R, 108N), which associated with high-level pyrimethamine resistance [10,11], were almost fixed in the African population [32,33]. High level of triple mutant genotypes was also found in the present study among isolates originates from Nigeria and Cameroon, which is in agreement with other studies [32,33]. Among the Indian sub-continent isolates, the double (59R/108N and 51I/108N) mutants genotypes were the most frequent genotypes followed by triple (51I/59R/108N) mutant genotypes, which are in agreement with previous reports from India [21,27,34–36].

Sulphadoxine resistance is mediated by a single point mutation at codon 437G of the *Pfdhps* gene. Higher levels of sulphadoxine resistance are associated with double mutation at codons 437G/581G and triple mutations at codons 436A/437G/613S [37]. In the present study, 52.8% isolates had the key mutation at codon 437G, whereas none of the isolates has key mutations at both double (437G/581G) and triple mutations [436A/437G/613S]. Approximately, 90% isolates from East African origin had double mutation whereas quadruple mutation arose in 19% isolates (Nigerian origin) where triple and quadruple mutations are

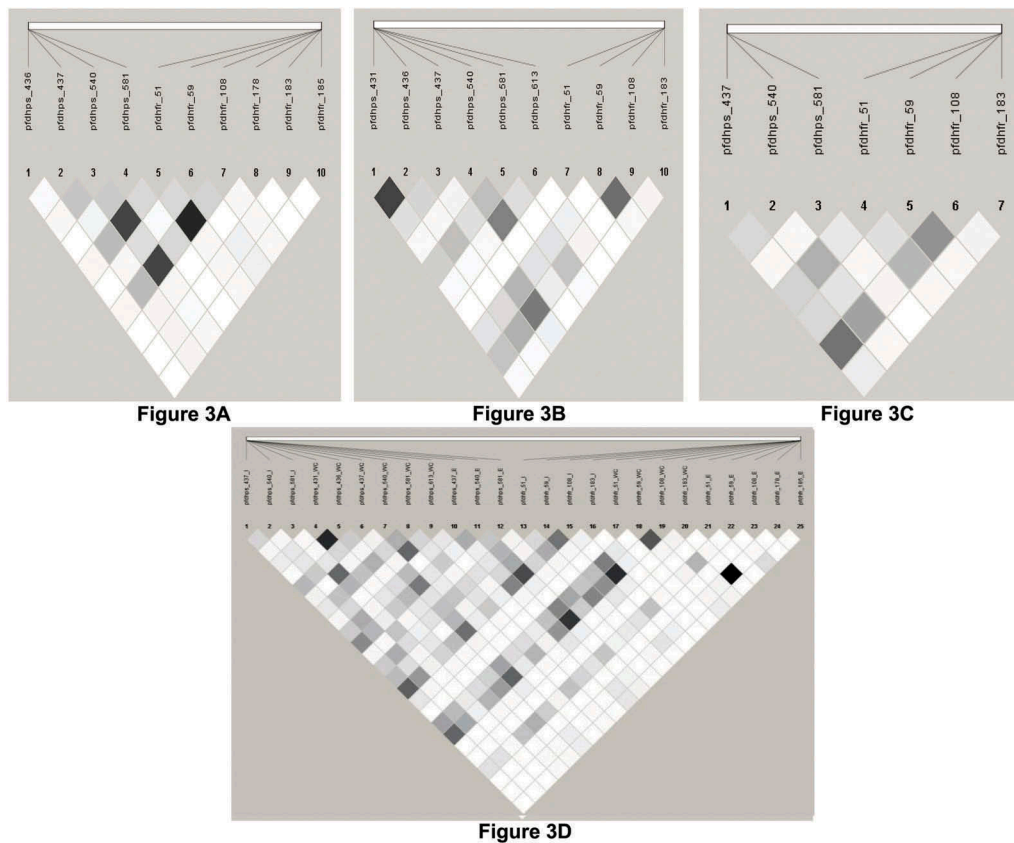


Figure 3. Linkage disequilibrium (LD) between pairs of SNPs located in *Pfdhfr*, *Pfdhps* genes implicated in SP drug resistance in imported *P. falciparum* cases in Qatar. The intra and inter-genic association between genes for the isolates collected from East Africa, West and Central Africa and Indian subcontinent were determined using the LD plot. The strength of LD between the SNPs was determined from the association of statistical significance by calculating the r^2 values and represented by the darkness of the boxes.

commonly prevalent [33]. Single point mutation at codon 437G was higher in Indian subcontinent isolates followed by West & Central Africa and East Africa. These findings corroborate with earlier reports from India [21,34,35]. Additionally, we found a novel mutation at codon 431V in five isolates imported from Nigeria and one isolate imported from Ghana, which corroborates with previous findings of imported malaria infections in the UK, which also originated from Nigeria [38] and also pregnant women from Cameroon [39], suggesting that this mutation is emerging especially in West Africa. Recently, mutation at 431V in combination with 436A, 437G, 581G and 613S was found to be the most common in a Nigerian cohort [40].

The presence of key mutations in *Pfdhfr* and *Pfdhps* genes along with the emergence of new mutations and quadruple mutations at *dhfr* locus and quadruple/quintuple mutations in *dhps* locus are important findings which might be the cause for multidrug resistance of antifolate drugs. The emergence of these novel mutations might have enhanced the level of antifolate resistance to *P. falciparum* hence it should be taken into consideration when using the combination of antifolate drugs with artemisinin derivatives nationwide and

also where the double mutant genotype of *Pfdhfr* (ACICNITYT) is common [21,41,42].

The artemisinin-combination therapy (ACT) is recommended by the WHO as the first-line treatment for *P. falciparum* infections in all endemic regions [1] and also in non-endemic countries like Qatar [4]. In spite of these efforts, there have been sporadic reports of an in-vivo and an in-vitro artemisinin resistance during the last few years [43–45]. However, the mechanism of artemisinin resistance is still under investigation. Subsequently, ACT resistance is considered a major risk to public health in Southeast Asia and Sub-Saharan Africa, where the burden is serious. The mutations of *Pfk13*-propeller are well established in Southeast Asia, whereas only limited polymorphisms of *Pfk13*-propeller are detected in Africa [16,46]. Recently, in China, polymorphism in *Pfk13* was reported in returned migrant workers from Africa [47]. Thus, there is now a clear need to acquire a greater understanding of *Plasmodium* parasites' genotypic resistance surveillance with *k13*-propeller polymorphism. In the present study, *k13* propeller sequence analysis of *P. falciparum* parasites from different malaria-endemic areas in East Africa, Indian

sub-continent and West & Central Africa did not detect the predicted artemisinin-resistant genotypes, but we observed only one non-synonymous mutation at codon G453A in a Kenyan isolate. Although anti-malarial drug resistance originates from the greater Mekong sub-

region and subsequently spread worldwide, still we do not have any functional mutation from sub-Saharan Africa [48–50]. No mutations in *PfATPase6* were found in the current study, which is in agreement with previous reports from India and Africa, where *PfATPase6* polymorphisms rarely reported [51–55]. Another marker *Pfmdr1* is also considered as quinine, mefloquine, lumefantrine and ACT resistant markers [56] and recently we have reported only 28% mutant or mixed genotype at N86 codon using the same samples [19].

Although the molecular findings were not further matched with treatment outcome and in-vitro drug sensitivity of the falciparum isolates, which does not allow us to make a correct evaluation about the level of sensitivity of *P. falciparum* isolates, including the possible role of the novel *Pfdhps*, *Pfdhfr* genotypes because of the limitations of the present study. But at the same time, many studies have proved that the quadruple *Pfdhfr/Pfdhps* combined haplotype (59R + 108N/437G + 540E) are directly associated with either adequate clinical and parasitological response, early treatment failures or late parasitological failures to SP [11,35,57]. Similarly, the reduced efficacy of artemisinin associated with the presence of the functional mutation in the *K-13* gene [44,45].

In conclusion, the present study shows a high prevalence of resistance patterns of SP drugs to *P. falciparum* in imported cases of malaria, which might be helpful for the enrichment of molecular surveillance of antimalarial resistance. In addition, the emergence of new mutations in *Pfdhfr* and *Pfdhps* genes requires further study to monitor the changes in the frequency of mutation. In addition, the current findings also raise a concern about the potential effectiveness of the current first line of drug, i.e. ACT. Hence, the baseline data on antimalarial drug resistance will help policymakers in updating national antimalarial guidelines for the treatment of imported malaria cases in Qatar.

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Availability of data and materials

Yes - all data are fully available without restriction and from the corresponding author on reasonable request.

Disclosure statement

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