Oxamniquine resistance alleles are widespread in Old World *Schistosoma mansoni* and predate drug deployment

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Short title: Standing variation for oxamniquine resistance in schistosomes

ABSTRACT

Do mutations required for adaptation occur *de novo*, or are they segregating within populations as standing genetic variation? This question is key to understanding adaptive change in nature, and has important practical consequences for the evolution of drug resistance. We provide evidence that alleles conferring resistance to oxamniquine (OXA), an antischistosomal drug, are widespread in natural parasite populations under minimal drug pressure and predate OXA deployment. OXA has been used since the 1970s to treat *Schistosoma mansoni* infections in the New World where *S. mansoni* established during the slave trade. Recessive loss-of-function mutations within a parasite sulfotransferase (SmSULT-OR) underlie resistance, and several verified resistance mutations, including a deletion (p.E142del), have been identified in the New World. Here we investigate sequence variation in *SmSULT-OR* in *S. mansoni* from the Old World, where OXA has seen minimal usage. We sequenced exomes of 204 *S. mansoni* parasites from West Africa, East Africa and the Middle East, and scored variants in *SmSULT-OR* and flanking regions. We identified 39 non-synonymous SNPs, 4 deletions, 1 duplication and 1 premature stop codon in the *SmSULT-OR* coding sequence, including one confirmed resistance deletion (p.E142del). We expressed recombinant proteins and used an *in vitro* OXA activation assay to functionally validate the OXA-resistance phenotype for four predicted OXA-resistance mutations. Three aspects of the data are of particular interest: (i) segregating OXA-resistance alleles are widespread in Old World populations (4.29 – 14.91% frequency), despite minimal OXA usage, (ii) two OXA-resistance mutations (p.W120R, p.N171IfsX28) are particularly common (>5%) in East African and Middle-Eastern populations, (iii) the p.E142del allele has identical flanking SNPs in both West Africa and Puerto Rico, suggesting that parasites bearing this allele colonized the New World during the slave trade and therefore predate OXA deployment. We conclude that standing variation for OXA resistance is widespread in *S. mansoni*.

AUTHOR SUMMARY

It has been argued that drug resistance is unlikely to spread rapidly in helminth parasites infecting humans. This is based, at least in part, on the premise that resistance mutations are rare or absent within populations prior to treatment, and take a long time to reach appreciable frequencies because helminth parasite generation time is long. This argument is critically dependent on the starting frequency of resistance alleles – if high levels of "standing variation" for resistance are present prior to deployment of treatment, resistance may spread rapidly. We examined frequencies of oxamniquine resistance alleles present in *Schistosoma mansoni* from Africa and the Middle East where oxamniquine has seen minimal use. We found that oxamniquine resistance alleles are widespread in the Old World, ranging from 4.29% in the Middle East to 14.91% in East African parasite populations. Furthermore, we show that resistance alleles from West African and the Caribbean schistosomes share a common origin, suggesting that these alleles travelled to the New World with *S. mansoni* during the transatlantic slave trade. Together, these results demonstrate extensive standing variation for oxamniquine resistance. Our results have important implications for both drug treatment policies and drug development efforts, and demonstrate the power of molecular surveillance approaches for guiding helminth control.

INTRODUCTION

The rate at which drug resistance alleles (or any other beneficial alleles) spread within populations in response to a drug treatment (or any other selection pressure) is critically dependent on the starting frequency of resistance alleles in the population when new drugs are deployed (1,2). If no such alleles are present when a novel drug is introduced, then there is a waiting time for resistance alleles to arise. Furthermore, because the starting allele frequency will be $1/(2N_e)$, where N_e is the effective population size, the vast majority of resistance alleles that arise will be lost due to genetic drift and fail to establish (2,3) (Fig. 1). The barrier to establishment is particularly severe for recessive traits because these will be present in heterozygotes at low frequency and therefore not exposed to selection. This effect, otherwise known as "Haldanes's sieve" (4), may be particularly relevant for drug resistance evolution in diploid pathogens, because resistance mutations in drug targets typically result in phenotypic resistance only when two copies are present. However, if resistance alleles are already segregating as standing variation in pathogen populations when drug treatment is initiated, then there is no waiting time for mutations to arise. Furthermore, there is a high probability of fixation and spread is rapid because many resistance alleles are present in homozygous recessive genotypes and therefore exposed to selection. Hence, whether resistance alleles (or alleles for other traits) arise *de novo* or are segregating as standing variation, is a central question in evolutionary biology and public health, and key to predicting the effective "shelf life" of new drug treatments (3,5).

There is growing evidence for resistance to anti-helminthics in several helminths infecting humans, including *Onchocerca volvulus* (6), the filarial nematode causing river blindness, and in soil transmitted helminths (hookworm, whipworm and *Ascaris* roundworms) (7) which cumulatively infect over one billion people worldwide (8). However, perhaps the best understood is oxamniquine resistance in schistosome blood flukes, for which the mechanism of drug action and the genetic and molecular basis for drug resistance are now known. Oxamniquine (OXA) kills *Schistosoma mansoni*, but is ineffective against two other major schistosome species infecting humans (*S. haematobium* and *S. japonicum*) (9). OXA is a pro-drug that is activated by a schistosome sulfotransferase (SmSULT-OR) encoded on chromosome

6 (10). Loss-of-function mutations within SmSULT-OR result in resistance: only parasites that are homozygous for resistance alleles are phenotypically resistant (OXA-R). We initially identified the locus and mutation, a single amino acid deletion (p.E142del), underlying OXA-R using a genetic cross involving a resistant parasite line selected from a parasite isolate from a Puerto Rican patient in 1971 (11). Additionally we identified a second mutation (p.C35R) in *S. mansoni* obtained from an incurable Brazilian patient (12). These two mutations result in disruption of the active site of the SmSULT-OR and inability to activate OXA (10). Both p.E142del and p.C35R, and two additional mutations resulting in truncated proteins, were subsequently identified in a field survey of SmSULT-OR genetic variation of parasites from a single Brazilian village (13). The combined allele frequency of these four resistant alleles was 1.85%.

OXA was widely used in the New World, where only *S. mansoni* is present, during the 1970s to early 2000's (14), so the OXA-R alleles we observed in Brazil (13) could conceivably have resulted from drug selection. In contrast, OXA saw minimal usage in Africa where both *S. haematobium* and *S. mansoni* are present. In South America, an estimated 6 million doses of OXA were used to treat the 7 million people infected with *S. mansoni* prior to 1987 (15). In contrast, 3 million doses had been used in Africa (Egypt, Ethiopia, Ivory Coast, Kenya, Malagasy, Malawi, Rwanda-Burundi, South Africa, Sudan, Tanzania, Uganda, Zambia, Zaire) and the Middle East (Arabian penensula) (15), where an estimated ~60 million people were infected with *S. mansoni* (16). Hence, OXA selection was minimal in Africa compared with South America. The central aim of this paper is to determine whether *de novo* mutation or standing variation best explains OXA-R in *S. mansoni* populations. To do this we examined *SmSULT-OR* genetic variation in Old World parasite populations where OXA treatment has been minimal.

RESULTS

1. Samples

We sequenced exomes from 92 miracidia from Tanzania (n=57), Niger (n=10), and Senegal (n=25) from the SCAN collection at the Natural History Museum (17), with each miracidium derived from a different patient. In addition, we included 112 samples collected from Oman: these included 86 single worms and 26 pools of cercariae from single infected snails. The Omani samples were derived from 11 human infections, 2 naturally infected rodents, and 26 naturally infected snails (Table 1). We obtained an average of 15.7 ± 8 (mean ± standard deviation, s.d.) million reads per library (supp. table 1). A very high proportion of these reads were mapped to the reference genome (91.9 ± 6.29 (s.d.) % on average). We captured on average 99.08 ± 3.92 (s.d.) % of the bait regions. We obtained an average read depth of 64.40 ± 32.27 (s.d.) in the bait regions. For *SmSULT-OR*, we obtained sequence across 95.06 ± 6.54 (s.d.) % of the coding sequence with an average read depth of 43.09 ± 26.96 (s.d.).

We compared these Old World parasite samples with: (i) the OXA-R parasite from Puerto Rico (HR) carrying the causative p.E142del mutation identified previously (10), for which whole genome sequence is available, and (ii) published *SmSULT-OR* sequences from a single Brazilian location (n=189) (13) (Table 1).

2. New and known mutations identified in the *SmSULT-OR* gene

We identified a total of 85 *SmSULT-OR* mutations across all three populations (West Africa, East Africa and Middle East), including 76 coding mutations and 9 non-coding mutations (supp. table 2). Exon 1 carried 24 mutations. These included 13 non-synonymous single nucleotide polymorphisms (SNPs), 8 synonymous SNPs, one duplication, one deletion, and one premature stop codon. Exon 2 carried 52 mutations: 26 non-synonymous SNPs, 23 synonymous and three deletions. There were no differences in the density of mutations in the two exons (Fisher's exact test, d.f.=1, p=0.09). The overall transition/transversion ratio was 1.94. Forty-three percent (37/85 mutations) showed an average allele frequency greater than 5%.

Among the 85 mutations, we have previously found three coding and one non-coding mutations in the New World (Caribbean and Brazil): the substitution p.P67L (g.200C>T), the deletion p.E142del (g.4348_4350delGAA), the substitution p.L256W (g.4691T>G) and the 3' untranslated region (UTR) substitution g.4720C>T (10,13). Just one of these mutations (p.E142del) encodes a confirmed OXA-R allele. Frequencies of all mutations in each population are shown in supp. table 2.

We measured nucleotide diversity (π) in both New and Old World populations. Nucleotide diversity was the highest in Oman ($\pi = 0.02424 \pm 2.4 \times 10^{-4}$) followed by East Africa ($\pi = 0.00195 \pm 2 \times 10^{-4}$), West Africa ($\pi = 0.00126 \pm 1.7 \times 10^{-4}$) and Brazil ($\pi = 0.00021 \pm 0.3 \times 10^{-4}$). If drug pressure drives the changes at *SmSULT-OR*, we might expect to see signals of positive selection. We examined sequence conservation by measuring proportions of non-synonymous difference per non-synonymous site relative to synonymous changes per synonymous site (K_a/K_s) between *S. mansoni* and a *S. rodhaini* outgroup. K_a/K_s ranged from 0.20 – 0.24 suggesting that changes at non-synonymous sites are 4-5 times less abundant than at synonymous sites, consistent with weak purifying selection. Similarly, the ratio of non-synonymous polymorphisms per non-synonymous site relative to synonymous polymorphisms per synonymous site (pN/pS) ranged from 0.111 to 1.36 and none of these values were significantly greater than unity (Table 2). These tests did not provide evidence that *SmSULT-OR* is under positive selection.

3. *In vitro* tests and *in silico* evaluation of impact of mutations

We used three approaches to identify *SmSULT-OR* mutations that are likely to result in OXA-R.

a. Visual assessment

Some mutations have obvious deleterious effect on the protein by introducing premature stop codons. This is the case for three mutations identified in *SmSULT-OR*. These mutations will generate truncated proteins that do not contain the active site. Other mutations, such as p.L179P, p.P225S or p.W120R, were either close enough to the OXA or the 3'-phosphoadenosine-5'-phosphosulfate (PAPS) binding sites or showed potential steric hindrance

or structural deformation likely to have an effect on protein activity. Other mutations, such as p.A74T, p.P106S or p.Q176R, were on the surface of the protein, distant to any active site, and therefore unlikely to have an impact.

b. Functional assay of OXA binding

We used an *in vitro* OXA activation assay to functionally assay the impact of mutations on SmSULT-OR activity for four newly discovered mutations and the two known OXA-R mutations (Fig. 3). The known resistant mutations, p.C35R and p.E142del, showed from zero to very low level of OXA activation, as expected (10). p.L179P showed a similarly low level of activation. The mutations p.S160L and p.P225S showed intermediate OXA activation: we conservatively classed these as OXA sensitive alleles. p.P106S showed similar activity to the wild type and p.S160L. We were able to produce recombinant protein p.W120R but all our attempts to fold this protein were unsuccessful. This mutation clearly has a dramatic impact on protein stability as predicted by visual inspection and thermodynamic modelling results (below). We considered this mutation to be OXA-R.

c. Thermodynamic modelling

We used thermodynamic modelling to evaluate the potential impact of substitutions on protein stability (indels such as p.E142del cannot be modelled). The difference in free enthalpy ($\Delta\Delta G$) ranged from -2.942 to 19.826 for the 37 mutations (Fig. 4). Among those, p.L179P and p.C35R which have the greatest impact on OXA activation (Fig. 3) showed the second and third highest $\Delta\Delta G$, respectively. p.W120R, for which we were unable to fold recombinant protein, showed the highest $\Delta\Delta G$, consistent with a dramatic impact on stability. p.S160L and p.P225S showed intermediate $\Delta\Delta G$ consistent with the results of the OXA activation assay.

In total, we identified 7 independent OXA-R mutations in Old and New World parasite populations examined using these three approaches (Table 3, Fig. 2). These included 3 indels and 4 amino acid mutations.

4. Frequency of OXA-R alleles

Having determined which of the mutations identified are likely to cause OXA-R, we measured the frequency of resistant variants and the frequency of resistant parasites in each population (Table 3, Fig. 5). To accurately identify resistant alleles and parasites, we phased our variant calling data on the first 3 Mb of the chromosome 6 (corresponding to 30,812 variable sites). West African samples carried only two resistant variants (p.S12X and p.E142del). East African samples carried five resistant variants, two of them at a frequency over 0.05 (p.W120R and p.N171IfsX28). The p.W120R mutation was also found at high frequency in Middle East (0.065). We found the highest frequency of OXA-R alleles in East Africa (14.91%, 17/114), followed by the Middle East (6.25%, 14/224), West Africa (4.29%, 3/70), and Brazil (1.85%, 7/378).

Most parasites carried OXA-R alleles in the heterozygous state and are predicted to be OXA sensitive. Heterozygous OXA-sensitive parasites were found in West and East Africa (8.6% and 24.6%, respectively), Middle East (13.4%) and in Brazil (1.06%). Parasites that are homozygous for OXA-R alleles at *SmSULT-OR* (but not necessarily carrying the same resistant variant) are OXA-R. We found homozygous parasites predicted to be phenotypically OXA-R at a frequency of 5.26% (3/57) in East Africa and 1.06% (2/189) in South America only (Fig. 5).

5. Haplotype analysis of *SmSULT-OR* and flanking regions

We used our phased data to investigate the haplotypes surrounding our resistant variant (p.E142del) in the Old and New World (Caribbean) (Table 1) and to investigate whether these resistant alleles derived from a common ancestor. This is of interest because it would suggest that these alleles predate the slave trade. We identified an identical 102.5 kb haplotype block around p.E142del shared between the Caribbean sample and one of the West African samples from Niger (Fig. 6A). This haplotype block contained 399 SNPs that varied in at least one of the 205 parasites examined (all samples except those from Brazil where haplotype data were not available). We used a minimum spanning network to investigate haplotype relationships using the 399 bi-allelic variants found in this 102.5 kb block across all phased haplotypes (Fig. 6B). The haplotypes associated with the p.E142del OXA-R alleles found in both Puerto Rico and Niger

clustered together, consistent with a common origin for West African and Caribbean p.E142del OXA-R mutations.

The p.E142del mutation was also identified in Brazil (13) but we sequenced the *SmSULT-OR* exons only, rather than complete exomes, for these Brazilian samples preventing reconstruction of extended haplotypes. This Brazilian p.E142del was also found associated with two mutations (p.P67L and g.4720C>T) found in West Africa but without the p.L256W found in samples from the Caribbean and Niger. Similarly, the p.E142del was also found in a Tanzanian sample but this sample has a distinct haplotype from those found in West Africa (Fig. 6). These results suggest either that there are several independent origins of East and West African p.E142del mutations, or alternatively, that the p.E142del is extremely old and has distinctive flanking haplotypes resulting from recombination and mutation.

DISCUSSION

1. Evidence for standing genetic variation for OXA resistance

Two lines of evidence support the view that standing variation is the source of OXA-R alleles in schistosomes. First, we have indirect evidence: OXA-R alleles are geographically widespread in Africa and the Middle East despite limited treatment with OXA (or hycanthone, its structural analog; (18)) in these regions. Furthermore, that OXA-R alleles are found at high frequency in East Africa, where there has been minimal use of OXA, while OXA-R alleles are found at low frequency in Brazil, where OXA has been used extensively, is also consistent with the idea that mutation and drift, rather than selection, explain the patterns of variation observed. The second line of evidence is more direct: we showed that an OXA-R mutation, p.E142del, with an identical 102.5 kb flanking haplotype, is sampled from both West African and Caribbean schistosomes. This result strongly suggests that p.E142del alleles were present in West Africa prior to the transatlantic slave trade (1501-1867) (19), and were transferred to the New World on ships carrying West African slaves. Hence, OXA-R alleles were segregating within *S. mansoni* populations at least 470 years before deployment of OXA in the 1970s (20).

Our molecular data are backed up by clinical observations from the early use of OXA. Resistant parasites were detected in Brazil in the 1970s (21,22), before any mass drug administration (14). Similar observations of *S. mansoni* infected patients resistant to OXA treatment were made in East Africa (23). The existence of OXA-R parasites was confirmed experimentally by infecting mice with parasites isolated from patients that were parasite positive following drug treatment (21–23). Together these observations support the existence of segregating OXA-R alleles in schistosome populations before OXA deployment for parasite control.

2. Differences in OXA treatment efficacy between East and West Africa

Given the variation in OXA-R frequencies that we observe in different geographical samples, it is interesting to examine the literature on clinical treatment efficacy of OXA for treating

schistosomiasis patients. Early trials of OXA to treat patients with intestinal schistosomiasis resulted in multiple treatment failures in Egypt, East Africa and South Africa (23–27). As a consequence, the WHO recommended use of higher doses of OXA in East Africa, compared with West Africa (28). Human host metabolism did not explain this lack of efficacy because the OXA availability in blood was the same or higher in the East African patient populations than in West African or South American populations (29,30). Therefore, the presence of resistant parasites was the most likely explanation. OXA-R parasites were identified in Kenya by treating mice infected with parasites from patients showing poor treatment response (23). We observed a 14.91% frequency of OXA-R alleles (and 5.26% frequency of homozygous OXA-R parasites) in East Africa compared with 4.29% frequency of OXA-R alleles (and no homozygous OXA-R parasites) in West Africa. Our results provide a molecular explanation for the poor treatment response observed in East Africa, relative to other locations.

3. Implications for development of OXA derivatives

OXA kills *S. mansoni* but not *S. haematobium* or *S. japonicum*. OXA derivatives are currently under development to obtain more potent molecules acting against all three schistosome species. In fact, OXA derivatives that kill adult worms of the three main species of schistosomes infecting humans *in vitro* have now been developed (31). The low frequency of homozygous OXA-R parasites in *S. mansoni* suggests that OXA derivatives will result in imperfect cure rate for this species, particularly in East Africa. However, the primary purpose of generating OXA derivatives is to treat *S. haematobium* and *S. japonicum*, perhaps as a partner drug for praziquantel (PZQ). Examining natural variation in homologous sulfotransferase genes from these two species (*ShSULT-OR* and *SjSULT-OR*) to better understand the potential for resistance evolution will be critical if OXA derivatives are to be developed to control these parasites.

4. Implications of standing variation for drug resistance evolution

Standing variation in drug resistance genes has a major impact on how fast resistance evolves (2). If resistant alleles are already present in the population prior to treatment, drug resistance has the potential to spread much more rapidly because there is no waiting time for a resistance mutation to appear *de novo* (Fig. 7A) (3). An increasing number of examples support this view. The nematode *Caenorhabditis elegans* carries a large diversity of *β-tubulin* alleles allowing worms to be resistant to benzimidazoles (BZ) (32). In the filarial worm *Onchocerca volvulus*, standing variation appears to be involved in resistance to ivermectin (6). Standing variation is also involved in herbicide resistance in plants: resistance alleles from the weed *Alopecurus myosuroides* were identified in plant collection almost 100 years before herbicides were used (33). Antibiotic resistance provides particularly dramatic examples of standing variation: plasmids encoding multidrug resistance were found in frozen bacteria isolated from the permafrost demonstrating that antibiotic resistance plasmids were already present thousands of years ago (34,35).

We do not want to give the impression that standing variation is the only source of variation for evolution of drug resitance. In the case of other well studied helminth parasites, such as *Haemonchus contortus* and *Teladorsagia circumcincta*, resistance alleles are consistent with evolution through recurrent *de novo* mutations or very rare standing variants. While selection of rare pre-existing BZ resistance alleles was shown in French farms (36), selection of *de novo* resistance mutations, associated with different haplotypes, was shown to be common in UK farms (37).

The fact that there is strong evidence of standing variation in OXA resistance but not in BZ resistance may reflect the differences in the nature of the mutation underlying resistance. In the case of OXA, resistance is due to loss-of-function mutations resulting in non functional SmSULT-OR. As a consequence, mutations can occur in any position that disrupts substrate binding or protein structure. Hence mutations are expected to arise frequently and will exist in natural populations. In contrast, mutations underlying BZ resistance occur in specific position within the *β-tubulin* gene. As consequence, such mutations occur much more rarely. Furthermore because *β-tubulin* is an essential gene, mutations that disrupt protein structure

and result in non functional proteins are strongly selected against and cannot reach high frequency.

Standing variation for OXA resistance alleles could arise by drift, or alternatively as a result of selective forces other than OXA treatment. For example, Hahnel *et al*. (32) demonsrated BZ resistance in natural population of *C. elegans* which are not targetted by BZ drugs and speculated that natural compound with similar structure to benzimidazoles could have pre-selected for benzimidazole resistance alleles. In the case of our OXA-R mutations in *SmSULT-OR*, we do not know what selective forces might be involved (see also discussion in section 5).

Drug resistance in parasitic helminths infecting livestock or humans is now recognized as a potential concern for control efforts, but was neglected for a long time using the argument that the slow reproduction rate of worms would greatly delay resistance evolution (38). The observation that resistance alleles exist as standing variation within multiple pathogen or parasite populations in the absence of drug treatment suggests previous optimism about the shelf life of drugs was poorly founded. If resistance alleles are already at relatively high frequency in populations when new drugs are deployed, resistance may evolve extremely rapidly (3,5).

5. Prediction of the resistance spread

We can use the frequency of resistance allele to model resistance spread in parasite populations. In the case of OXA resistance, using an N_e estimate of 65,000 (39), OXA-R alleles spread from 15% starting frequency to fixation in 170 generations in 100% of simulations when selection is strong (s=0.1). Assuming a generation time between 3 months and 1 year, this is equivalent to a period of 42.5 to 170 years (Fig. 7A). However, if OXA-R alleles were evolving *de novo*, simulations indicate that fixation will occur rarely (0.04% of the simulations) and this would take 1,197 generations (corresponding to a period of 299.25 to 1,197 years) from the time a mutation arises. We can use the observed frequency of OXA-R alleles segregating in East African populations to make predictions about the spread of phenotypically resistant parasites (i.e. those homozygous for OXA-R alleles) (Fig 7B). If we use a frequency of 10% resistant

parasites to denote unacceptable efficacy (this threshold is used for antimalarial drugs (40)) then this threshold will be reached in 19 to 444 generations (4.75 to 444 years) using a range of selection coefficients (from 0.01 to 0.2). The selection coefficients driving spread of drug resistance alleles in schistosomes is not known, but the range we have used covers measured selection coefficients driving drug resistance spread in another human parasite (*Plasmodium falciparum*) (41,42). These simulations suggest that, while OXA-R allele frequencies are relatively high in East Africa, OXA derivatives could still be extremely effective for schistosome control in the short-medium term, particularly if deployed as a combination therapy, partnered with a second drug with a different mode of action (e.g. PZQ).

Our simple models for predicting spread of OXA-R alleles under drug selection ignore fitness costs of OXA-R alleles, which might limit the rate of spread. The fitness cost of inactive SmSULT-OR in the absence of drug treatment still needs to be assessed accurately (13) but the occurrence of natural homozygotes for defective alleles suggests limited costs. The exact role of this enzyme in schistosome biology is not known. Sulfotransferases transfer the sulfo group from a donor (usually PAPS) to the substrate, resulting in inactivating or solubilizing of the substrate (43). Substrates can be endogenous signal molecules (hormones, neurotransmitters) or exogenous chemicals. In the latter case, sulfotransferases play a role in detoxifying natural or synthetic toxins (43), but sometimes they do the opposite by activating pro-drugs as observed with the anti-tumor drug N-benzyl indolecarbinols (44) or OXA (10,45). Because the same enzyme can sulfate both endogenous and exogenous compounds, it is often difficult to determine their exact biological role. In schistosomes, we speculate that SmSULT-OR could have roles in regulating endogenous molecules as well as detoxifying chemicals present in their environment (*i.e.* in the feces, water, snail or human blood, etc.).

6. Molecular markers for resistance surveillance

Molecular markers of OXA-R now allow efficient monitoring of the distribution of OXA-R alleles in schistosome populations. This approach is widely used for other parasites and pathogens such as malaria parasite (46) and HIV (47). For schistosome, collections such as SCAN which

382 contain thousands of parasite samples from multiple locations (17) will be extremely valuable
383 for this work: regular sampling in different endemic regions will help to update the resistance
384 landscape. However, not all identified *SmSULT-OR* mutations will lead to resistance, so it is
385 critical that molecular screening is paired with functional evaluation or computational
386 prediction, as we have done here.

387 PZQ is the only drug currently available to treat schistosomiasis and effort in mass drug
388 administration has recently been expanded 10 fold (48), with a target of administering 250
389 million treatments per year, increasing selective pressure for PZQ resistance. We suspect that
390 standing variation for PZQ resistance is also likely, because this trait is easy to select in the
391 laboratory. This has been done by several groups using independent laboratory populations,
392 and resistance has spread within very few generations (49–54), strongly suggesting that
393 resistance alleles were already present in these laboratory populations. Furthermore, the
394 laboratory populations used for selection were isolated before PZQ was available (23,55) and so
395 were not exposed to drug selection. Molecular markers for monitoring the frequency of PZQ-R
396 in natural parasite populations would be extremely valuable, as demonstrated by our work on
397 OXA-R.

MATERIALS AND METHODS

1. Ethics statement

a. African samples

Samples from Senegal and Niger were collected as part of the EU-CONTRAST project (56), a multidisciplinary alliance to optimize schistosomiasis control and transmission surveillance in sub-Saharan Africa, as detailed in Webster *et al.* (57) with ethical approval granted by ethical committees of the Ministry of Health (Dakar, Senegal), and the Niger National Ethical Committee (Niamey, Niger) with additional ethical approval obtained from the St Mary's Hospital Local Ethics Research Committee, R&D office (part of the Imperial College Research Ethics Committee (ICREC; EC no. 03.36. R&D no. 03/SB/033E)), in combination with the ongoing CONTRAST and Schistosomiasis Control Initiative (SCI) activities.

For the Tanzanian samples collected as part of the Schistosomiasis Consortium for Operational Research and Evaluation (SCORE), ethical approvals were granted by the Imperial College Research Ethics Committee and the SCI Ethical approval (EC no. 03.36. R&D no. 03/SB/033E); the National Institute for Medical Research (NIMR, reference no. NIMR/HQ/R.8a/Vol. IX/1022); University of Georgia Institutional Review Boards, Athens, GA (2011-10353-1).

Following routine procedures in the field, the objectives of the study were first explained to the local village chiefs and political and religious authorities who gave their consent to conduct the study. Written consent for the schoolchildren to participate in longitudinal monitoring of the national control programme for schistosomiasis was given by head teachers, and/or village chiefs where there were no schools, due to the fact that in African villages, written consent of the child's guardian is often very difficult to obtain owing to the associated impoverished conditions and often low literacy. Each individual child also gave verbal consent before recruitment. Following sampling, a praziquantel treatment (40 $mg.kg^{-1}$) was offered to infected participants.

b. Omani samples

We obtained ethical clearance from the Sultan Qaboos University and the Ministry of Health of Oman to use positive stool samples for schistosomiasis collected by the Ministry of Health of Oman during epidemiological screening. Ethical approval was given by the Medical Research and Ethical Committee (MREC) of the Non-Communicable Disease Control Section of the Directorate General of Health Affairs, Headquarters, Ministry of Health, Oman (no. MH/DGHA/DSDC/NCD/R&S/167/01).

We obtained ethical approvals of animal studies in France from the French Ministère de l'Éducation Nationale, de la Recherche et de la Technologie, from the French Ministère de l'Agriculture et de la Pêche (agreement no. A 66040), and from the French Direction Départementale de la Protection des Populations (no. C 66-136-01 with prefectoral order no. 2012-201-0008). Certificate for animal experimentation was given to H.M. (authorization no. C 66.11.01; articles no. R 214-87, R 214-122 and R 215-10). Housing, breeding and animal care followed the guidelines of the French CNRS. The different protocols used in this study had been approved by the French veterinary agency from the DRAAF Languedoc-Roussillon (Direction Régionale de l'Alimentation, de l'Agriculture et de la Forêt), Montpellier, France (authorization no. 007083).

2. Sampling

a. African samples

S. mansoni miracidia were collected from individual patients in three different West African countries in 2007: 27 patients from two locations in Senegal, and 17 patients from two locations in Niger (supp. table 3) (57,58). Additionally, *S. mansoni* miracidia were collected as part of the SCORE program from 64 children in seven villages on the shores of Lake Victoria in Tanzania (East Africa) in January 2012 (supp. table 3) (59).

Collection of miracidia was performed as previously described (57,60). Briefly, individual stool samples from positive patients were homogenized through a mesh and washed through with water. The content was then transferred in a Pitchford funnel assembly, washed with

454 additional water, and the filtered homogenate was drained into a Petri dish. The Petri dish
455 containing the homogenate was then left in bright ambient light (not direct sunlight) to allow
456 hatching of miracidia. Miracidia were visualized under a dissecting microscope and individually
457 captured in 3-5 µL of water using a micropipette. Miracidia were then pipetted individually onto
458 Whatman FTA cards for DNA preservation. Cards were allowed to dry for 1 hour and then
459 stored for future research (57,58,60).

460 b. Omani samples

461 The Omani schistosome samples were collected during 8 field trips, from 2001 to 2015, in
462 different areas in Dhofar, Oman and originated from either *Homo sapiens*, *Rattus rattus* or
463 *Biomphalaria pfeifferi* (supp. table 3): 11 patients from 4 localities, 2 rats from 2 localities, 26
464 snails from 3 localities.

465 We obtained schistosome adult worms from naturally infected rats and from laboratory
466 infected mice. The mice were infected with cercariae from naturally infected snails or from
467 laboratory snails infected with miracidia isolated from stool samples. We collected miracidia
468 from stool samples as described in Moné *et al.* (61). We exposed *Biomphalaria pfeifferi* snails to
469 miracidia as described in Mouahid *et al.* (62). We maintained laboratory and naturally infected
470 snails at constant temperature (26°C) and balanced photoperiod (12h light / 12h dark) and fed
471 them with fresh lettuce *ad libitum*. Prior to infection, we anaesthetized the mice by
472 intraperitoneal injection of an anesthetic solution (0.01 $mL.g^{-1}$ of mouse body weight). We
473 prepared the anaesthetic solution using 0.5 mL of Rompun (20 $mg.mL^{-1}$; Bayer) and 1 mL of
474 Imalgène (100 $mg.mL^{-1}$; Rhône Mérieux) diluted in 8.5 mL of autoclaved NaCl 8.5 ‰. Abdomens
475 of anesthetized mice were shaved and exposed during 1 hour to cercariae shed from laboratory
476 or naturally infected snails. Cercariae from naturally infected snails were kept in 95° ethanol
477 when the number of cercariae was too low for mouse infection. Laboratory infected mice or
478 naturally infected rats were euthanized by intraperitoneal injection of sodium pentobarbital
479 solution (1.1 mL diluted in 10 mL of ethanol 10%). We recovered adult worms by perfusion (63);
480 the worms were washed in NaCl 8.5 ‰, and single worms (female or male) were fixed in 95°

ethanol and preserved at -20°C. Worms and cercariae were washed in 1X TE buffer for 1 hour prior to DNA extraction.

3. DNA processing and library preparation

We amplified DNA and sequenced exomes from single miracidia preserved on FTA cards (1 miracidium per patient) for African samples or from DNA extracted from worms or cercariae for Omani samples. FTA-preserved samples were processed following our published protocol (64). Briefly we punched a 2 mm disc containing the miracidium from the FTA card, washed it with the FTA Purification Reagent (GE Healthcare Life Sciences), rinsed it twice with TE^{-1} buffer, and finally dried it. DNA from single worms and cercariae were extracted using the DNeasy Blood and Tissue kit (Qiagen) following the tissue protocol with an incubation time of 2h at 56°C and an elution in 200 µL. Samples were quantified using the Qubit dsDNA HS assay kit (Invitrogen).

We then performed whole genome amplification (WGA) on each FTA punch or on 2 µL or 4 µL of DNA solution using the Illustra GenomiPhi V2 DNA Amplification kit (GE Healthcare Life Sciences). Amplified DNA was purified with the SigmaSpin™ Sequencing reaction Clean-up (Sigma-Aldrich), following the manufacturer protocol. We quantified purified samples using the Qubit dsDNA BR assay (Invitrogen). DNA samples that failed WGA were cleaned up and concentrated using the Genomic DNA Clean & Concentrator kit (Zymo Research) following the manufacturer protocol and these samples with concentrated DNA were used to perform a new WGA.

Because WGA reactions are non-specific, we performed qPCR on each sample from FTA cards to quantify proportion of schistosome DNA (i.e., check for an excess of amplified DNA from the environment (water, fecal matter, etc.)). We excluded samples that showed less than 100 schistosome genomes copies in 20 ng of DNA which were not suitable for subsequent exome capture. We assessed genome copies by quantifyng the *S. mansoni α-tubulin* single copy gene (64).

We prepared exome capture libraries on the selected African samples and on all the successfully amplified Omani samples using the pre-capture pooling method of the SureSelect XT^2 Target Enrichment System (Agilent) (64). Finally, we sequenced libraries on a HiSeq 2500 and data were demultiplexed using the Casava pipeline. Raw sequencing data are accessible from the NCBI Sequence Read Archive under BioProject accession numbers PRJNA439266, PRJNA560069, PRJNA560070.

4. Alignment, variant calling and phasing

We aligned sequences as described in Le Clec'h *et al.* (64). Briefly, we aligned data against the v5 *S. mansoni* genome using BWA and SAMtools, realigned around indels using GATK, PCR duplicates were marked using picard and Q-score were recalibrated using GATK.

To identify variants in the *SmSULT-OR* (Smp_089320) gene, we performed a variant calling using FreeBayes (v1.1.0-46-g8d2b3a0) (65) in the first 3 Mb of the chromosome 6. We used a minimum base quality (-q) of 20 and a minimum mapping quality (-m) of 30. We included mutation sites identified previously (10,13) in order to genotype these sites specifically for further comparison. We defined 4 populations: Caribbean (HR), West Africa (SN and NE), East Africa (TZ) and Middle-East (OM). We excluded variants supported by less than 4 reads using VCFtools (v0.1.14) (66). We then used vcf-subset from VCFtools to remove sites with reference alleles only. We adjusted variant positions using vt normalize (v0.5772-60f436c3) (67). We finally used Beagle (v4.1) (68) to first estimate genotypes and to then phase data. This approach resolves haplotypes using statistical models rather than by direct linkage of SNPs on short reads. Unphased variant calling data and scripts used to analyze the data are available on Zenodo (DOI: 10.5281/zenodo.2850876 and 10.5281/zenodo.3370039, respectively).

5. Genetics analysis

We performed all the genetics analysis using phased exome data. We handled the VCF data in R (R v3.5.0 (69)) using the vcfR package (v1.8.0.9) (70). We determined the longest haplotype

534 block from the samples carrying the p.E142del using a custom R code after filtering invariable
535 sites in these samples. We built the haplotype network using the R package poppr (v2.8.1)
536 (71,72) after selecting variants within the longest haplotype coordinates showing no more than
537 20% of missing data. We computed the frequency of the OXA-R allele using a custom R script
538 and functional annotation obtained through a custom bash script.

539 We generated haplotype sequences of the coding sequence only for the Old World samples
540 using the updated phased VCF data exported from R and the BCFtools (v1.2) (73). We
541 generated haplotypes of the South American samples from previous genotyping using a custom
542 bash script. We included the *SmSULT-OR* homologue sequence from *S. rodhaini* previously
543 identified (13). We aligned the haplotypes using Clustal Omega (v1.2.2) (74). We determined
544 nucleotide diversity, number of synonymous and non-synonymous sites using DnaSP software
545 (v6.12.01) (75). Populations were defined as described in the previous section. Scripts used to
546 analyze the data are available on Zenodo (DOI: 10.5281/zenodo.3370039).

547

548 **6. Recombinant SmSULT-OR protein production and OXA activation assay**

549 We produced recombinant SmSULT-OR proteins following Chevalier *et al.* (13). Briefly,
550 mutations were introduced in the cloned *SmSULT-OR* gene sequence (Smp_089320; GenBank
551 accession no. HE601629.1) and introduced into *Escherichia coli* for protein production. Proteins
552 were extracted from bacterial culture and purified on an affinity chromatography column. His-
553 tag was removed using Tobacco etch virus (TEV) protease, the solution was dialyzed overnight
554 and passed through affinity chromatography again to remove His-tag and TEV protease. The
555 sample was loaded onto a GE-pre-packed Q anion exchange column and eluted, and the pooled
556 fractions were dialyzed overnight. The protein was finally concentrated at 10 $mg.mL^{-1}$.

557 We tested the impact of a subset of the mutations observed on OXA activation using an *in*
558 *vitro* assay (13). We tested the ability of recombinant SmSULT-OR proteins to activate OXA in a
559 protease inhibitor cocktail with sheared *S. mansoni* gDNA as a final target for the tritiated OXA
560 pre-mixed with ATP, $MgCl_2$ and PAPS co-factor. After 2.5 h of incubation at 37°C, the reaction
561 was stopped and DNA was extracted three times. Radioactivity in the remaining aqueous phase

562 containing the DNA and in water (blank) was counted in a liquid scintillation spectrometer.
563 Blank values were subtracted from sample values. We performed three independent reactions
564 for each recombinant protein.

565

566 **7. Evaluation of impact of mutations on protein stability**

567 We first visually assessed the scored mutations on the SmSULT-OR protein structure (PDB code
568 4MUB (10)) using the mutagenesis function of PyMol software (v2.3.0; Schrödinger, LLC).

569 We then used the Rosetta package (v3.9) to test the impact of scored mutations on protein
570 stability. We used the ddg_monomer application to compute the difference in free enthalpy
571 ($\Delta\Delta G$) between the mutated (amino acid substitutions only) and the wild-type protein. The
572 higher the $\Delta\Delta G$, the more unstable is the mutated protein. For this, we prepared ligand files
573 (OAQ and A3P) by downloading SDF files containing all ligand structures from SmSULT-OR
574 crystals available from the Protein Data Bank website. We modified SDF files to add hydrogens
575 using Openbabel (v2.4.0) (76), and generated params files using molfile_to_params.py from
576 Rosetta. We used the structure of SmSULT-OR to generate a constraint file using the
577 minimize_with_cst application and the convert_to_cst_file.sh script. We removed ligand
578 information from the constraint file. For each mutation, we finally generated a resfile and ran
579 the ddg_monomer application with 50 iterations and options adapted from the protocol 16 of
580 Kellogg *et al.* (77). Scripts used to analyze the data are available on Zenodo (DOI:
581 10.5281/zenodo.3370039).

582

583 **8. Statistical analysis**

584 We conducted statistical analyzes using R (v3.5.0) (69). We performed simulations using a
585 modified version of the driftR simulator (78). The OXA activation assay data were tested for
586 normality using a Shapiro-Wilk and compared by a parametric ANOVA followed by a Tukey
587 post-hoc test.

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TABLES

Table 1 – Summary statistics for sequence variation in *SmSULT-OR*.

Location	Sample size	Parasite stage sampled	Host	Sequence	Notes[b]
South America (Brazil)[a]	189	Miracidia	Human	Sanger sequence of *SmSULT-OR* exons	1-11 miracidia from each of 49 people from single village (13)
West Africa (Niger/Senegal)	25/10	Miracidia	Human	Exome sequence	1 miracidia from each person
East Africa (Tanzania)	57	Miracidia	Human	Exome sequence	1 miracidia from each person
Middle East (Oman)	112	Miracidia/adult worms/cercariae	Human/Rat/Snail	Exome sequence	1-53 parasite genotypes analysed per host from 11 people, 2 rats and 26 snails from 8 locations
Caribbean (Puerto Rico)[a]	1	Adult worms	Hamster	Genome sequence	OXA-resistant parasite used in a genetic cross (10)

[a] published data

[b] see supplementary table 2 for detailed information on sample locations

Table 2 – Summary statistics for sequence variation in *SmSULT-OR*.

Location	Nucleotide diversity ($\pi \pm$ standard deviation)	Dn	Pn	Ds	Ps	N	S	pN/pS	Ka/Ks
South America (Brazil)[a]	$2.1 \pm 0.3 \times 10^{-4}$	17	4	23	0	598.19	163.81	N/C	0.202
West Africa (Senegal / Niger)	$7.2 \pm 1.5 \times 10^{-4}$	19	9	23	2	600.93	164.07	1.229	0.225
East Africa (Tanzania)	$22.8 \pm 2.3 \times 10^{-4}$	18	19	23	9	593.80	162.20	0.577	0.214
Middle East (Oman)	$247.5 \pm 3.4 \times 10^{-4}$	10	15	11	36	598.80	160.20	0.111	0.243
Overall	$148.1 \pm N/C \times 10^{-4}$	10	39	11	40	583.61	157.39	0.263	0.245

[a] Data from Brazil from a previous study (13) added for comparison.

Dn, Ds: Number of fixed non-synonymous and synonymous differences between species (*S. mansoni* and *S. rodhaini*)

Pn, Ps: Number of polymorphic non-synonymous and synonymous differences within species (*S. mansoni*)

N: Number of non-synonymous sites

S: Number of synonymous sites

pN/pS=(Pn/N)/(Ps/S)

Ka/Ks=(Dn/N)/(Ds/S)

N/C: not calculable

850 **Table 3 – OXA-R mutations scored in the *Schistosoma mansoni SmSULT-OR* gene and their frequency in the New and Old World.**

Nucleic acid mutation	Amino acid mutation	Mutation frequency			
		South America (Brazil)[a] n=189	West Africa (Senegal / Niger) n=25 / n=10	East Africa (Tanzania) n=57	Middle East (Oman) n=112
c.3dupGTTTATCCATAATG	p.I2VfsX3	-	-	0.0096	-
c.35C>A	p.S12X	-	0.014	-	-
c.103T>C	p.C35R	0.0027	-	-	-
c.358T>C	p.W120R	-	-	0.0510	0.065
c.424_426delGAA	p.E142del	0.008	0.035	0.0098	-
c.510delT	p.N171IfsX28	-	-	0.0625	-
c.536T>C	p.L179P	-	-	0.0089	-
Total frequency		0.0107	0.044	0.1418	0.065

851 The code used for nucleic acid mutations indicates the sequence type (c = coding), the position, and the mutation type (X>Y = substitution of X
852 by Y, insN = insertion of N, delN = deletion of N, dup = duplication). The code used for amino acid mutations indicates the sequence type (p =
853 protein), the reference amino acid, the position, and finally the alternative amino acid, and when frame shift (fs) occurs, the position of the stop
854 codon (X) after the mutation. For details about the nomenclature, see Ogino *et al.* (79).
855 [a] Data from Brazil were obtained in a previous study (13) and added for comparison.

856 **FIGURES**

857 **Fig. 1 – Drug resistance evolution from standing variation or *de novo* mutation**. Drug
858 resistance alleles spread rapidly and reach fixation with a high probability when drug resistance
859 alleles are already present as standing variation. In contrast, if resistance alleles are absent
860 when treatment is initiated, resistance mutation must arise *de novo*, so there is a waiting time
861 before the resistance alleles appear, and most resistance alleles are lost by genetic drift, so the
862 probability of establishment and fixation is low.

863

864 **Fig. 2 – Mapping of the resistance mutations on the gene sequence and structure of**
865 ***Schistosoma mansoni* SmSULT-OR sulfotransferase.** Exon 1 and exon 2 are represented in
866 orange and beige, respectively. Single nucleotide polymorphisms and insertion/deletion events
867 are represented in cyan and magenta, respectively. (A) Linear representation of the *SmSULT-OR*
868 gene showing the relative position of the mutations and their translation in amino acid
869 sequences. (B) Positions of mutations on the SmSULT-OR protein. Oxamniquine is represented
870 in yellow, 3'-phosphoadenosine-5'-phosphosulfate (PAPS) co-factor is represented in green.

871

872 **Fig. 3 – Enzymatic activity of recombinant *Schistosoma mansoni* SmSULT-OR sulfotransferase**
873 **expressed from different allelic variants.** This *in vitro* oxamniquine activation assay quantifies
874 DNA-oxamniquine complexes by scintillation (counts per minute). (A) Bars show the mean of
875 three replicates, while error bars are S.E.M. (B) The triangular matrix shows the p-values from
876 the pairwise comparisons (Tukey's HSD, $p < 0.05$). The color is proportional to the level of
877 significance, from white (not significant) to red (most significant). Enzyme carrying known loss-
878 of-function mutations, such as p.C35R or p.E142del, as well as a newly identified variant
879 (p.L179P) showed no or low oxamniquine activation, while two newly identified variants
880 (p.S160L and p.P225S) showed intermediate activation. The newly identified p.P106S did not
881 impair oxamniquine activation.

882

883 **Fig. 4 – *In silico* evaluation of mutations on protein stability.** We computed the difference in
884 free enthalpy ($\Delta\Delta G$) between the mutated and the wild type proteins. The higher the $\Delta\Delta G$, the
885 more unstable is the mutated protein. Only single amino acid changes within the resolved
886 crystal structure were examined. For completeness, we included mutations from our current
887 dataset and from previous studies (10,13). Grey bars correspond to known sensitive alleles. Red
888 bars correspond to validated resistant alleles. Grey labels correspond to mutations identified
889 previously from South America (13).

890

891 **Fig. 5 – World map showing proportion of resistance and sensitive alleles in South America**
892 **(Brazil), West Africa (Senegal and Niger), East Africa (Tanzania) and Middle East (Oman).**
893 Number of homozygous (hmz) and heterozygous (htz) parasites for resistant alleles, and total
894 number of parasites sampled (n) are shown below the pie charts. East Africa showed the

895 highest frequency of resistant alleles and resistant parasites. Data from Brazil from a previous
896 study (13) was added for comparison.

897

898 **Fig. 6 – Common origin of the p.E142del mutation in the Old and New World.** (A) Haplotype
899 variation in all the samples bearing p.E142del from Caribbean (HR9), Niger (NE) and Tanzania
900 (TZ) across a 102.5 kb region of chr. 6. Each row represents a chromosome, HR9 was used as
901 reference, blank squares reflect HR9 allele state, and black squares correspond to the
902 alternative allele. Relative bp position to p.E142del (0 bp) is shown on the x-axis. The first and
903 last variants showed on the block correspond to the break of the haplotype block. The
904 Caribbean sample (HR9) and a Nigerien sample (Sm.NE_Di158.1) share an identical haplotype
905 block of 102.5 kb. (B) Minimum spanning network of 410 haplotypes of the 102.5 kb region
906 previously identified. The network was built using 399 bi-allelic variants. Node size is
907 proportional to sample size (smallest node: n=1; biggest node n=50). Nodes with samples
908 carrying p.E142del are circled in blue. Caribbean and West African haplotypes carrying
909 p.E142del clustered together indicating a common origin. The p.E142del from East Africa has
910 different flanking haplotypes.

911

912 **Fig. 7 – Impact of starting allele frequency on OXA-R allele change.** (A) Monte Carlo simulation
913 over 1,500 generations using strong selection (selection coefficient (*s*) = 0.1) on a population
914 size (N) of 65,000 with a starting allele frequency (p(R)) of 0.15 for standing variation or 1/(2N)
915 for new mutation. These simulations underestimate time to fixation for true *de novo* mutation,
916 because we do not account for the waiting time for resistance to appear which is dependant on
917 the rate of drug resistance mutations and N_e (3). The starting frequency of 0.15 corresponds to
918 the frequencies of OXA-resistance alleles observed in Kenya. (B) Change in frequency of
919 resistant parasites (i.e. homozygotes for OXA-R alleles) from standing variation under a range of
920 selection coefficients. The dashed line corresponds to the two thresholds (10% and 20%) at
921 which treatment efficacy would be compromised. The numbers at the dashedlines correspond
922 to the parasite generations needed to cross these thresholds. These predictions are
923 deterministic, because we expect minimal stochastic variation when starting resistance allele
924 frequencies are high.

SUPPLEMENTARY TABLES

Supp. table 1 – Library sequencing statistics.

Supp. table 2 – Mutations scored in samples from West Africa (Senegal and Niger), East Africa (Tanzania) and Middle East (Oman).

Supp. table 3 – Sampling information for the schistosome material used.

Standing variation

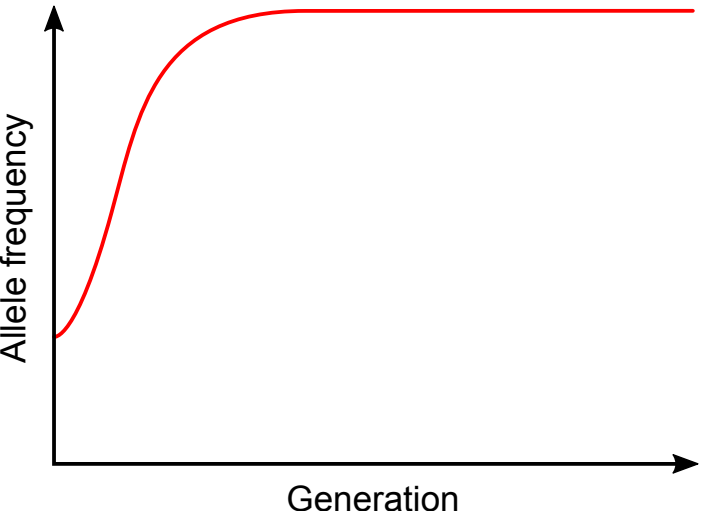
Mutation **present** before selection

Starting allele frequency = p(resistant allele)

→ **No** waiting time

Drug resistance evolves rapidly

High probability of fixation



De novo variation

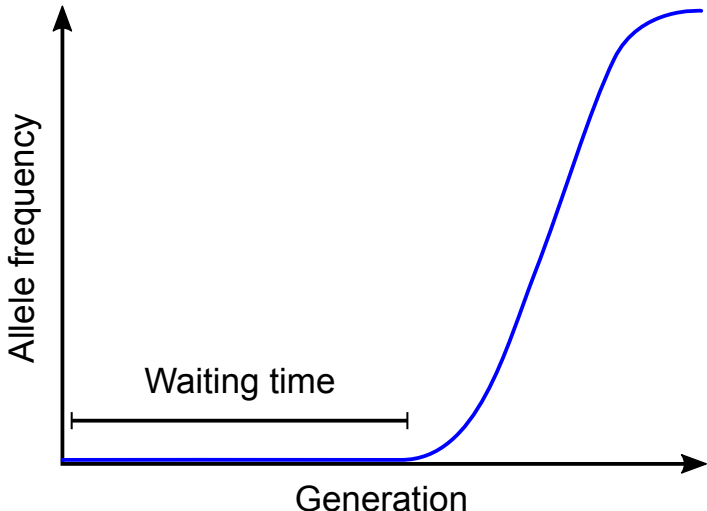
Mutation **not present** before selection

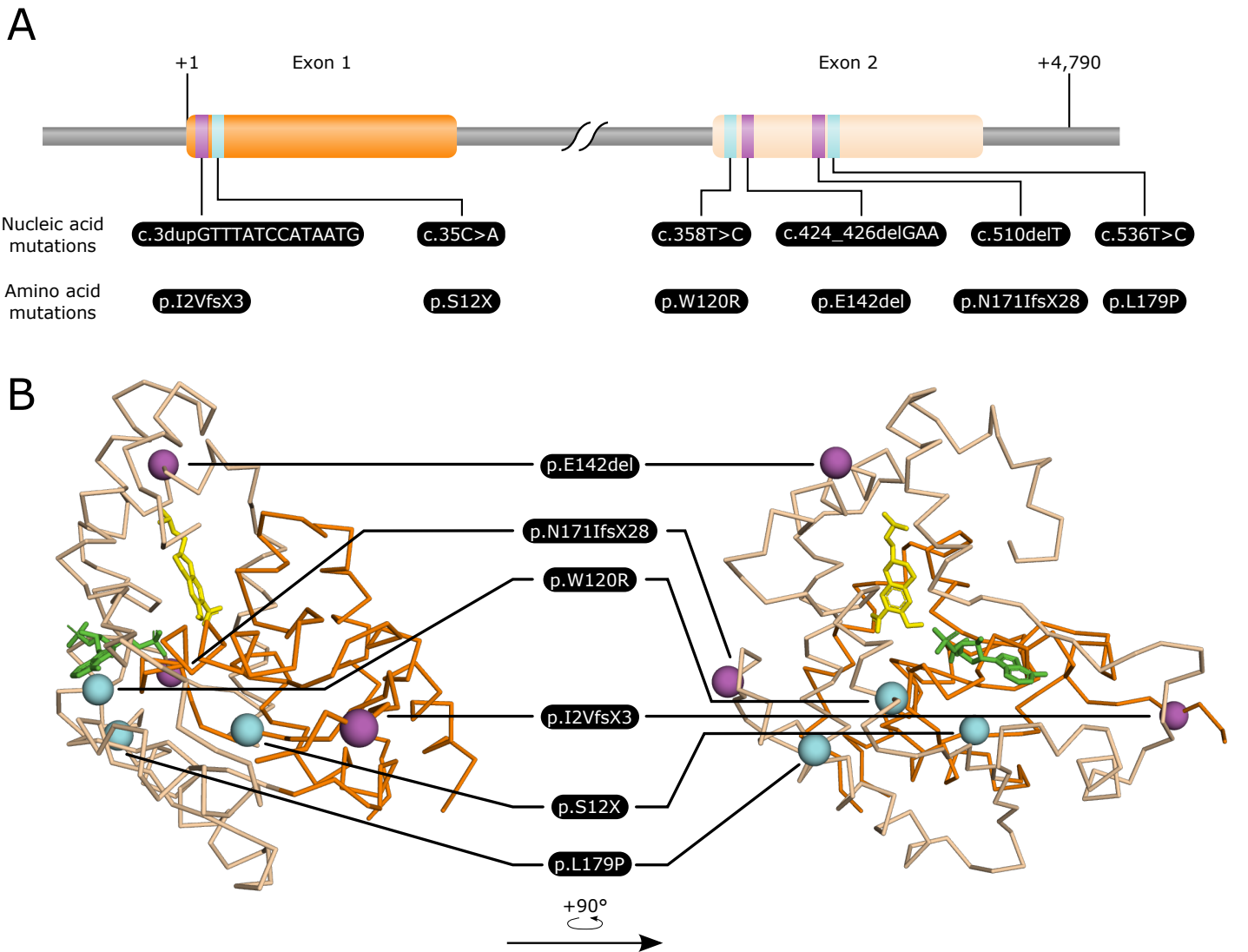
Starting allele frequency = $1/(2N_e)$

→ Waiting time

Drug resistance evolves slowly

Low probability of fixation




A
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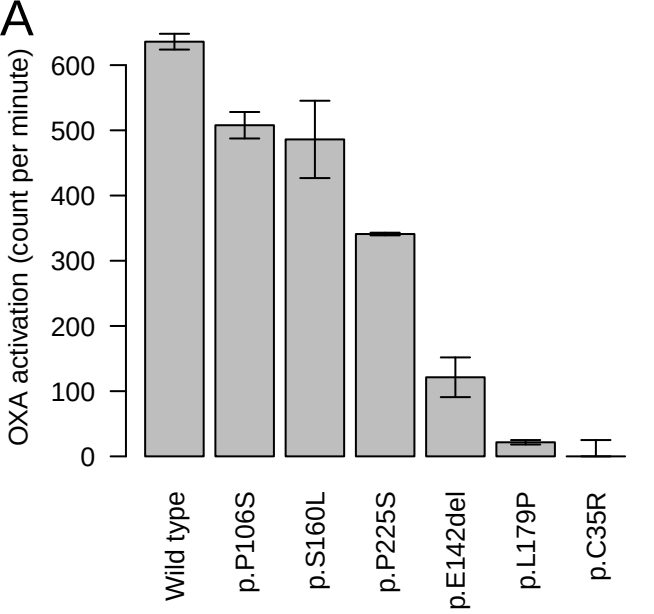
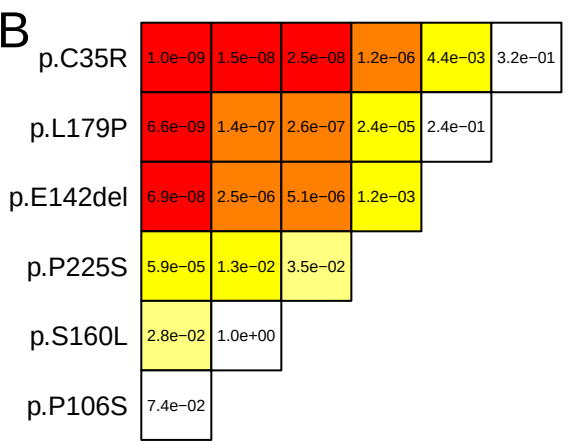
Exon 1
Exon 2
+4,790
Nucleic acid mutations
c.3dupGTTTATCCATAATG
c.35C>A
c.358T>C
c.424_426delGAA
c.510delT
c.536T>C
Amino acid mutations
p.I2VfsX3
p.S12X
p.W120R
p.E142del
p.N171IfsX28
p.L179P
B
p.E142del
p.N171IfsX28
p.W120R
p.I2VfsX3
p.S12X
p.L179P
+90°


A
OXA activation (count per minute)
600
500
400
300
200
100
0
Wild type
p.P106S
p.S160L
p.P225S
p.E142del
p.L179P
p.C35R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p.L179P
p.E142del
p.P225S
p.S160L
p.P106S
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3.2e−01
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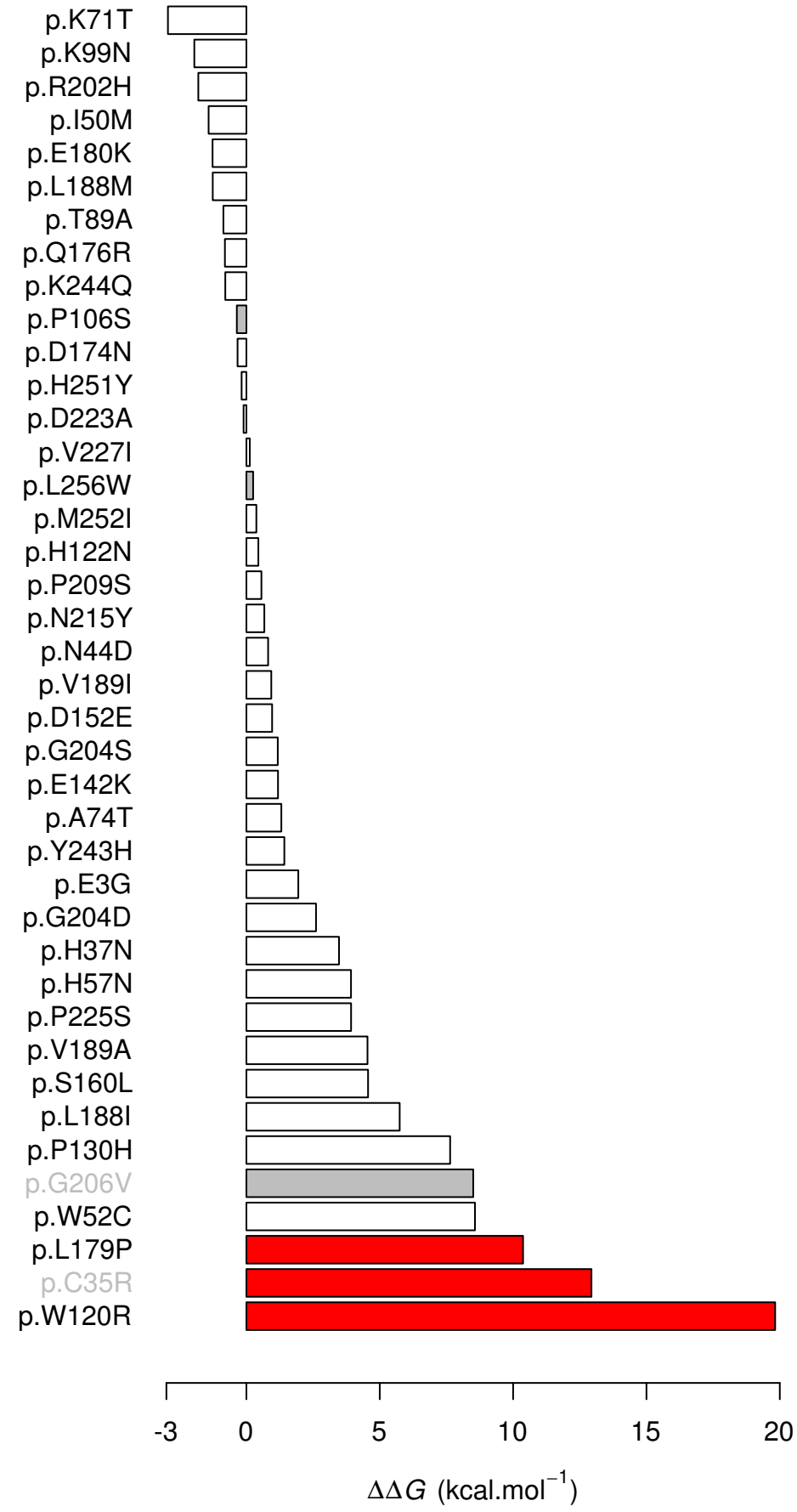
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p.P106S
p.D174N
p.H251Y
p.D223A
p.V227I
p.L256W
p.M252I
p.H122N
p.P209S
p.N215Y
p.N44D
p.V189I
p.D152E
p.G204S
p.E142K
p.A74T
p.Y243H
p.E3G
p.G204D
p.H37N
p.H57N
p.P225S
p.V189A
p.S160L
p.L188I
p.P130H
p.G206V
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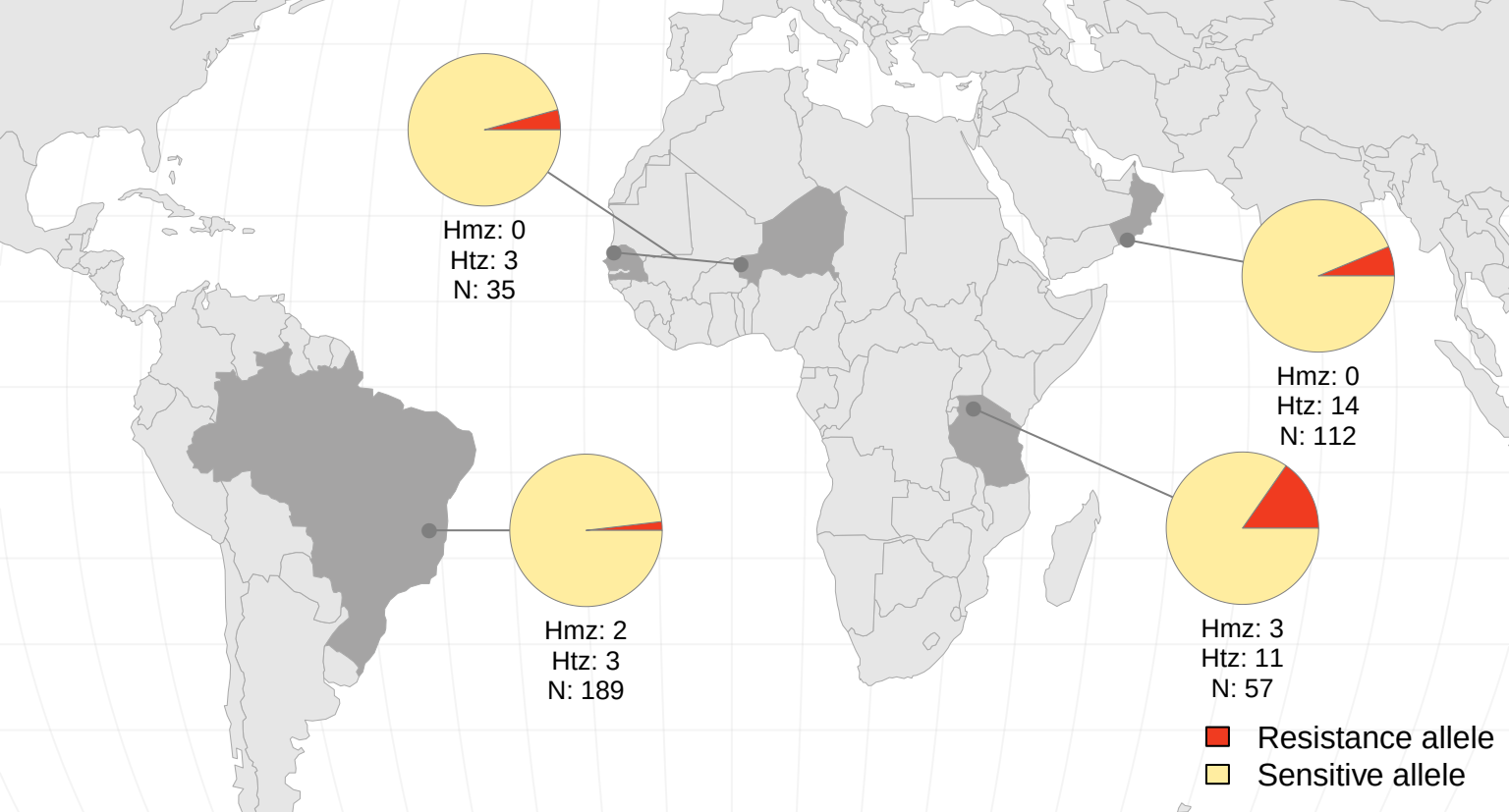
p.W120R
-3
0
5
10
15
20
ΔΔG (kcal.mol−1)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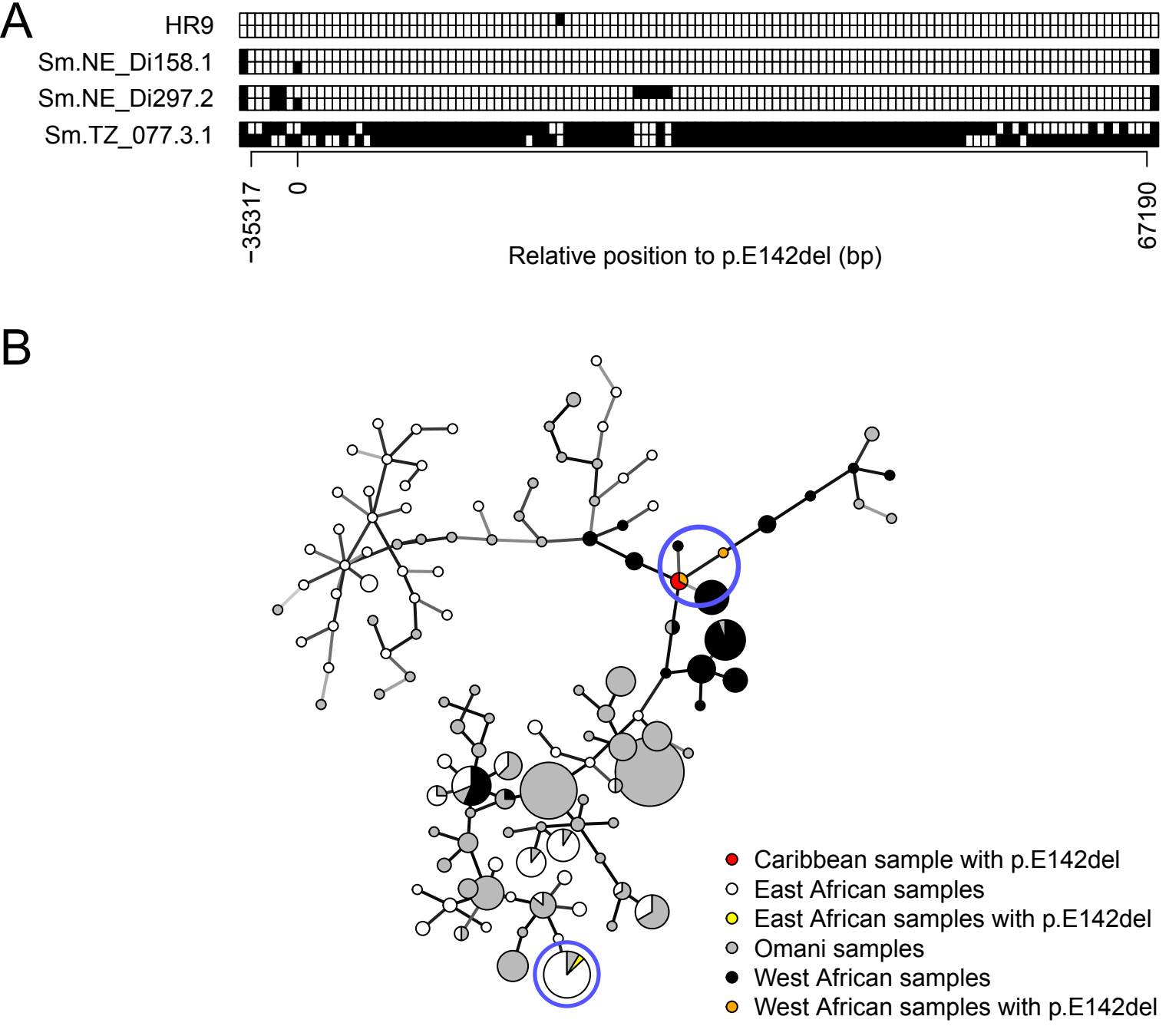
Htz: 3
N: 35
Hmz: 0
Htz: 14
N: 112
Hmz: 2
Htz: 3
N: 189
Hmz: 3
Htz: 11
N: 57
Resistance allele
Sensitive allele


A
HR9
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Sm.NE_Di297.2
Sm.TZ_077.3.1
−35317
0
67190
Relative position to p.E142del (bp)
B
Caribbean sample with p.E142del
East African samples
East African samples with p.E142del
Omani samples
West African samples
West African samples with p.E142del