Metabolic and Target-Site Mechanisms Combine to Confer Strong DDT Resistance in Anopheles gambiae

Citation

Published Version
doi:10.1371/journal.pone.0092662

Permanent link
http://nrs.harvard.edu/urn-3:HUL.InstRepos:12152876

Terms of Use
This article was downloaded from Harvard University’s DASH repository, and is made available under the terms and conditions applicable to Other Posted Material, as set forth at http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA

Share Your Story
The Harvard community has made this article openly available. Please share how this access benefits you. Submit a story.

Accessibility
Metabolic and Target-Site Mechanisms Combine to Confer Strong DDT Resistance in Anopheles gambiae

Sara N. Mitchell, Daniel J. Rigden, Andrew J. Dowd, Fang Lu, Craig S. Wilding, David Weetman, Samuel Dadzie, Adam M. Jenkins, Kimberly Regna, Pelagie Boko, Luc Djogbenou, Marc A. T. Muskavitch, Hilary Ranson, Mark J. I. Paine, Olga Mayans, Martin J. Donnelly

Introduction

Physiological resistance to insecticides often involves either mutations in the insecticide target site (target-site resistance), or elevated activity of detoxifying enzymes that metabolise and/or sequester insecticides (metabolic resistance). Resistance may result from selection upon standing genetic variation [1] or from a de novo mutation [2]. In Anopheles gambiae, a primary African malaria vector, a third route has been described, involving introgression of resistance-bearing haplotypes between molecular forms which are thought to be in the process of speciation [3]. There is overwhelming evidence that the mutation L1014F, a replacement change in the voltage-gated sodium channel (Vgsc), the target of both DDT and pyrethroid insecticides, is significantly associated with increased phenotypic resistance in both the donor S- and recipient M- form populations across Africa [4,5,6]. However, what remains unknown is whether such introgressed resistance alleles interact with allelic variants in the recipient genetic background.

In An. gambiae metabolic resistance has been linked to elevated expression of detoxifying enzymes through microarray-based analyses and quantitative PCR [7,8,9]. An epsilon-class glutathione-S-transferase in An. gambiae, GSTE2, and its orthologue in the dengue and yellow fever vector Aedes aegypti, have been linked to DDT resistance through elevated gene expression [10,11]. Recombinant protein expression and in vitro assays also support a role for this enzyme in DDT metabolism [11,12]. In previous studies, GSTE2 was found to be 5–8 fold over-expressed in An. gambiae of the ZAN/U strain, which displays DDT resistance in the absence of mutations in the voltage-gated sodium channel, compared to a susceptible East African mosquito colony (Kisumu) [12,13,14]. The rationale for the current study arose from the serendipitous discovery of allelic differences in GSTE2 in recently re-established colonies of Kisumu and ZAN/U (source www.MR4.org), which exhibited the expected DDT susceptibility/resistance profiles but not the level of differential expression observed previously [12,13]. The ZAN/U colony showed only a 2.34-fold greater expression of
Table 1. GSTE2 allelic variants from the An. gambiae Kisumu and ZAN/U strain used for recombinant protein expression.

<table>
<thead>
<tr>
<th>Cloned variant</th>
<th>Amino acid position</th>
<th>Specific activity (µmoles/mg)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>114</td>
<td>120</td>
</tr>
<tr>
<td>Kisumu 1B</td>
<td>Isoleucine</td>
<td>Leucine</td>
</tr>
<tr>
<td>Kisumu 2B</td>
<td>Isoleucine</td>
<td>Phenylalanine</td>
</tr>
<tr>
<td>ZAN/U 1C</td>
<td>Threonine</td>
<td>Phenylalanine</td>
</tr>
</tbody>
</table>

The position of variant amino acids proximal to the putative DDT binding site are shown; together with the specific activity of the recombinant GSTE2 with substrate CDNB. Protein concentrations were determined using a commercial assay (Fluka – Sigma-Aldrich) based on Bradford assay chemistry[40]. CDNB activity was determined by colorimetric assay and spectrophotometric reading.

doi:10.1371/journal.pone.0092662.t001

Results

Recombinant protein expression and DDTase activity screens

Based upon amino acid sequence, three allelic variants were identified, two within the Kisumu colony and one in the ZAN/U colony (Table 1; GenBank accession numbers: JX840597-JX840599). The three alleles were expressed in Ecoli and each exhibited activity with the substrate CDNB in the presence of GSH; confirming that the expressed proteins were glutathione-S-transferases (Table 1). DDT metabolism assays were performed to determine optimal conditions for kinetic analysis of each variant GSTE2 enzyme with a substrate (DDT) dilution series. At lower concentrations all three variant enzymes displayed comparable activity (Figure 1). However, the ZAN/U-derived GSTE2 protein displayed a significantly higher mean enzyme rate than the two Kisumu proteins at the higher concentrations tested (Figure 1). Enzyme kinetic measurements did not produce markedly different values for maximum enzyme rate (V_max) and the K_M (substrate concentration at half maximum velocity) for the three variants (Table 2). However, the Kisumu alleles did not exhibit standard Michaelis-Menten kinetics (Figure 1), but rather displayed profiles typical of enzymes experiencing substrate inhibition [16,17].

Structural analysis of non-synonymous changes in GSTE2

Molecular modelling was used initially to investigate the mechanistic effect of the amino acid replacements on catalysis. Previously, Wang et al. [15] proposed that a hydrophobic pocket in close proximity to the GSH binding site was the site of DDT binding. Predicted to be of particular importance was the inclination of the C-terminal section of helix H4, which brought residues 112, 116 and 120 closer to the GSH cofactor. These residues also helped to form a pocket ‘cap’ for the putative DDT binding site, which would potentially increase hydrophobicity and therefore affinity for the highly hydrophobic DDT molecule. Our study focused upon two residue exchanges, I114T and F120L, which are located in the C-terminal section of helix H4 and, thus, have the potential to influence DDT binding.

The variable mutation found at position 120, F120L, in the Kisumu strain had potential to affect the formation of the putative DDT pocket cap as the aromatic phenylalanine is replaced with the shorter aliphatic chain of leucine. F120 is predicted to make hydrophobic contact with one of the aromatic rings of the DDT molecule. A leucine residue at this position, being smaller, may not form as tight an interaction with the DDT and, thereby, weaken its binding. The importance of the phenylalanine residue at this position is supported by the likelihood that this is the ancestral allele, as it is fixed in an extensive collection of An. arabiensis from Sudan, Ethiopia, Tanzania and Malawi (collection details in [18] (GenBank accession numbers: JX627247-JX627266). However, enzyme kinetics parameters (Table 2) indicate that the F120L exchange has little influence on substrate affinity or catalysis, suggesting that the aromatic group of phenylalanine is dispensable at this position and not deterministic of DDT affinity.

Position 114 is also situated in close proximity to the predicted DDT binding pocket. The effect of the change from isoleucine, inferred to be ancestral from comparisons with the same An. arabiensis data, to threonine at position 114 was difficult to estimate through modelling. In this case, a destabilizing polar hydroxyl group is introduced in a hydrophobic core region of the protein in ZAN/U, with the potential for marked effects on protein conformation. To better understand the effect of this substitution in enzyme activation, we elucidated the structure of ZAN/U:GSH using X-ray crystallography (Figure 2). The structure, determined to 2.3 Å resolution (R-factor/R-free 17.57/22.78 %; Table S2 in File S1), closely resembles that of the Kisumu enzyme previously reported [PDB entry 2IMI; [15]] (0.5 Å overall rmsd calculated using RAPIDOT [19] (Figure 2) as well as that of GSTE2 from An. funestus most recently elucidated (PDB entry 3ZML). Similar to the Kisumu variant from An. gambiae, the latter carries Ile at position 114. Both enzymes share 93% sequence identity and their structures superimpose with an rmsd of 0.3 Å. The model of ZAN/U calculated in this study shows that the introduced hydroxyl group is stabilized by hydrogen bond formation to the main chain carbonyl group of R110 (calculated using HBOND, J. Overington, unpublished), so that the presence of this polar group in the hydrophobic core does not lead to structural alterations in the enzyme (Fig 2a; a comparison to GSTE2 from An. funestus is shown in Figure S3 in File S1). Interestingly, inspection of electron density maps for all GSTE2 enzymes (Figure 3), calculated using PDB_REDO [20], reveal a disorder of residues F113 and Y133,
Screening of I114T and Vgsc variants in wild-caught, DDT-phenotyped specimens of An. gambiae

We screened for the presence of the I114T mutations in a number of collections of both molecular forms of An. gambiae. Unexpectedly, given that the ZAN/U colony is of the S-molecular form and originates from East Africa, the I114T allele was most common in M-form populations from West Africa (Figure 5). For example in both Benin and Burkina Faso 114T allele was significantly more frequent in M-form (Benin Freq = 0.79; 95%CIs 0.73–0.83; Burkina Faso Freq = 0.59; 95%CIs 0.54–0.63) than sympatric S-form populations (Benin Freq = 0.05; 95%CIs 0.03–0.09; Burkina Faso Freq = 0.12; 95%CIs 0.08–0.17) suggestive that the mutation originated in M-form populations. Consequently we focused genotype: phenotype studies on West African populations, where in addition we were able to investigate potential interactions between the Gste2 variant and two known DDT-linked Vgsc variants that are rare or absent in East Africa.

Female An. gambiae from Benin and Burkina Faso that survived or were killed by 60 minute DDT exposure in standard WHO susceptibility tests[21], were genotyped at the Gste2-114 codon and at the resistance-associated mutations in the voltage gated sodium channel (Vgsc-1014F, commonly termed kdr, and Vgsc-1575Y) [5]. In the M-form specimens from Benin there was a significant association between 114T and DDT survival (allelic test of association p = 8×10−4: Odds Ratio(OR) = 2.35 ; 95%CIs 1.42–3.88). The trend was similar in Burkina Faso specimens but did not reach statistical significance (p = 0.28: OR = 1.27; 95%CIs 0.83–1.93). As expected the Vgsc-1014F mutation was associated with DDT resistance in both locations, Benin (p = 6×10−3; OR = 2.21; 95%CIs 1.40–3.50) and Burkina Faso (p = 5×10−7; OR = 3.05 95%CIs 1.97–4.74).

For the Benin data, where both Gste2-114T and Vgsc-1014F were significantly associated with DDT resistance in univariate analyses, we fitted a general linear model with a logistic link function. In this analysis both mutations remained significantly associated with the ability of mosquitoes to survive DDT exposure (Gste2-114T p = 0.002; Vgsc-1014F p = 0.018). The additive effects of the resistance loci was revealed in both Benin and Burkina Faso by elevated odds ratio for a double mutant haplotype relative to wildtype (OR Benin = 3.13 (95% CIs 1.59–6.15); p = 0.0012: OR Burkina Faso 5.00 (95% CIs 2.51–9.98; p<0.001; Figure 6; Datasets S1 and S2). The third mutation, Vgsc-1575Y, is at low frequency in Benin (Freq = 0.055; 95%CIs 0.02–0.06) precluding association analysis but at a higher frequency in Burkina Faso (Freq = 0.12; 95%CIs 0.09–0.16). In Burkina Faso Vgsc-1575Y was strongly resistance-associated (p = 6.6×10−7) whereas both Gste2-114T (p = 0.051) and Vgsc-1575T (p = 0.039) were on the margins of significance. However, for the triple mutant (Gste2-114T: Vgsc-1014F : Vgsc-1575Y) the odds ratio relative to wild type rose to 12.99 (95% CIs 2.55–66.10; p<0.001; Dataset S2), which

### Figure 1. Comparison of GSTE2 catalysed DDT metabolism for three variant recombinant proteins over a DDT dilution series.

Three allelic variants of enzyme GSTE2 from An. gambiae are compared over a range of DDT concentrations and the mean production of DDE plotted from three replicate assays. Fitted curves used the Michaelis-Menten equation for the ZAN/U allele and a substrate inhibition equation for the two Kisumu alleles doi:10.1371/journal.pone.0092662.g001

which are involved in the mutual packing of two H4 helices across the dimer interface, at a spot that is immediately local to the predicted DDT pocket. This suggests that this region, which constitutes the DDT pocket ‘cap’, has high intrinsic dynamics. Such dynamics could facilitate the motions that take place during substrate binding and/or product release and, thereby, influence catalytic turn-over. Our data suggest that mutations can influence catalysis even when not resulting in detectable structural alterations, most likely by affecting the molecular dynamics of this region.

### Heterologous expression of GSTE2 in Drosophila melanogaster

Heterologous expression in Drosophila melanogaster was achieved for both the Gste2-ZAN/U and Gste2-Kisumu1B alleles (Figure 4). For both alleles ubiquitous expression of An. gambiae Gste2 resulted in an increase in resistance to DDT as assessed by resistance ratio of LC50s (LC50 transformed line/LC50 control). Although, contrary to the recombinant E.coli work (Figure 1), and our a priori expectations, the resistance ratios were apparently higher for Gste2-Kisumu1B (15.15) than Gste2-ZAN/U (5.24).

| Table 2. Enzyme kinetic parameters of three GSTE2 alleles with substrate DDT. |
|-----------------|-----------------|-----------------|-----------------|
|                 | Kisumu 1B       | Kisumu 2B       | ZAN/U 1C        |
| Km_DDT (μM)     | 50.9            | 97.8            | 66.4            |
| Vmax (μmol DDE/min/mg) | 17.0           | 27.2            | 22.9            |
| Kcat (s⁻¹)      | 14.1            | 22.5            | 18.9            |

Three variant GSTE2 proteins were expressed from a DDT resistant (ZAN/U) and susceptible (Kisumu) strain of An. gambiae and assayed with substrate DDT over a range of concentrations. The maximum enzyme rate (Vmax), substrate concentration at half the maximum rate (Km) and catalytic turn-over (Kcat) were calculated for each protein from a Michaelis-Menten or substrate inhibition equation (Figure 1).
translates into an increase in probability of surviving a one hour DDT exposure from 50% to 93%. Nonetheless, over 50% of the variation remained to be explained and may reflect the effects of environmental factors or additional resistance mechanisms (e.g. [8]).

Full-length Gste2 sequences were obtained from 18 M-form individuals used in the Burkinabe genotype: phenotype tests (Genbank accession numbers: KC533009-KC533026). There were no additional non-synonymous mutations that segregated with the 114T mutation providing further evidence that mutation is causal, rather than merely a marker of DDT resistance.

**Discussion**

Our data demonstrate how introgression of adaptively advantageous alleles between the molecular forms of *An. gambiae* can bring together combinations of alleles that enhance insecticide resistance phenotypes. This is yet another example of the evolutionary plasticity of this species complex and vividly illustrates why its members are so extremely difficult to control. The triple mutant described in this study is almost completely resistant to DDT, as assessed using the standard World Health Organization exposure assay. There is no simple association between resistance phenotype and epidemiological outcomes but these data raise...
Figure 4. Dose-response curves for *Drosophila melanogaster* adults transformed with *Anopheles gambiae* Gste2 alleles. The left panel shows survival of control (CyO × UAS+Gste2-Kisumu1B; black circles) and Kisumu allele expressing lines (Actin-Gal4 × UAS+Gste2-Kisumu1B; open circle) together with 95% confidence intervals. The right panel shows survival of control (CyO × UAS+Gste2-ZANU; black circles) and ZAN/U allele (Actin-Gal4 × UAS+Gste2-ZANU; open circle) together with 95% confidence intervals.

doi:10.1371/journal.pone.0092662.g004

Figure 5. Geographical variation in frequency of Gste2-I114T in the S and M molecular forms of *An. gambiae* across Africa. Blue represents the I114 and red the T114 frequency. The molecular form of the collection is indicated by the letter overlaid on each chart. Samples were from: Benin S-form n = 111; M-form n = 223. Burkina Faso S-form n = 115; M-form n = 216. Cameroon S-form n = 55; M-form n = 652. Ghana S-form n = 29; M-form n = 758. Guinea-Bissau S-form n = 38; M-form n = 39. Mali S-form n = 31; M-form n = 26. Uganda S-form n = 207. The base map was obtained from http://en.wikipedia.org/wiki/File:Africa_satellite_orthographic.jpg and was created by NASA. Details of the locations are given in Table S3 in File S1.

doi:10.1371/journal.pone.0092662.g005
Concerns about the efficacy of indoor residual spraying with DDT in parts of West Africa for controlling malaria.

Insecticide resistance in mosquitoes [7,9,11,12,22,23], and other insects [24,25], is commonly linked to elevated expression of detoxifying enzymes. Indeed Gste2 was first implicated in DDT resistance as a result of elevated expression rather than allelic variation [12,13]. However, it seems that the ZAN/U strain used in earlier work bears little relation to that used in this study: in addition to the higher levels of Gste2 expression observed, the amino acid at codon 114 was an asparagine [12,13,26] not the threonine we identify here. The occurrence of the I114T mutant in our ZAN/U strain is probably a result of a contamination event, most likely from an M form colony, followed by selection during routine colony husbandry to maintain the DDT-resistant phenotype. Such inter-colony contamination events are a major problem when rearing morphologically identical mosquito strains[27]. The involvement of metabolic allelic variants in conferring an insecticide resistance phenotype is not without precedent. In the sheep blowfly, Lucilia cuprina, Newcomb et al. [1] highlighted a G135D substitution within a carboxylesterase gene, E3, which conferred broad-spectrum organophosphate (OP) hydrolase activity. The same mutation was subsequently found to confer OP resistance in the housefly Musca domestica [28]. Next generation sequencing of individual An. gambiae (http://www.malariagen.net/node/287) will permit genome-wide association studies of insecticide resistance phenotypes to simultaneously uncover coding and regulatory variants.

The data that were obtained from the heterologous expression of Kisumu and ZAN/U alleles in D. melanogaster are somewhat at odds with our contention that the ZAN/U allelic variant is DDT-resistance associated. However, these data may point to the influence of genotypic background in the penetrance of a resistance-associated variant, as has been observed previously in both An. gambiae and D. melanogaster [6,30]. In an earlier study Drosophila transformed with the Gste2-ZAN/U allele showed DDT LC50 values in excess of those observed here [29].

**Figure 6.** Summary of haplotypic association tests for the combination of four possible allele combinations at the Vgsc-1014 (kdr) and Gste2-114 loci with DDT susceptibility in An.gambiae M-form females from Benin (Panel A) and Burkina Faso (Panel B). Susceptibility to 4% DDT, was determined following a 1hr exposure to followed by 24hr recovery. Odds ratios are given with significance indicated by asterisks (P < 0.0502, **P < 0.01, ***P < 0.001). The arrow is oriented from least to most resistant. The allele combination in bold (Gste2-114T; kdr-Phe) is the double mutant which is significantly associated with DDT resistance. wt = wildtype.

doi:10.1371/journal.pone.0092662.g006

**Mechanism of action of Gste2-114T**

The importance of mutation I114T most likely arises from the creation of an enzyme with increased catalytic activity through predicted increased conformation dynamics and reduced product affinity, facilitating metabolic turnover. The relationship between structure, stability and catalysis of enzymes has been studied extensively in the context of protein thermostability [31]. Enzymes from hyperthermophiles, which grow optimally at elevated temperatures, are often barely active at room temperature but are as active as their mesophilic homologues at high temperatures. It has been proposed that the low activity of the thermostable enzymes at mesophilic temperatures is due to a high structural rigidity, which is relieved at their elevated physiological temperatures. This concept of “corresponding states” highlights the importance of protein dynamics in catalysis [32]. In agreement with this concept, rational protein design and directed evolution have shown that enzyme mutants with reduced stability often exhibit improved catalytic activity compared to the wild-type form, even though structural alterations are often minimal or undetectable (e.g. [33,34]). The lack of notable structural differences between the Kisumu 2B and ZAN/U IC variants and the intrinsic dynamics of the region vicinal to the catalytic site in GSTE2 enzymes led us to speculate an effect of the residue exchanges in protein stability. We predicted changes in stability that might result from mutation of amino acids, I114 and F120, to their smaller replacements, T114 in ZAN/U IC and L120 in Kisumu 1B. The I114T change was predicted as strongly destabilising at 2.85 kcal/mol [35], while the F120L was classified as neutral at –0.98 kcal/mol. The destabilizing effect of the T114 exchange is likely due to the reduction in side chain volume, with the introduced polarity apparently well accommodated in the local environment. The change in volume is greater for position 120, but volume changes in protein cores are especially disruptive [36] and I114 is buried while F120 is largely solvent-accessible. It is position 114 that correlates better with activity and which was shown to associate with phenotype in the phenotypic work conducted in Benin and Burkina Faso (Figure 6). It appears that the 114 mutant drives DDT resistance through dynamic rather than static conformational changes.

**Conclusion**

We describe a variant Gste2-114T that is significantly associated with DDT resistance in M molecular form females from West Africa. This mutation in concert with Vgsc mutations confers...
highly elevated resistance to DDT. Whilst individually the mutations may have a modest effect on resistance phenotype the effect of acquisition of these incremental changes relative to wild-type may be large.

Materials and Methods

Strains

The DDT resistant ZAN/U strain was derived from the ZANDS strain, colonised from Zanzibar and displaying resistance to DDT as larvae [10,37]. ZAN/U was derived from this strain via selection of 1-day old adults with 4% DDT [38]. ZAN/U displays DDT resistance in the absence of known knockdown resistance (kdr) mutations in the sodium channel. The Kisumu strain is fully susceptible to DDT and originates from Kisumu in Western Kenya. Both of these laboratory colonies are of the S molecular form and originate from East Africa. These studies did not involve human participants or endangered or protected species and therefore no ethical clearance of specific permissions were required.

Sequencing of Gste2

Gste2 (GenBank accession number XM3199663.3), for which only a single transcript has been reported, is situated on chromosome 3R at position 28,597,686–28,598,594 (AgamP3.5). Sequence assembly of An. gambiae genome assembly of 3R indicated that only a single transcript has been reported, is situated on chromosome 3R at position 28,597,686–28,598,594 (AgamP3.5). To investigate non-synonymous changes between the strains, sequence data were obtained from ten individual female mosquitoes from both ZAN/U and Kisumu. Primers were designed to amplify a 680 bp fragment encompassing the majority of the three exons. Total DNA was purified from single insects using the DNeasy Blood and Tissue spin column kit (Qiagen). All twenty DNA extracts were confirmed as the S-form of An. gambiae using a PCR-RFLP approach [39]. Gste2 amplicons were sent for direct sequencing (Macrogen, South Korea). Those individuals yielding poor-quality data from direct sequencing were re-amplified and cloned in Escherichia coli using a pGEM-T Easy Vector (Promega) prior to sequencing. All sequences were aligned versus the full Gste2 genomic sequence obtained from VectorBase (http://www.vectorbase.org/) using CodonCode Aligner software (CodonCode Corporation) and synonymous and non-synonymous polymorphisms identified.

Full-length cDNA sequences for Kisumu and ZAN/U Gste2 were produced from RNA extracted from three batches of ten female mosquitoes from each strain using the PicoPure RNA Isolation Kit (Arcturus). RNA concentration was measured (NanoDrop spectrophotometer, Thermo) and approximately 2 µg from each pool used for cDNA synthesis (SuperScript III Reverse Transcriptase, Invitrogen). The cDNA sequence was amplified from cDNA pools using primers situated in the 5' and 3' untranslated regions (Table S1 in File S1) to produce a 683 bp fragment. The amplified Gste2 fragment from each cDNA pool was then cloned into a pGEM-T Easy vector using a PCR fragment. Positive clones from each cDNA pool were selected for sequencing. Selected clones were used to inoculate a 5ml overnight culture from which plasmid DNA was extracted (QIAprep Spin Miniprep Kit, Qiagen). An aliquot of each plasmid was then sent for sequencing (Macrogen, South Korea; GenBank accession numbers: JX940597–JX940599).

Modelling of non-synonymous changes on to the GSTE2 protein structure

The amino acid changes identified in the ZAN/U and Kisumu sequence data were interpreted in the context of the Kisumu GSTE2 crystal structure [ProteinDataBank (PDB) accession code 2IL3] and their potential importance in DDT binding inferred with respect to the residues highlighted by Wang et al. [15] as amino acid positions likely to be involved with DDT binding/metabolism, henceforth termed the catalytic triad. This in silico approach was used to select Gste2 haplotypes that were likely to have differing DDT-ase activity for further recombinant protein and crystallography work. PoPMuSiC [35,36] was used to predict protein stability changes occurring as a result of amino acid changes between the polymorphisms.

Recombinant protein expression and DDTase activity screens

Recombinant protein expression was performed for three Gste2 allelic variants that had non-synonymous changes proximal to the DDT binding site. Gste2 was re-amplified from clones of the cDNA extracts using primers that incorporated a 3'NotI site and a 5' BamHI restriction site (Table S1 in File S1). These restriction sites were exploited to clone the Gste2 alleles into protein expression vector pET15b (Novagen) before transformation into E. coli BL21 (DE3) (New England Biolabs). Cultures were incubated at 37°C (150 RPM) until an optical density of 0.8 (wavelength 600 nm) was reached, then protein production was induced by addition of 1 mM isopropyl-β-D-thiogalactoside (IPTG) at 30°C (150 RPM). A pET15b encoded polyhistidine (6XHis) tag was exploited for purification of GSTE2 using nickel affinity chromatography. Bacterial lysates were prepared by sonication in buffer TSE (50 mM Tris-HCl pH 7.4, 1 mM EDTA, 150 mM NaCl, 10 mM β-mercaptoethanol (β–ME), 1.25 mM MgCl2 and 250 U benzonase) and cell debris removed through centrifugation (10,000 g for 20 minutes at 4°C) and filtration (0.2 µm filter). Crude cell lysate was then applied to a 1 ml nickel-nitrilotriacetic acid (Ni-NTA) agarose (Qiagen) column and washed with 10 column volumes of buffer A (50 mM sodium phosphate, 200 mM NaCl, pH 8.0) containing 20 mM imidazole. Protein was eluted in 10 ml of buffer B (50 mM sodium phosphate, 300 mM NaCl, pH 8.0) containing 250 mM imidazole. Purified GSTE2 was then applied to a PD-10 Desalting Column (GE Healthcare) and eluted in storage buffer [50 mM sodium phosphate, 20 mM Dithiothreitol (DTT), pH 7.4].

Protein concentration was determined using a commercial protein quantification kit (Fluka – Sigma-Aldrich) based on the Bradford protein assay [40] and GST activity confirmed for each purified recombinant variant using the GST substrate 1-chloro-2,4-dinitrobenzene (CDNB) in a standard colorimetric activity assay [41]. The recombinant proteins produced for each of the three GSTE2 variants were of extremely high and consistent purity (Figure S4 in File S1).

The DDT dehydrochlorinase activity of all GSTE2 variants was assessed using an enzymatic assay and High Performance Liquid Chromatography [10]. GSTE2 catalyses the dehydrochlorination of DDT in the presence of glutathione (GSH) to produce 1,1-dichloro-2,2-bis(p-chlorophenyl) ethylene (DDE).[12]. Reverse-phase HPLC using a silica based stationary phase and a 90%:10% methanol:water mobile phase was used to separate DDT, DDE and the spike-in control dicofol according to their polarity. Standard curves were produced for DDT, DDE and dicofol using a doubling dilution series (200 – 12.5 µg/ml). The mobile solvent phase was pumped through the HPLC system (Ultimate 3000) at a rate of 1 ml/minute and 20 µl of each sample injected. Data acquisition was set at 18 minutes as DDE elutes at approximately 14 minutes with DDT eluting at ≥12 minutes, and the UV wavelength 232 nm selected. Compound concentration (µg/ml) was then plotted against the HPLC peak area to produce a graph.
standard curve with the intercept fixed at zero. The equation of this curve was employed to assess DDT, DDE and dieldrin concentration in subsequent assays.

Enzyme kinetics

To compare enzyme activity between variants, a doubling dilution series of DDT from 200–3.125 μg/ml was employed using optimised reaction parameters. Each assay contained 60 μg of GSTE2 enzyme. All variant GSTE2 proteins were assayed at each DDT concentration and a series of three technical replicates performed. The DDE peak area from the HPLC trace was normalised against the dieldrin spike-in area and the adjusted area used to calculate micrograms of DDE produced per ml reaction using the DDE standard curve. The DDE concentration was used to calculate the enzyme rate, expressed as μmol DDE/mg GSTE2 protein/min. Michaelis-Menten and substrate inhibition plots were produced to compare the kinetics of each GSTE2 allele based upon initial substrate concentration (DDT) and rate of product (DDE) formation in R [42]. The maximum enzyme rate (Vmax), the point at which all enzyme active sites are bound to substrate, the Michaelis-Menten constant (Km), which is the substrate concentration for an enzyme at half its maximum velocity and Kcat, a measurement of overall catalytic turn-over rate, were derived from the fitted equations.

X-ray crystallography and corresponding recombinant protein production

The Gste2 variant ZAN/U was cloned into the expression vector pOPIN (Oxford Protein Production Facility-UK) via the In-Fusion PCR cloning system (Clontech). This vector incorporates His6- and SUMO-tags, as well as a SUMO protease cleavage site, N-terminal to the target insert. Protein expression was in E. coli BL21(DE3) Rosetta2 (Novagen). Cultures were grown at 37°C up to an OD600 of 0.6 in Terrific broth supplemented with 50 μg/ml kanamycin and 34 μg/ml chloramphenicol. Expression was induced with 1 mM IPTG and cultures grown for a further 18hr at 25°C. Cells were harvested by centrifugation. The bacterial pellet was re-suspected in lysis buffer (25 mM Tris-HCl pH 8.0, 500 mM NaCl, 5 mM β-ME) and supplemented with 1.25 mM MgCl2 and 250 units of benzamidine before sonication on ice. The homogenate was clarified by centrifugation and affinity purified using a 3 ml Ni-NTA agarose (Qiagen) column equilibrated in wash buffer (lysis buffer supplemented with 20 mM imidazole). Protein was eluted using 250 mM imidazole before over-night dialysis at 4°C against 25 mM Tris-HCl pH 8.0, 200 mM NaCl, 5 mM β-ME to remove imidazole and reduce salt concentration. Tags were removed by incubation with SUMO protease overnight at 4°C (1.7 μl SUMO protease/mg fusion protein). Further purification used subtractive metal affinity and size exclusion chromatography in a Superdex 75 HR16/60 column (GE Healthcare) equilibrated in dialysis buffer. Purified samples were concentrated to 13 mg/ml via Vivaspin column (GE Healthcare). As the apo enzyme was unstable and degraded rapidly, it was supplemented with GSH (1:1.2 molar ratio) and the stabilized complex stored at 4°C until further use.

Crystals of ZAN-U:GSH were grown at 22°C in VDX 24-well plates in hanging drops. Drops consisted of 1 μl protein solution and 1 μl mother liquor containing 30% PEG 6000, 0.1 M Bis-Tris pH 6.5, 1 mM β-ME. Crystals grew within 3 days and exhibited rod morphologies with approximate dimensions of 0.2×0.05×0.05 mm². Crystals were then soaked in mother liquor supplemented with 40% PEG 400 and DDE at saturation for 2 days. For X-ray data collection, crystals were retrieved and shock-frozen in liquid nitrogen. Diffraction data were collected at 100 K on beamline I04 at Diamond (Didcot, UK) and processed using XDS/XSCALE [43]. Processing statistics and crystallographic parameters are given in Table S2 in File S1. The crystal form used in this study contained two biological dimers in its asymmetric unit (four molecular copies). Phasing was by molecular replacement in Phaser[44] using a single molecular copy (A) from PDB entry 2IL3 [15]. The model was manually rebuilt in COOT [45] and TLS refined in Refmac5 using local NCS restraints [46]. Solvent building was in Phenix [47] and COOT. In the final model, the four molecular copies of ZAN/U:GSH were virtually identical (0.42 A overall rmsd calculated with RAPIDO [19]). DDE binding could not be identified in electron density maps. Model and refinement statistics are given in Table S2 in File S1. Model coordinates and diffraction data have been deposited with the ProteinDataBank (PDB accession code 4GSN).

Heterologous expression of GSTE2 in Drosophila melanogaster

cDNA clones including the open reading frames for Gste2-ZAN/U and Gste2-Kisumu1B, were PCR-amplified using high fidelity AccuPrime Pfx polymerase (Invitrogen). The PCR primers used contained EcoRI and Ndel restriction sites within the forward and reverse primers, respectively (Table S1 in File S1). PCR products were gel-purified using the GenElute Gel Extraction Kit (Sigma) and subsequently ligated into a pUASTattB plasmid (obtained from Dr. Konrad Basler, University of Zurich) using T4 DNA ligase (New England Biolabs). Ligation mixtures were transformed into competent DH5α cells for plasmid production, and individual colonies were verified using PCR. The EndoFree Plasmid Maxi Kit (Qiagen) was utilized to obtain purified plasmid DNA for subsequent steps. pUAST-attB clones containing Gste2 inserts were sent to Rainbow Transgenic Flies, Inc. (Camarillo, CA, USA) for injection into Bloomington stock #9750 (y¹ w¹; P{Act5C-GAL4}25FO1/CyO, y¹) and 8–12 experimental transgenic flies were added to each tube. The tubes were capped with cotton wool saturated with a 10% (w/v) sucrose solution. The tubes were placed on their sides and continually oscillated until the entirety of the interior of tube was recorded and LC50 values calculated in the R language [42].

Larvae were kept at 25°C, and G0 flies that eclosed were sorted by sex prior to mating. To establish families of homozygous transgenic flies, G0 flies were crossed to obtain homozygous insertion lines. The following D. melanogaster stocks were obtained from the Bloomington Drosophila Stock Center (Bloomington, IN, USA): y¹ w¹; P{Act5C-GAL4}25FO1/CyO, y¹ and w¹ (BL3605). Virgin females from both types of Gste2 insertion stocks were crossed with Act5C-GAL4/Cyo (ubiquitous Actin5C driver) flies. Control crosses were set up in parallel by crossing heterozygous (Act5C GAL4) driver males to virgin w¹ females.

To create dose response curves Drosophila adults were exposed to a range of DDT concentrations (Figure 4). DDT, dissolved in 100 μl of acetone, was added to 16×100 mm glass disposable culture tubes (VWR Scientific). Tubes were placed on their sides and continually oscillated until the entirety of the interior of tube was coated and all acetone had evaporated. A total of 8–12 control and 8–12 experimental transgenic flies were added to each tube. The tubes were capped with cotton wool saturated with a 10% (w/v) glucose/water solution. Tubes were then incubated at 25°C for 24hr. After 24hr, mortality, (as indicated by absence of movement) was recorded and LC50 values calculated in the R language [42].
Screening of allelic variants in wild-caught, DDT-phenotyped specimens of *Anopheles gambiae*

Data from catalytic assays, modelling and X-ray crystallography suggested that one of the non-synonymous changes had a marked effect on DDTase activity. A TaqMan SNP genotyping assay was designed to screen for the mutation in individual mosquitoes (see Table S1 in File S1 for primer and probe sequences). DNA extracts from adult female mosquitoes from a number of locations in sub-Saharan Africa were genotyped for the *Gste2* allelic variants. In addition female mosquitoes with known DDT susceptibility phenotypes, as defined by the standard WHO protocol, were obtained from Burkina Faso[49] and Benin. SNP genotyping assays were performed in 10 μl volume containing 1x Sensimix (Bioline), 1x primer/probe mix and 1 μl template DNA with a temperature profile of 95°C for 10min followed by 40 cycles of 92°C for 15s and 60°C for 1min on an Agilent Mx3005 real-time PCR machine. VIC and FAM fluorescence was captured at the end of each cycle and genotypes called from endpoint fluorescence using the Agilent MXPro software. Specimens from Benin and Burkina Faso were also screened for known DDT-resistance associated variants in the voltage-gated sodium channel [5,50].

Genotype: phenotype associations were assessed using a generalized linear model with a logit link function [42], chi-squared tests associated variants in the voltage-gated sodium channel [5,50].

Supporting Information

File S1  This file contains Figure S1-S4 and Table S1-S3. Figure S1, Mean normalised expression of *GSTe2* in female *An. gambiae* s.s. of the DDT resistant ZAN/U strain and susceptible Kisumu strain. Expression of *GSTe2* and ribosomal S7 were assessed from ten RNA pools comprised of ten 3 day old female mosquitoes using the GeXP quantitative PCR system (Beckman-Coulter). The ZAN/U colony showed 2.34 fold greater expression of *Gste2* compared with the Kisumu colony. *GSTE2* expression was normalised against housekeeping gene ribosomal S7. Standard error of the normalised mean expression is also indicated. Figure S2, Western blot comparison of *GSTe2* protein level in the Kisumu (Kis) and ZAN/U (Zan) *An. gambiae* s.s. strains. Whole mosquito extracts from 10 unmated 3 day old female mosquitoes from each strain was probed with *An. gambiae* *GSTe2* polyclonal antibody. Approximately 1.7 times more *GSTe2* protein was present in the ZAN/U extract as determined by background corrected pixel intensities using the ImageJ v1.43 software. Ac. aegypti recombinant *GSTe2* was run as a positive control (+). Figure S3, Superimposition of the *GSTe2* enzymes of *An. gambiae* (ZAN/U variant generated in this study containing Thr114; orange) and *An. funestus* (containing Ile114; blue). The GSH ligand is shown in red. a. Overall view; b. close-up of the mutated region of helix H4 showing the altered residue in position 114, and Phe113 at the dimer interface. Figure S4, SDS PAGE gel illustrating the purity of three recombinant variants of *Gste2* isolated from *An. gambiae* s.s. The left panel represents 2.5 μg and the right 1.25 μg of each glycerol stored protein. SDS PAGE performed as previously outlined. Table S1, PCR primers used in the study. Numbers 1 and 2 - *Gste2* promoter region amplification and sequencing. Numbers 3 and 4-amplification of the *Gste2* coding region. Numbers 5 and 6- amplification of the coding region of *Gste2* incorporating the Ndel and BanHI restriction enzyme sites for subsequent cloning into expression vector pET-15b (Novagen). Numbers 7 and 8 Heterologous expression of *GSTE2* in *Drosophila melanogaster*. Numbers 9–12 primers and probes used in the Taqman assay for variants at the 114 codon. Probes 11 and 12 carried a non-fluorescent quencher at the 3’end. Table S2, Statistics for X-ray data and model refinement. The model contains all protein residues with the exception of Ala221 in chain A and C and Lys220-Ala221 in chain D that were disordered in the electron density maps. Table S3, Showing exact collection latitudes and longitudes of the collections used in figure 5. (DOCX)

Dataset S1  (CSV)

Dataset S2  (CSV)

Acknowledgments

Thanks to the Oxford Protein Production Facility for assistance with recombinant protein expression and to the Diamond Light Source for synchrontron radiation time. Dr. Chris Jones provided the specimens from Burkina Faso, which were collected with the assistance of Dr Sagnon N’Fale. Barbara Franke provided support with protein purification.

Author Contributions

Conceived and designed the experiments: SNM DJR MATHM MR JNP OM MJD. Performed the experiments: SNM DJR AD FL CSW DW SD NL AMJ KR PB LD. Analyzed the data: SNM DJR AMJ KR DW OM MJD. Wrote the paper: SNM DJR OM MJD.

References


