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An *ace-1* gene duplication resorbs the fitness cost associated with resistance in *Anopheles gambiae*, the main malaria mosquito

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Widespread resistance to pyrethroids threatens malaria control in Africa. Consequently, several countries switched to carbamates and organophosphates insecticides for indoor residual spraying. However, a mutation in the *ace-1* gene conferring resistance to these compounds (*ace-1^R* allele), is already present. Furthermore, a duplicated allele (*ace-1^D*) recently appeared; characterizing its selective advantage is mandatory to evaluate the threat. Our data revealed that a unique duplication event, pairing a susceptible and a resistant copy of the *ace-1* gene spread through West Africa. Further investigations revealed that, while *ace-1^D* confers less resistance than *ace-1^R*, the high fitness cost associated with *ace-1^R* is almost completely suppressed by the duplication for all traits studied. *ace-1* duplication thus represents a permanent heterozygote phenotype, selected, and thus spreading, due to the mosaic nature of mosquito control. It provides malaria mosquito with a new evolutionary path that could hamper resistance management.

Vector-borne diseases, among which malaria is preeminent, cause a considerable burden on human population¹. In West-Saharan Africa, *An. gambiae* is the major malaria vector. Malaria accounts for 11% of the total population and accounts for an estimated 2.5 million deaths annually, with the majority of deaths occurring in children under the age of five². The use of chemical insecticides has been a major strategy for malaria control. However, the widespread resistance to pyrethroids (PYR), carbamates (CX) and organophosphates (OP)³. The control of *Anopheles* breeding sites is also important, and the main objective of malaria control is to reduce the mosquito population by using insecticide-treated bed nets (ITN) and indoor residual spraying (IRS).

Until recently, PYR was the only insecticide used for ITN and the most effective for IRS^{4,6,12}. However, the use of PYR has been hampered by the emergence of resistance to PYR in *Anopheles* populations. This has led to a decline in the effectiveness of PYR, and the use of alternative insecticides such as IRS and CX is being explored. However, the use of IRS and CX is limited by the high cost of these insecticides and the need for specialized personnel to apply them. The use of IRS and CX is also limited by the high cost of these insecticides and the need for specialized personnel to apply them.

In order to overcome the resistance to PYR, alternative insecticides are needed. However, the use of alternative insecticides is limited by the high cost of these insecticides and the need for specialized personnel to apply them. The use of IRS and CX is also limited by the high cost of these insecticides and the need for specialized personnel to apply them.

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high mortality of PYR-resistant (*kdr^R*) *An. gambiae* in Iwo Coa and Benin^{22, 24}, following the American Pesticide Resistance Monitoring Initiative in collaboration with the National Malaria Control Program, and the African Consortium for the Elimination of the Anopheles Gambiae from PYR-resistant CX (i.e. bendiocarb) or OP (i.e. chlordane) if necessary for IRS^{22, 25, 26}.

However, a critical concern for the use of OP and CX is the emergence of insecticide resistance in *An. gambiae* following the introduction of organophosphate and carbamate insecticides to the region of Iwo Coa and Benin^{31, 32}, highlighted by the emergence of a mutation in the *ace-1* gene: a single amino acid substitution in the binding site of the organophosphate esterase (AChE1) encoded by the *ace-1* gene: a point mutation of glutamic acid to valine at position 119 (G119S) resulting in a major conformational change³³. This *ace-1^R* is an allele that is widespread in the region of Iwo Coa and Benin^{34, 35}. In *Culex pipiens* mosquito, the emergence of insecticide resistance is also associated with the *ace-1^R* mutation in *An. gambiae* (a single amino acid substitution in the binding site of the organophosphate esterase) (Fig. 1), highlighting the importance of insecticide resistance management in the absence of OP and CX insecticides, and the need to monitor the spread of insecticide resistance in the region of Iwo Coa and Benin (Fig. 1), highlighting the importance of insecticide resistance management in the absence of OP and CX insecticides, and the need to monitor the spread of insecticide resistance in the region of Iwo Coa and Benin.

Work in the region of Iwo Coa and Benin has shown that the *ace-1* allele has been found in *An. gambiae* and *An. coluzzii* in the West African region (e.g. Iwo Coa and Bkina Faso)^{41, 42}. This allele, named *ace-1^D*, consists of a duplication of the *ace-1* gene, resulting in a resistant and a sensitive copy, probably on the same chromosome. Several duplicated alleles have been observed in *Cx. pipiens*^{43, 44}, where they have been shown to be selected because they reduce the mortality of the G119S mutation^{45–47}. An insecticide resistance allele is also described in *Drosophila melanogaster* in the duplication of the *ace-1* gene⁴⁸. A similar insecticide resistance allele of *An. gambiae* *ace-1^D* allele is also found in the region of Iwo Coa and Benin, the emerging OP and CX insecticide resistance in malaria control programs. This is a critical case of the emergence of the *ace-1^D* duplication in the region of Iwo Coa and Benin, both in the presence and absence of insecticides.

To do so, we conducted a laboratory experiment using the *ace-1^D* allele and having a genetic background similar to the *An. gambiae* *ace-1^S* and *ace-1^R* allele, a mosquito population of the region of Iwo Coa and Benin. We analyzed the genetic structure of the duplicated *ace-1* gene by a phylogenetic approach and compared the heterozygous form of OP and CX insecticide resistance, a well-established life history trait. This is demonstrated by the *ace-1^D* allele indeed emerged, highlighting the emergence of the *ace-1^D* allele in the region of Iwo Coa and Benin.

Results

Characterization of the *Acerduplikis* strain carrying *ace-1* gene duplication. We collected larvae from a field population of *An. gambiae* in Bagida⁴⁹, a region selected to contain *ace-1^D* allele, because of the large area of emergence of the *ace-1* locus⁴². A non-mutational molecular epidemiological approach for the detection of *ace-1* duplication, identified the genetic structure of the *ace-1* gene in *Cx. pipiens* mosquito, or identify female having *ace-1^D* allele (S vs. Fig. 1). The *ace-1^D* allele is composed of sensitive, D(S), and resistant, D(R), copies (see nomenclature in Labbe *et al.*⁴³), respectively, and were identified in 16 female (2241 bp PCR fragment from 2000–2007), and all D(S) copies were found identical, as were all D(R) copies. The D(R) copy is identical to the known *ace-1^R* allele³² and differs from the D(S) copy by 24 mutations (S vs. Fig. 2). Both D(S) and D(R) copies were found identical to the sequence of the *ace-1^D* allele first identified in *An. gambiae* in Mali⁴¹. Phylogenetic analysis of the 16 founding female demonstrated a close relationship with the *Acerduplikis* strain.

The mean length of *ace-1* gene copies was estimated for 20 *Acerduplikis* and *KimP* mosquito in the Real-time quantitative PCR. Differences in copy number among D/D and S/S genotypes are expected by comparing the following linear model $Cn = \text{Geno} + \varepsilon$, where Cn is the copy number, Geno is the genotype (S/S or D/D) of each individual and ε is the error term (Gaussian distribution). I compared the *Acerduplikis* and *KimP* (1.00 ± 0.05; LRT, $F = 329.9$, $\Delta df = 1$, $p < 0.001$, S vs. Fig. 3).

A search for *in situ* hybridization (FISH) approach was used to identify the location of the *ace-1* D(S) and D(R) copies of *Acerduplikis* *ace-1^D* allele on the chromosome. To overcome the complexity of *ace-1* and AGAP001373 (probe 2), which are separated by about 500 kb on the 2R chromosome of *An. gambiae*. One approach was to use a single signal with the *ace-1* probe, as the same location for both *KimP* and *Acerduplikis* (Fig. 1A, B). However, the signal was observed for *Acerduplikis*. When the probe was co-hybridized on *Acerduplikis* chromosome, the observed signal was a single signal, the observed copy number of the *ace-1* probe and the *ace-1* probe 2 (Fig. 1C). This result indicates that the *ace-1* duplicated allele is in tandem and separated by a distance less than 500 kb.

Finally, since we aimed at determining the impact of *ace-1^D* allele on mosquito survival, we performed a competition experiment to compare the fitness of the sensitive *KimP* genotype with the duplicated *ace-1^D* allele on mosquito survival. We compared the fitness of the *KimP* and *Acerduplikis* (a mixture of

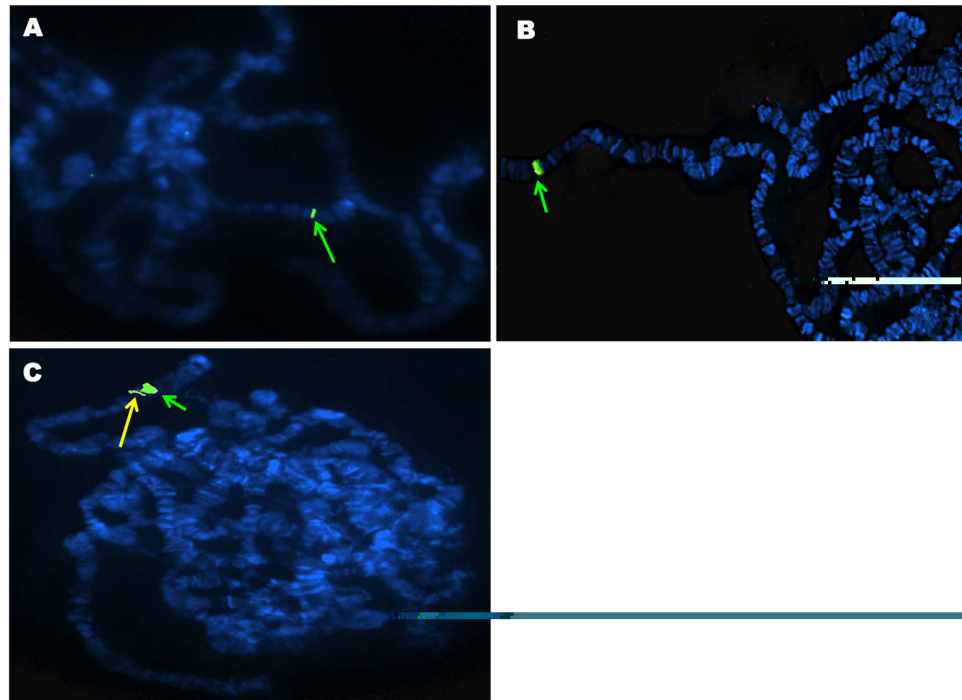


Figure 1. *In situ* hybridization with Cy3 fluorescently labelled DNA probes performed on polytene chromosomes of *An. gambiae* strains. Green and yellow arrows indicate *ace-1* and AGAP001373 probe hybridization. (A) *ace-1* probe hybridized on Ki m P strain; (B) *ace-1* probe hybridized on Ace d _liki strain; (C) *ace-1* and AGAP001373 probe co-hybridized on Ace d _liki strain.

10 individuals from the Bagida field population (collected on each chromosome (S₁–S₁₀, Table 1). The Ace d _liki strain had all the Ki m P markers, although the Ace d _liki genomic background is similar to that of Ki m P. Although recombination and the *ace-1* gene is not, most of the background is eliminated, allowing a clean assessment of the duplication's effect.

***ace-1^D* provides less resistance to carbamates and organophosphates insecticides than *ace-1^R*.** Bioassays were carried out on larvae from the heterozygous Ki m P (S/S), Ace ki (R/R) and Ace d _liki (D/D) strains and from the F1 offspring (R/S, D/S and D/R genotypes). One CX (bendiocarb), three OP (chlorfenvinphos, fenitrothion and dichlorvos) and one PYR (permethrin) were tested. For all larval bioassays, mortality in control was not exceeded 5%. Statistical analysis (chi-square test) were observed and the *ace-1^D* strain (dead number) indicated good for the log-dose mortality regression (all *p*-value > 0.05, Table 1, S₁–S₁₀, Fig. 4). Moreover, the same susceptibility to permethrin was observed for Ki m P, Ace ki (RR₅₀ = 1, *p* > 0.05) and Ace d _liki (RR₅₀ = 1, *p* > 0.05) although the absence of the hybrid resistance mechanism (Table 1). In larval competition with only *ace-1* combined with OP and CX resistance in the heterozygous Ace d _liki strain (D/D) did not affect the resistance to CX (bendiocarb, RR₅₀ = 3.14 vs 229.3, *p* < 0.001) and OP (chlorfenvinphos, RR₅₀ = 1.91 vs 9.03, *p* < 0.001; fenitrothion, RR₅₀ = 6.56 versus 23.74, *p* < 0.001; dichlorvos, RR₅₀ = 8.78 vs 12.61, *p* < 0.001) than Ace ki (R/R; Table 1, S₁–S₁₀, Fig. 4). While D/D individuals did not affect the resistance to the R/S heterozygote for all the tested OP (all *p*-value > 0.05), and significantly affected the resistance to the CX (bendiocarb) (*p* < 0.001). For all the tested insecticides, D/S and D/R heterozygotes did not affect the resistance, significantly and significantly higher resistance to all pesticides (all *p*-value < 0.001) than D/D individuals (Table 1), but D/R individuals did not affect the resistance to the R/R individuals (all *p*-value < 0.001). From the least to the most resistant, the genotype order is: SS < DS < DD ≈ RS < DR < RR.

***ace-1* duplication induces low, if any, fitness cost.** To measure the net cost of the *ace-1* duplication, the adult life history parameters were compared in Ace ki (R/R), Ace d _liki (D/D) and Ki m P (S/S).

Larval mortality and development time. Pre-imaginal mortality was followed from egg hatching to adult emergence. The number of dead larvae at each developmental stage was recorded, allowing the

ace-1 genotypes	Insecticides														
	Bendiocarb			Chlorpyrifos-methyl			Fenitrothion			Dichlorvos			Permethrin		
	^a LC ₅₀ (mg/L)	^b RR ₅₀	^c Chi(p)	^a LC ₅₀ (mg/L)	^b RR ₅₀	^c Chi(p)	^a LC ₅₀ (mg/L)	^b RR ₅₀	^c Chi(p)	^a LC ₅₀ (mg/L)	^b RR ₅₀	^c Chi(p)	^a LC ₅₀ (mg/L)	^b RR ₅₀	^c Chi(p)
S/S (Ki m)	0.22	NA	0.99	0.004	NA	0.99	0.003	NA	0.99	0.008	NA	1	0.006	NA	0.99
R/R (Ace ki)	50.1	229.3	0.99	0.036	9.04	1	0.061	23.74	0.99	0.096	12.61	0.99	0.006	1	0.99
R/S	27.04	123.9	0.99	0.007	1.72	0.99	0.021	8.39	0.91	0.05	6.4	0.99	NA	NA	NA
D/S	0.28	1.29	1	0.006	1.56	0.99	0.016	6.28	0.99	0.04	5.4	0.99	NA	NA	NA
D/R	26.96	123.5	0.99	0.013	3.21	0.99	0.042	16.57	0.99	0.06	7.62	0.99	NA	NA	NA
D/D (Ace d liki)	0.68	3.14	1	0.007	1.91	0.99	0.022	8.78	0.99	0.05	6.56	1	0.006	1	0.99

Table 1. Dose-mortality responses to different insecticides observed in reference strains of *Anopheles*

***gambiae* s. s.** ^aLC₅₀: lethal concentration in milligram per liter indicating a mortality of 50%. ^bRR₅₀: relative resistance to LC₅₀ = LC₅₀(reference strain)/LC₅₀(Ki m). ^cChi(p): the *p*-value of chi-square test for linearity of the dose-response; *p*-value > 0.05 indicates acceptable (i.e. linearity not rejected).

found to be in accordance with the theoretical model. A Co-spatial model (Co-spatial model) was fitted to the data: $S \sim G + \epsilon$, where S is the proportion of dead larvae at each developmental age, G is the expected proportion of dead larvae based on the di-allelic genotype (S/S, D/D, R/R) and ϵ is the error term, following a binomial distribution. The expected proportion of dead larvae for each genotype was calculated as follows: $m_{RR} = 0.71$ [0.60–0.79]; $m_{DD} = 0.43$ [0.32–0.52]; $m_{SS} = 0.29$ [0.20–0.38] (the 95% confidence interval, or CI, are given in brackets).

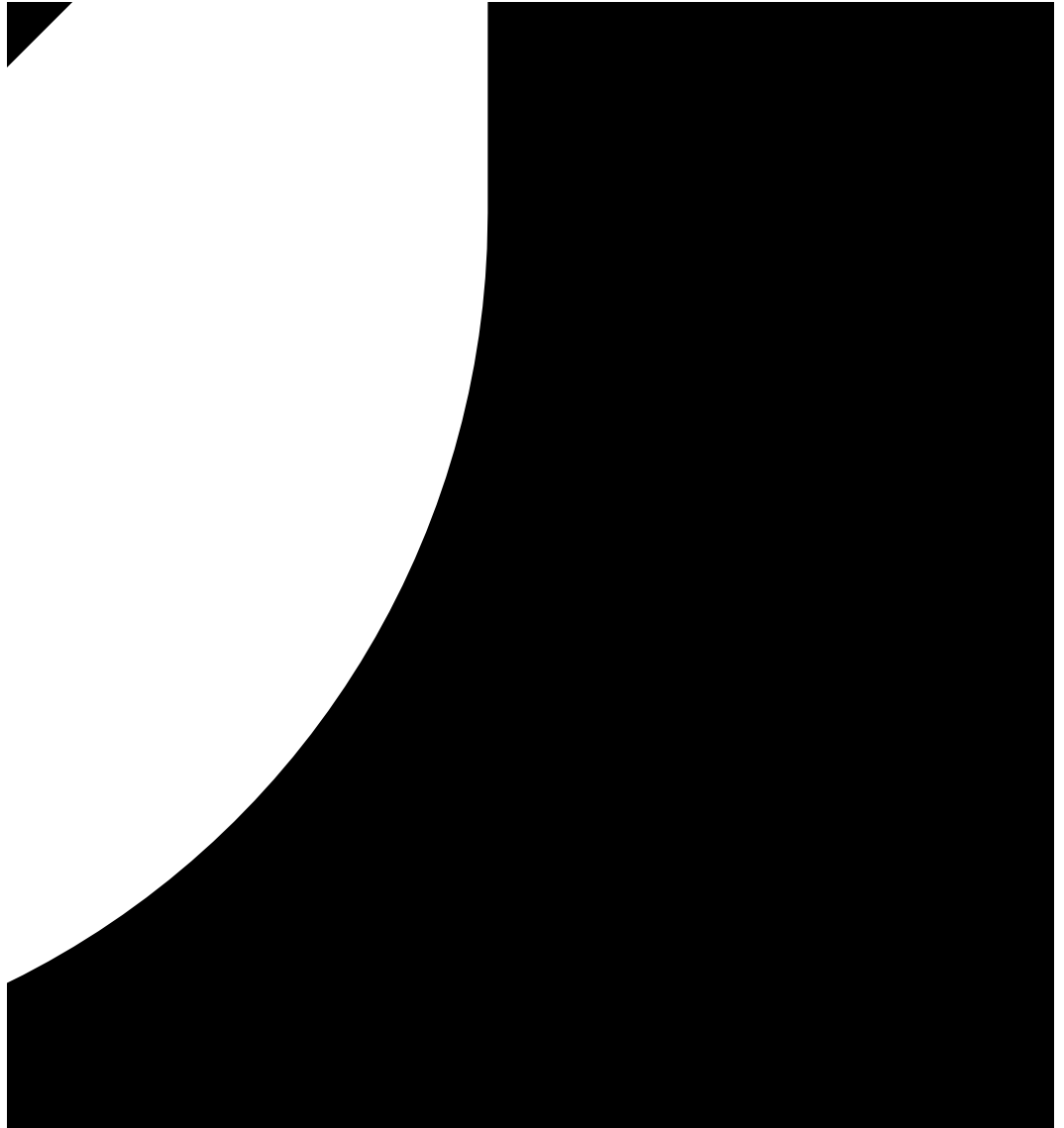
Development time. The number of days taken for a larva to reach adulthood (i.e. the emergence time) was recorded for each genotype and/or sex. The expected emergence time for each genotype was calculated using the following model: $D = G + S + G + S + \epsilon$, where D is the number of days taken for a larva to reach adulthood, G is the expected emergence time for each genotype, S is the sex effect (male or female), and ϵ is the error term (binomial distribution).

No interaction between genotype and sex was detected ($\chi^2 = 2.22$, $\Delta df = 2$, $p = 0.33$) allowing the comparison of each genotype independently. A sex effect was detected in *An. gambiae*⁵⁰, male emergence time was significantly longer than female (mean ± SD: 8.5 ± 1.2 and 9.2 ± 1.3 days; $\chi^2 = 8.9$, $\Delta df = 1$, $p < 0.01$). D/D individuals emerged significantly faster than R/R individuals (mean ± SD: 8.7 ± 1.3 and 10.5 ± 0.84; $t = 7.85$, $df = 76.05$, $p < 0.001$). The mean emergence time was not significantly different between D/D and S/S individuals (mean ± SD: 8.7 ± 1.3 and 8.2 ± 0.7; S den = 0.83, $df = 50.67$, $p = 0.41$; Fig. 2B). However, the Co-spatial model showed a significant difference between D/D and S/S individuals (i.e. emergence time was longer and the adult emergence was lower; $z = 3.8$, $p < 0.001$; Fig. 2B).

Mating competition. Mating competition was tested between pairs of male of different genotypes or combinations of genotypes in a pair of Ki m P (S/S) or Ace d liki (D/D) female. A generalized linear model (GLM) was used to compare the proportion of mating success among competing males: $P = P + F + P + F + \epsilon$, where P is the proportion of mating success (number of eggs laid by a given male genotype), F is the sex effect (male or female), and ϵ is the error term (binomial distribution).

The female genotype did not significantly affect the proportion of mating success, either among the pairs (F: $\chi^2 = 0.07$, $\Delta df = 2$, $p = 0.97$) or for a given pair (F: $\chi^2 = 2.22$, $\Delta df = 1$, $p = 0.33$). However, the proportion of mating success was significantly affected by the genotype of the male (P: $\chi^2 = 11.25$, $\Delta df = 2$, $p < 0.01$). Both the D/D and the S/S male showed a higher proportion of mating success than R/R male (i.e. Δ proportion > 0.5): in DD vs RR pair, D/D proportion of mating success was 0.68 ± 0.11 (> 0.5, Binomial test: $p < 0.001$), while in SS vs RR pair, S/S proportion of mating success was 0.68 ± 0.12 (> 0.5, Binomial test: $p < 0.001$). Pairwise comparisons of the D/D and S/S males showed no significant difference in the proportion of mating success for the R/R male ($\chi^2 = 0.02$, $df = 1$, $p = 0.89$) or for each of the: in DD vs SS pair, D/D proportion of mating success was 0.48 ± 0.08 (no difference from 0.5, Binomial test: $p = 0.63$) (Fig. 2C).

Female fecundity and fertility. In order to assess the influence of the different alleles on the female fecundity and fertility, the number of eggs laid and the number of eggs that hatched were recorded for each genotype (S/S, D/D and R/R) and for each sex.



Overall, the proportion of R/R female progeny can be (on average 21.5 ± 22 lae female) than D/D or S/S female (respectively, on average 33.1 ± 24 and 37.6 ± 33 lae female; Fig. 2D) (GLM $R^2 = \text{Geno} + \varepsilon$ (Gaussian distribution), $F = 7.04$, $\Delta df = 1$, $p < 0.01$). Moreover, the difference between D/D and S/S female progeny can ($F = 0.56$, $\Delta df = 1$, $p = 0.46$). The observed difference is due to the fact that R/R female larvae are egg-eaten by the mother; the number of female larvae ingested and the hatching rate are not significantly different between the two genotypes. For detailed analysis see Supplemental Material S11 Fig. 3.

Overall, the order of the genotype from the mother is: $SS \approx DD < RR$.

Discussion

A more detailed African continent-wide survey of the *ace-1* gene duplication in *Anopheles gambiae* is needed to clarify the evolutionary history of the *ace-1* gene duplication in *An. gambiae*. We conducted a laboratory-based survey of the *ace-1^D* allele, highlighting the background of the *ace-1* gene duplication in *An. gambiae* in Mali, Burkina Faso, and Benin. We then conducted a field survey of the *ace-1* gene duplication in *An. gambiae* in Mali, Burkina Faso, and Benin. We found that the *ace-1^D* allele is widespread in *An. gambiae* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides. Our findings suggest that the *ace-1* gene duplication is a recent event in *An. gambiae* and is associated with resistance to insecticides.

A new resistance allele at the *ace-1* locus. In *Cx. pipiens*, 13 distinct *ace-1* duplication alleles have been identified so far^{44,51,52}, some of which are also found in *An. gambiae*. Although the exact evolutionary history of these alleles is unclear, they appear to have originated in *An. gambiae* and spread to *Cx. pipiens* through gene flow.

In *An. gambiae*, a single *ace-1^D* allele was first reported in West Africa: the *ace-1^D* allele was first identified in Mali in 2006⁴¹. It is now widespread in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides. The *ace-1^D* allele is also found in *Cx. pipiens* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides. The *ace-1^D* allele is also found in *An. gambiae* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides. The *ace-1^D* allele is also found in *An. gambiae* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides.

***ace-1* duplication sets a new evolutionary path for *Anopheles gambiae* resistance.** Current models for the evolution of the *ace-1* locus in *An. gambiae* are based on the assumption that the *ace-1^D* allele arose from a duplication of the *ace-1* gene. However, recent studies have shown that the *ace-1^D* allele is associated with a specific haplotype of the *ace-1* locus, suggesting that the *ace-1^D* allele may have arisen from a duplication of a specific *ace-1* allele. This suggests that the *ace-1^D* allele may have arisen from a duplication of a specific *ace-1* allele, rather than from a duplication of the *ace-1* gene.

Insecticide resistance is a major public health problem in many parts of the world. The *ace-1* gene duplication is a key factor in the evolution of insecticide resistance in *An. gambiae*. The *ace-1^D* allele is associated with resistance to insecticides, and is widespread in *An. gambiae* in Mali, Burkina Faso, and Benin. The *ace-1^D* allele is also found in *Cx. pipiens* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides. The *ace-1^D* allele is also found in *An. gambiae* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides.

An. gambiae major life history traits, such as the timing of emergence, mating, and feeding, are influenced by the *ace-1* gene duplication. The *ace-1^D* allele is associated with a specific life history phenotype, and is widespread in *An. gambiae* in Mali, Burkina Faso, and Benin. The *ace-1^D* allele is also found in *Cx. pipiens* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides. The *ace-1^D* allele is also found in *An. gambiae* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides.

While the *ace-1^D* allele is associated with resistance to insecticides, it is also associated with a specific life history phenotype. The *ace-1^D* allele is associated with a specific life history phenotype, and is widespread in *An. gambiae* in Mali, Burkina Faso, and Benin. The *ace-1^D* allele is also found in *Cx. pipiens* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides. The *ace-1^D* allele is also found in *An. gambiae* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides.

As a result of the *ace-1^D* allele, the *ace-1^D* allele is associated with a specific life history phenotype. The *ace-1^D* allele is associated with a specific life history phenotype, and is widespread in *An. gambiae* in Mali, Burkina Faso, and Benin. The *ace-1^D* allele is also found in *Cx. pipiens* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides. The *ace-1^D* allele is also found in *An. gambiae* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides.

***ace-1^D* is bad news for malaria vector control in areas with high PYR resistance.** Although the *ace-1^D* allele is associated with resistance to insecticides, it is also associated with a specific life history phenotype. The *ace-1^D* allele is associated with a specific life history phenotype, and is widespread in *An. gambiae* in Mali, Burkina Faso, and Benin. The *ace-1^D* allele is also found in *Cx. pipiens* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides. The *ace-1^D* allele is also found in *An. gambiae* in Mali, Burkina Faso, and Benin, and is associated with resistance to insecticides.

Genetic background characterization. A eighth backcross, most of the Ace d₁ liki strain are expected to be in genetic background: a 5% ik, all the genome except 30cM around the *ace-1* locus expected to have recombined³⁶. To check his in origin, we developed a lea-one molecular marker for *An. gambiae* chromosome has a polymorphic been individual from the Kisumu P strain and a third of individuals from the Bagida wild population are able to Ace d₁ liki (S₁ Table 1). The polymorphic marker is then screened on DNA extracted from a mixture of about 100 Ace d₁ liki in a larvae.

Specific molecular tests. All PCR were performed with 50 ng of genomic DNA in 40 μL final volume following conditions: 94 °C for 30 s, annealing temperature for 30 s, and 72 °C for 1 or 2 min for a total of 33 cycles (time and annealing temperature are listed in S₁ Table 1).

D(S) copy specific PCR-RFLP test. A PCR using En3 primer and AgE 4e 2 primer amplified a 511 bp fragment from all *An. gambiae ace-1* allele (S₁ Tab. 1 and S₁ Fig. 2). The restriction enzyme AalI cut the *ace-1^S* and *ace-1^R* allele in order of fragments (28 bp and 483 bp), and the D(S) copy in order of fragments (28 bp, 119 bp and 363 bp). 10 μL of the PCR product were digested with 5 μL of enzyme for 1 h at 37 °C.

KisumuP specific PCR test. A PCR using Kisumu 2 and Kisumu 1 primer is specific to the Kisumu P *ace-1^S* allele; none of the other *ace-1* allele were amplified (S₁ Fig. 2).

***ace-1^D* sequencing.** Genomic DNA from single mosquito was amplified using the AgE 2di 1 and AgE 4e 2 primer (2241 bp PCR fragment, from exon 2 to exon 7 (S₁ Fig. 2). PCR product were purified using the QIAquick Gel Extraction Kit (QIAGEN). For the Kisumu P and Ace ki strain, the purified PCR product was directly sequenced. For Ace d₁ liki, the purified PCR product was cloned using the TOPO TA Cloning kit following the manufacturer instructions (In vitro Gen Life Science Technologies), ordered and then sequenced. D(S) or D(R) clones were screened for the presence of the G119S mutation, and a lea-one clone were screened for each copy. Sequencing was conducted on an ABI Prism 3100 sequencer (BigDye Terminator 3.1, Applied Biosystems, Foster City, CA). Each clone was sequenced using the primer AgE 2di 1 and AgE 4e 2, in an internal primer distance of the fragment length, AgIn di 1 (S₁ Fig. 2). Exon 2 to exon 7 sequence of the sequenced single-copy allele from Kisumu P (Ag-*ace-1^S*), of the internal single-copy allele from Ace ki (Ag-*ace-1^R*) and of the sequenced (Ag-*ace-1^D*-S) and internal (Ag-*ace-1^D*-R) copy of the duplicated allele is deposited in GenBank (accession numbers: KM875634, KM875637, KM875635 and KM875636, respectively).

***ace-1* duplication mapping.** Only the Kisumu P and Ace d₁ liki were used as his age.

Chromosomes preparation. Ovaries were collected from 4 day-old half-grown female, 25 h blood-feeding, a Chiohe's Stage III of development⁶⁷, and were embedded in fresh Carnoy's solution (3 volumes ethanol: 1 volume glacial acetic acid). Ovaries were fixed for 24 h at room temperature and ordered at -20 °C. Polyene chromosome slides were prepared as described by Shaakhov et al.⁶⁸.

Probes preparation. Probe 1 is specific to the *ace-1* gene and probe 2 is specific to the AGAP001373 gene, located about 500 kb from *ace-1* on chromosome 2R in *An. gambiae* genome (http://www.cebola.eo.g/Ano.gambiae). Using Kisumu P DNA, the probe 1 2241 bp fragment was amplified with AgE 2di 1 and AgE 4e 2 primers and the probe 2 1861 bp fragment was amplified with Ag0.5MBdi 2 and Ag0.5MB e 2 primer (S₁ Table 1). The fragments were cloned in the TOPO TA Cloning kit following the manufacturer instructions (In vitro Gen Life Science Technologies). DNA probes were labeled with a ³²P in the DIG-Nick Translation Mix (DIG-labelling kit) according to the manufacturer protocol (Roche Diagnostic). Hybridization and detection followed a standard procedure⁶⁹. Fluorescence images were recorded using a Zeiss 10 microscope equipped with a e-con and a e-cence image analysis (Cytion 3.93.2). The polymorphic chromosome slides were hybridized for each strain and each probe hybridized for Ace d₁ liki strain with probe 1 and probe 2.

Acerduplikis *ace-1* copy number quantification. The number of *ace-1* gene copies was estimated using the qPCR method. The primer pair AGAP010592 = AgR 17 (found in a single copy in the Peruvian genome, VectorBase http://www.vectorbase.org/). Real-time quantitative PCR was performed with a LC480 Light Cycler (Roche). For each PCR performed on each DNA, one specific of *ace-1* locus (Agace1 idi 2 and Agace1 i e 2 primer) and the other specific of the reference gene (AgS7E 5 idi and AgS7E 5 i e primer) (S₁ Table 1). 1 ng of each genomic DNA (normalized with the Qiagen 2.0 Fluorometer - In vitro Gen) was amplified with 0.6 μM or 0.8 μM of *ace-1* or *Rps7* specific primers respectively and 3 μL of master mix (Light Cycler 480 SYBR Green, Roche). PCR was performed with a 95 °C activation for 8 min followed by 45 cycles of 95 °C for 14 s, 67 °C for 13 s, and 72 °C for 19 s. Each DNA was analyzed in triplicate for both genes. The ratio between *ace-1* and *Rps7* was a concentration was determined with the Advanced Relative Quantification method of the Light Cycler 480 software 1.5.0.

Bioassays with Carbamate and Organophosphate insecticides. Resistance data for the hee strain (Kisumu P, Ace ki and Ace d₁ liki) and the F1 offspring (*ace-1* genotype R/S (Ace ki

Ki m P), D/S (Ace d \bar{l} iki \rightarrow Ki m P) and D/R (Ace d \bar{l} iki \rightarrow Ace ki)) e e com \bar{l} ed. Fi e in ecicide of echnical g ade ali e e ed, one CX: bendioca b (99.5% \bar{l} e), h ee OP : chl \bar{o} ifo me h l (99.9% \bar{l} e), feni o hion (95.2% \bar{l} e) and dichlo o (98.9% \bar{l} e), and one PYR: e me \bar{h} in (98.3% \bar{l} e). In ecicide ol ion e e \bar{l} ed in 70% e hanol and o ed a 4 C in a da k oom o a oid ho ol i. A e of 25 la e hi d- and ea l fo h-in a la ae a inc ba ed in 99 ml of di illed a e in la ic c \bar{l} , o hich 1 ml of in ecicide ol ion a he e i ed concen a ion a dded. Fo e lica e e e \bar{l} fo med fo each concen a ion. Si \bar{e} o el e in ecicide concen a ion \bar{l} o iding a ange of mo ali f, om 0 o 100% e e ed fo each in ecicide e ed. La al mo ali a eco ded a e a 24 ho e \bar{l} e. Con ol bioa a e e \bar{l} fo med b adding 1 ml of g hanol \bar{v} 99 ml of di illed a e. Tem e a e a main ained a 27 C \pm 2 C d ing bioa a y (em e a e mea ed ing Wa ne echnolog, Wa ne Sol ion, SAS, A ch, F ance).

T \bar{l} e anal e of do e-mo ali e \bar{l} on e in bioa a e e \bar{l} fo med ing he R o a e (.3.0.0). e R ci \bar{l} BioR a (.6.1;7 $\bar{4}$) a ed; i i feel a ilable on he eb i e of he In i de Science de l'E o \bar{l} jon de Mon \bar{l} ellie. i c i \bar{l} com \bar{l} e y he do e of in ecicide killing 50% and 95% of he e ed \bar{l} la ion o ain (Le hal Concen a ion 50 and 95, o LC $\bar{50}$ and LC $\bar{95}$) and he a ocia ed con dence in e al, and e fo he linea j of he do e-mo ali e \bar{l} on e (χ^2 e). Final, i allo he com a i on of o o mo e \bar{l} ain o \bar{l} la ion and calc la e he e i ance a io, i.e. RR $\bar{50}$ o RR $\bar{95}$ (=LC $\bar{50}$ o LC $\bar{95}$ of e ed \bar{l} la ion/LC $\bar{50}$ o LC $\bar{95}$ of he efe ence ain, e \bar{l}) and hei 95% con dence in e al.

Fitness cost parameters. *Larval mortality and development time.* To a e \bar{l} he de elo men ime and \bar{l} e-imaginal mo ali a ocia ed i h di e en *ace-1* allele, a a e e \bar{l} fo med a de c ibed b Agne *et al.*⁷¹. Female \bar{y} , o i b i ion a nch on i ed fo he h ee ain. A egg ha ching, 96 \bar{y} -in a la ae f om each ain e e indi id \bar{y} all an fe ed o *Drosophila* be fo ea ing in 1 ml of mine al a e a 2 g/L concen a ion of Te aM \bar{n} \bar{l} o de ed h food (Te amin Bab Min, Te a Gmbh, Melle, Ge man). Food a \bar{l} o ided once, he da of e \bar{l} imen. T be e e a \bar{l} rged on ack and main ained in in ec a condi ion (27 \pm 2 C, 80 \pm 2 h midi, 12 h: 12 h high :da k). e ack e e andoml mo ed e e da \bar{y} o ed ce \bar{l} o i onal e ec. Dead la ae o \bar{l} ae e e con ed e e da o a e he mo ali \bar{y} a e a \bar{y} each de elo men age. Timing of ad l eme gence a al o eco ded \bar{y}

Mating competition. Vi gin ad l (o-da old) ea ed nde labo a o anda d condi ion e e c o ed in cage (30 cm \times 30 cm \times 30 cm). T ial e e \bar{l} fo med be een \bar{y} o male of each com e ing geno e (S/S vs R/R, S/S vs D/D o D/D vs R/R) \bar{l} aced in he \bar{l} e ence of ei en S/S o en D/D female \bar{y} . Each com e i ion cage a e lica ed en ime. Mo i oe had acce *ad libitum* o a hone ol ion. A e h ee da \bar{y} , female e e blood-fed on abbi and allo ed o la egg indi id all. A \bar{y} ha ching, each female \bar{l} ogen a elec ed i h an in ecicide do e ha allo \bar{y} \bar{l} a e ni a \bar{l} ig \bar{n} a ion. When female e e S/S, \bar{l} a e ni in he S/S vs R/R and S/S vs D/D ial a a igne d i h \bar{l} o o a a 1 mg/L (hich kill onl S/S \bar{l} ogen); in he D/D vs R/R ial, \bar{l} a e ni a a igne d i h bendioca b a 1 mg/L (hich kill D/S b no R/S \bar{l} ogen). When female e e D/D, \bar{l} a e ni in he S/S vs R/R and S/S vs D/D ial a a igne d i h bendioca b a 1 mg/L, hile \bar{l} a e ni in he DD vs RR ial a a igne d i h bendioca b a 5 mg/L (hich kill D/D b no D/R \bar{l} ogen). e \bar{l} a e ni cce of a gi en geno e a de ned in each e lica e of ial a he e cen age of egg- a i had \bar{y} ed.

Female fecundity and fertility. All ain e e ea ed nde he ame o en i onmen al condi ion and c o e e e \bar{l} fo med be een 200 male and 200 female. A e a lea h ee da \bar{y} , female e e blood-fed and 40 g a id female f om each ain e e allo ed o o i b i indi id all \bar{y} in la ic c \bar{l} con aining 70 mL dechlo ina ed a e. e e da a e blood feeding, he n mbe of egg-la ing female and he amo n of egg \bar{l} female e e eco ded. T o da \bar{y} a e, he n mbe of ha ching la ae e female a con ed.

Statistical analyses. *ace-1* gene co \bar{l} n mbe a ia ion among S/S and D/D geno e a ana l ed ing linea model. No mali of he model e id al and homo ceda ici e e checked ing Sha \bar{l} o-Wilk and Be ch-Pagan e \bar{y} , e e ec i el⁷⁰.

La al mo ali and de elo men ime e e anal ed ing Co \bar{e} o b i onal ha a d e g e ion model⁷⁰.

Di e ence in \bar{l} a e ni cce be gen ail e e e ed ing gene ali ed linea model (GLM), i h a binomial e o di \bar{y} ib ion. De a e f om he e ec ed \bar{l} o b i on of 0.5 i hin each ial (i.e. if he o male geno e di la he ame abili o fec nd female) a hen e ed ing e ac binomial e⁷⁰.

Di e ence among geno e in he a e of female la ing egg and in he ha ching a e e e e ed ing GLM i h binomial e \bar{y} o di ib ion. Di e ence among geno e in egg n mbe and la ae n mbe e female e e e ed ing GLM i h Ga ian e o di ib ion⁷⁰.

All com \bar{l} a ion e e \bar{l} fo med ing he R f ee o a e (.3.1.1, h \bar{l} // . \bar{l} ojec o g). Co \bar{e} model and GLM e e im li ed a follo : igni cance of he di e en e m a e ed a ing f om he highe o de e m ing likelihood a io e (LRT). Non- igni can e m ($p > 0.05$) e e emo ed⁷². Fac o le el of ali a i e a iable ha e e no igni can l di e en e e g o ed (LRT⁷²).

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