Antimalarial drug resistance markers and treatment outcome in travellers: a retrospective cohort study in Sweden

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Background: In response to emerging antimalarial resistance in Africa, this study aimed to investigate the presence and temporal trends of pfKelch13 mutations and pfmdr1-duplications among P. falciparum infections in imported malaria cases in Sweden, and to evaluate effects on early and late treatment failures since the introduction of artemether-lumefantrine.

Materials and methods: Targeted PCR and Sanger sequencing were used to detect pfKelch13 mutations and pfmdr1-duplications in archived samples from acute P. falciparum malaria cases in Stockholm 1997–2025 (n = 341). Clinical and demographic data were extracted from medical records. Detailed data on malaria diagnostics, including exact sampling times and microcopy parasite counts, were available for episodes after 2009 (n = 188) and were used to model clearance rates and detect artemether-lumefantrine treatment failures.

Results: In total, 19 treatment failures, 11 early failures and 8 recrudescences were observed among the 188 patients with genotyping data from 2009 to 2025. PfKelch13 mutations were present in 2/11 early failures, and pfmdr1-duplications in 1/8 recrudescences. Among all successfully analyzed samples, pfKelch13 mutations were found in 2.9% (8/278), and pfmdr1-duplications in 2.9% (9/313). All cases of pfKelch13 mutations were from Africa, and validated ART-R markers were detected in samples from 2020 to 2025. The median time to parasite clearance increased from 2009 to 2025.

Conclusion: Mutations previously linked to reduced artemisinin and lumefantrine efficacy were detected among imported malaria cases and signs of association with increased treatment failures were observed. Continued surveillance of antimalarial drug resistance markers and treatment failures is needed.