Efficient population modification gene-drive rescue system in the malaria mosquito *Anopheles stephensi*

Adriana Adolfi[a,1], Valentino M. Gantz[b], Nijole Jasinskiene[a], Hsu-Feng Lee[a], Kristy Hwang[a], Emily A. Bulger[b,c,2], Arunachalam Ramaiah[d,e], Jared B. Bennett[f], Gerard Terradas[b,c], J.J. Emerson[d], John M. Marshall[g], Ethan Bier[b,c], Anthony A. James[a,h]*.

[a] Department of Microbiology & Molecular Genetics, University of California, Irvine, CA 92697-3900, USA.
[b] Section of Cell and Developmental Biology, University of California, San Diego, La Jolla, CA 92093-0349, USA.
[c] Tata Institute for Genetics and Society (TIGS)-UCSD, La Jolla, CA 92093-0335, USA.
[d] Department of Ecology and Evolutionary Biology, University of California, Irvine, CA 92697-2525, USA.
[e] Tata Institute for Genetics and Society (TIGS)-India, Bangalore, KA 560065, India.
[f] Biophysics Graduate Group, Division of Biological Sciences, College of Letters and Science, University of California, Berkeley, CA 94720, USA.
[g] Division of Epidemiology & Biostatistics, School of Public Health, University of California, Berkeley, CA 94720, USA; Innovative Genomics Institute, Berkeley, CA 94720, USA.
[h] Department of Molecular Biology & Biochemistry, University of California, Irvine, CA 92697-4025, USA.

*Corresponding author: Anthony A. James, aajames@uci.edu

Current addresses:
[1] Liverpool School of Tropical Medicine, Vector Biology Department, L3 5QA Liverpool, UK.
[2] Developmental and Stem Cell Biology Graduate Program, University of California, San Francisco, CA 94158, USA; The Gladstone Institutes, San Francisco, CA 94158, USA.

ABSTRACT

The development of Cas9/gRNA-mediated gene-drive systems has bolstered the advancement of genetic technologies for controlling vector-borne pathogen transmission. These include population suppression approaches, genetic analogs of insecticidal techniques that reduce the number of vector insects, and population modification (replacement/alteration) approaches, which interfere with competence to transmit pathogens. We developed a recoded gene-drive rescue system for population modification in the malaria vector, *Anopheles stephensi*, that relieves the load in females caused by integration of the drive into the *kynurenine hydroxylase* gene by rescuing its function. Non-functional resistant alleles are eliminated via a dominantly-acting maternal effect combined with slower-acting standard negative selection, and a functional resistant allele does not prevent drive invasion. Small cage trials show that single releases of gene-drive males robustly result in efficient population modification with ≥95% of mosquitoes carrying the drive within 5-11 generations over a range of initial release ratios.

INTRODUCTION

The challenges faced by current programs to eliminate malaria from high-endemic areas[1] have fostered the development of novel control strategies including those based on genetically-modified mosquitoes. These genetic approaches are bolstered by the development of Cas9/guide RNA(Cas9/gRNA)-based gene-drives[2–4], with pioneering studies demonstrating effective mosquito population suppression[5–7] or modification[8–10], the latter aimed at impairing the ability of adult females to transmit the *Plasmodium* parasites causing the disease.

Our population modification approach is to express multiple anti-parasite effector molecules in the form of single-chain antibodies directed against sexual stages of *P. falciparum* in relevant mosquito tissues[8,11,12]. This strategy relies on efficient copying of a drive system carrying these molecules from one chromosome to its homolog in the germline by homology-directed repair (HDR) of Cas9/gRNA induced double-stranded DNA breaks, resulting in the rapid increase in frequency of the parasite-refractory trait in the population. However, competing end-joining (EJ) repair mechanisms often result in insertions or deletions (INDELs) that are usually resistant to subsequent Cas9-mediated cleavage and can greatly impede the copying process[9,13]. These resistant alleles can be generated at different developmental stages including in early embryogenesis due to parental deposition of Cas9/gRNA complexes or somatic expression from 'leaky' promoters[14–16]. When targeting a coding region, INDELs at the cut site often disrupt protein function (non-functional EJ), however mutations that maintain protein function (functional EJ) can also occur. Both outcomes can affect the persistence of the drive element and, in the absence of strategies that prevent or mitigate EJ events[16–18], gene-drives can stall or be eliminated from a population if they carry a fitness cost[9,13].

One resistance-mitigation strategy for population modification approaches is to design a drive that targets an essential gene while concomitantly providing a recoded rescue sequence[19]. Under these conditions, EJ resistant alleles that lack the rescue sequence are eliminated from the population as they suffer from the fitness load associated with the loss-of-function of the targeted gene. The feasibility of 'rescue systems', such as CleaveR (Cleave and Rescue) and TA (Toxin-Antidote), was demonstrated in *Drosophila melanogaster* by targeting essential genes using alternative combinations of *trans*- or *cis*-acting drive elements and rescue sequences. These systems are independent of HDR copying of the drive and result in threshold-dependent drive invasion dynamics[20,21]. When arranged in a split configuration, where the Cas9 and gRNAs are not located in the same transgenic construct, these systems are predicted to remain confined locally[21,22]. Alternative designs based on the HDR-mediated spread of rescue sequences and the use of multiple gRNAs showed high non-confinable invasion capabilities in model-based simulations and *D. melanogaster* cage experiments[23,24].

Here we report an HDR-based autonomous gene-drive rescue system in *Anopheles* mosquitoes and provide the first experimental evidence of its ability to sustain long-term population modification in caged mosquito populations powered by a drive system that dominantly eliminates non-functional EJ events. This efficient performance is based on a phenomenon referred to as lethal/sterile mosaicism, recently reported in *D. melanogaster*[25], which converts recessive non-functional resistant alleles into dominant deleterious mutations

that are eliminated from the mosquito population as they arise. The drive system, designated 'Recoded' (Rec), was developed in the Indo-Pakistan malaria mosquito *Anopheles stephensi*, the major vector in urban areas of India[26] that also has recently invaded the Horn of Africa[27]. The drive element is inserted into the autosomal gene *kynurenine hydroxylase* (*kh*), involved in the tryptophan metabolism pathway[28], and carries a partial recoded *kh* sequence that restores full activity of the *kh* gene (Rec*kh*). Homozygous loss-of-function mutations in *An. stephensi kh* locus result in a pleiotropic phenotype that includes loss of the black eye pigment (white eyes) and reduced female survival, fertility, and fecundity following blood feeding[8,9]. The recoded *kh* sequence carried by the drive construct supports normal survival and reproductive capacity in females; while females failing to inherit the Rec*kh* construct from their mothers and carrying non-functional mutated copies of *kh* are promptly eliminated from the populations. This elimination, however, does not rely only on the standard negative selection of recessive alleles but is remarkably boosted by lethal/sterile mosaicism, that takes advantage of the maternal deposition of Cas9/gRNA complexes that mutate the wild type (WT) paternal allele in a sufficient percentage of cells to dominantly eliminate females that do not inherit the Rec*kh* drive element from the reproductive pool. The combination of lethal/sterile mosaicism and negative selection results in robust drive outcomes demonstrable in population cage experiments with initial Rec*kh*-to-WT male seeding ratios of 1:1, 1:3, and 1:9. Finally, we also report a Cas9/gRNA-mediated cassette exchange[29] in mosquitoes, called 'Swap', that permits the rapid and flexible replacement of specific sequences within genomically-integrated transgenes without the need for docking sites.

RESULTS

Generation of Rec*kh* gene-drive mosquitoes by Swap

The first *An. stephensi* Cas9/gRNA-based gene-drive system, AsMCRkh2 (referred hereon as 'non-recoded', nRec), was inserted into the coding region of the *kh* locus[8]. Homozygous (kh^{nRec-}/kh^{nRec-}) or heteroallelic (kh^{nRec-}/kh^{-}) loss-of-function allelic combinations cause a white-eye phenotype and impairment of blood-fed female survival and reproduction, resulting in a suppression drive that limits its spread in caged populations[9].
We modified this loss-of-function prototype drive system by inserting a recoded portion of the *kh* cDNA precisely at the 3'-end junction of the gRNA cleavage site producing an in-frame chimeric functional *kh* gene that restores endogenous gene activity (kh^{Rec+}) (Fig. 1a). A Cas9/gRNA-mediated cassette exchange system, Swap, facilitates integration of the recoded cDNA through the coordinated action of two gRNAs in the presence of a donor template carrying homology arms matching the flanking regions of each of the cut sites. A mixture comprising a donor plasmid marked with GFP (pRec*kh*) and two plasmids each encoding one of two gRNAs was injected into 504 embryos of the DsRed-marked nRec gene-drive line, which carries *vasa*-Cas9 and U6Akh2-gRNA transgenes targeting the *kh* locus in the germline. Successful cassette replacement was visualized by loss of the DsRed marker and concomitant acquisition of the GFP-marked Rec*kh* cassette. Two independent

transformation events were recovered from the 184 G_0 individuals surviving microinjection, one in a female and one in a male founder, totaling 96 transformants among the 25,293 G_1 progeny screened (Supplementary Table 1).

In the recovered Rec*kh* transgenic lines, the recoded *kh* sequence is integrated at the junction where insertion of the original nRec line disrupted the *kh* gene, restoring the coding sequence (Supplementary Fig. 1). As a result, individuals from these GFP-marked mosquito lines exhibit WT eye color and maintain the nRec autonomous gene-drive components (Fig. 1b). This updated line, Rec*kh*, should therefore sustain efficient copying onto unmodified WT *kh* alleles (kh^+) while producing a fully functional partially recoded *kh* allele (kh^{Rec+}) (Fig. 1c).

Transmission of the Rec*kh* element is affected by maternal deposition of Cas9/gRNA complexes

Drive performance of the Rec*kh* element was evaluated when this was inherited either through male or female lineages by sequentially outcrossing heterozygous Rec*kh* individuals to WT mosquitoes and assessing the percentage of individuals inheriting the drive allele (i.e. transmission) and the percentage of *kh* alleles converted to Rec by HDR copying (i.e. gene conversion or HDR rate) (Fig. 2; Supplementary Table 2).

As found previously[5,6,8,18], near-complete drive transmission (99.8% ± 0.15% SEM) and gene conversion (99.5% ± 0.29% SEM) were observed in progeny whose drive-bearing parent was a male. Similar experiments using Rec*kh* females showed reduced transmission (57% ± 2.2% SEM) and weak gene conversion (14% ± 4.4% SEM), which is consistent to that reported for the original non-recoded drive element[8]. This greatly reduced level of drive via females is largely due to maternal deposition of Cas9/gRNA complexes in the unfertilized egg which accumulate to significant levels when using the *vasa* promoter to express the Cas9 transgene[5,8,18]. A large fraction of individuals that failed to inherit the drive element through the female lineage displayed a white-eye phenotype and are likely to reflect early somatic mutagenesis of the WT paternal allele in eggs that inherited a non-functional maternal EJ (kh^-) allele from drive mothers to generate large sections of homozygous mutant cells that give rise to the eyes and other tissues.

Rec drives efficiently in caged mosquito populations

Because loss-of-function *kh* alleles are recessive, the Rec*kh* element, which produces a protein of WT sequence under native transcriptional control, was predicted to rescue *kh* activity in a single copy. Consistent with this, fitness assessments indicate that Rec*kh* drive females are comparable to WT in their ability to reproduce (Supplementary Table 3-4) and that males carrying a drive allele have an equal ability to contribute to the following generation compared to WT male counterparts (Supplementary Table 5). In contrast, homozygous EJ events resulting in non-functional kh^- alleles reduce viability, fecundity, and fertility in blood-fed females relative to WT, heterozygous, or homozygous Rec*kh* (Supplementary Tables 3-4). These resistant non-functional alleles are expected to be eliminated from the population in cage experiments as a combination of two processes. 1) The first process, lethal/sterile mosaicism, relies on the maternally-deposited Cas9/gRNA complexes acting

somatically on the WT kh^+ paternal allele to mutate it by EJ-induced INDEL formation rendering part of or all embryonic cells homozygous for *kh* loss-of-function. 2) The second process by which kh^- alleles are culled from the population is the standard Mendelian inheritance wherein mating of two kh^- carriers results in 25% of the progeny being kh^- homozygous of which the females will be unable to contribute effectively to the following generation. We hypothesize that the combination of fast-acting lethal/sterile mosaicism and slower-acting Mendelian processes results in the drive achieving full introduction (i.e. all individuals carrying at least one drive allele).

We tested the performance of Rec*kh* in small laboratory populations by assessing the drive dynamics in the presence of competition in three sets of triplicate experiments (A, B, and C), each starting with a specific release ratio of heterozygous Rec*kh* to WT males, 1:1 (drive allele frequency 25%), 1:3 (drive allele frequency 12.5%), or 1:9 (drive allele frequency 5%) and an equal total number of WT females (1:1 sex ratio) (a schematic of the set-up is in Supplementary Fig. 2). The proportion of eye-phenotype combinations (GFP^+ or GFP^- fluorescence; and black, white, or mosaic color) was scored in a randomly-selected sample of ~500 individuals for eighteen discrete (non-overlapping) generations. Data for all cages are reported in Fig. 3 and Supplementary Tables 6-8. Cages seeded with 1:1 Rec*kh*:WT males reached ≥95% introduction within 5-7 generations (Fig. 3a). Interestingly, cages $1{:}3_A$ and $1{:}3_C$ achieved ≥95% introduction within a comparable timeframe, generations 6-7, while $1{:}3_B$ fluctuated below 30% for 7 generations before increasing with dynamics similar to that of the other two cages and reaching >90% by generation 11 (Fig. 3b); the drive dynamics in this outlier cages were further evaluated and are reported in the next section. Finally, cages seeded with the lowest release ratio (1:9) reached ≥95% introduction by generation 10-11 (Fig. 3c), consistent with an expected ~3-generation delay relative to cages seeded at 1:1. Population levels fluctuated in all cages, but did not show any obvious decline associated with the increasing prevalence of the drive (Supplementary Fig. 3).

Potential drive-resistant individuals (GFP^-/white) could be scored first in generation 3. Sequencing their *kh* loci confirmed that the phenotype was due to both gene copies being inactivated by non-functional homozygous or trans-heterozygous mutations (Supplementary Table 9). As expected from the load observed in adult kh^-/kh^- females, the proportion of GFP^-/white individuals decreased progressively over the generations (Fig. 3). However, as hypothesized, the rate of decrease exceeded that expected for the elimination of homozygous recessive individuals by negative selection and Mendelian inheritance. We believe this is driven by lethal/sterile mosaicism (Fig. 4), which accelerates the elimination of kh^- mutations inherited through females. Perduring Cas9/gRNA complexes mutagenize WT paternal kh^+ alleles somatically rendering EJ-derived loss-of-function mutations functionally dominant when transmitted by females. Inheriting a copy of the kh^{Rec+} allele restores WT *kh* activity, including eye-color and female reproductive capacity, therefore Rec*kh* females are protected from the deleterious effects of mosaicism (Fig. 4b). Whereas females carrying a non-functional EJ-derived kh^- allele can have somatic tissues comprised of double-mutant cells and therefore fail to contribute significantly to the following generation (Fig. 4c). Consistent with this interpretation, the frequency of EJ-induced kh^- alleles (implied by that of individuals with white eyes) was highest at the steepest phase in the drive curves (Fig. 3;

Supplementary Fig. 4) reflecting the generation of mosaic individuals. Evidence of somatic mutagenesis affecting small patches of tissue in the eyes was observed by the transient appearance of non-drive individuals with mosaic eyes (GFP^{-}/mosaic) in generations 3-9 (Fig. 3).

Rare (n = 20) white-eyed drive (GFP^{+}/white) individuals also were recovered. Sequencing of their *kh* loci showed they carry a drive allele with an out-of-frame INDEL at the 5'-end insertional site junction that disrupts *kh* recoding (kh^{Rec-}) despite integration of the transgenic cassette, in combination with a kh^{-} allele (Supplementary Table 10). Such kh^{Rec-} alleles may be generated by inaccurate HDR or EJ events resulting from the drive allele being targeted at low frequency by the endogenous gRNA. While such alleles may still retain drive capacity, they also suffer from the load observed in white-eye females, consistent with these genotypes being rare and not accumulating in any of the cages. The rarity of this class of events and their failure to thrive provide clear experimental support for robust HDR-mediated rescue of endogenous gene function.

When comparing the performance of Rec in population cages to studies conducted on the nRec drive[9] (Supplementary Fig. 5) we found little difference in the dynamics of the initial exponential phase of the drive curves at all seeding ratios. At later generations, however, drive trajectories diverged significantly during the middle and final phases of the drive process. All Rec cages reached maximum introduction and the drive system was maintained stably for the remaining observed generations. In contrast, only two of the three 1:1 and 1:3 nRec cages, and none of the 1:9 replicates, reached >95% introduction before driving to extinction due to fixation of *kh* double-mutant genotypes and associated female load. We also observed a delay in mid-stage growth in the nRec 1:3 cages, most likely resulting from the elimination through lethal/sterile mosaicism of female progeny receiving a kh^{nRec-} or a kh^{-} allele from drive mothers.

A functional resistant allele does not prevent drive introduction in caged populations

Cage replicate $1{:}3_B$ displayed anomalous drive dynamics where the drive stalled for the first 7 generations before increasing and reaching full introduction (Fig. 3). We examined the potential basis for this outlier cage by assessing whether the presence and relative abundance of specific Cas9-induced mutations might have accounted for the observed drive delay. To do so, we deep-sequenced a PCR product generated by amplifying the sequence surrounding the cut site in non-drive alleles from pooled individuals from generations G_0, G_8, and G_{14} (Supplementary Table 11).

A total of 98% of the non-drive *kh* alleles found in G_0 conformed to the unmutated WT sequence and 2% of the reads revealed indels adjacent to the gRNA-directed cut site. Such kh^{-} mutations were likely carried by the heterozygous males selected at random to seed the first cage from a founder cage that had been intercrossing for several generations as part of the regular maintenance of the line. By the time the drive reached 50% introduction (in generation G_8), 83% of the non-drive *kh* alleles were still unmodified kh^{+} alleles, while the most prevalent mutated non-drive alleles were indels of various lengths (1-3% each) and two in-frame substitutions (1-2% each) causing non-synonymous amino acid changes (TACG>CGAT:Y328R-G329W and

CAG>GCA:Q330A) potentially functional and resistant to the drive. In generation G_{14}, where the drive had reached >95% introduction and WT *kh* alleles had virtually disappeared (<0.1%), the Y328R-G329W substitution was also absent, suggesting it caused protein malfunction, while the Q330A substitution had increased in frequency to 12% of the total non-drive alleles.

Further investigation of the CAG>GCA:Q330A mutation confirmed that it maintains *kh* function, as individuals homozygous for the mutation or trans-heterozygous for the mutation and a kh^{-} allele isolated from generation G_{16} had black eyes (Supplementary Table 12). This functional mutation affects the PAM site creating a *kh* allele that is resistant to further Cas9 cleavage (kh^{+R}), as demonstrated by the nearly Mendelian segregation of the GFP marker observed in the progeny of kh^{Rec+}/kh^{+R} males crossed to WT females (57% GFP^{+} and 43% GFP^{-} individuals, n = 1718).

Resistant EJ events that preserve gene activity could be 1) under negative selection relative to the kh^{Rec+} if they affect protein function, 2) positively selected if they cause a relative increase in fitness compared to drive individuals, or 3) neutral if the fitness of the two modified *kh* alleles is comparable. Population analysis of the late stages in the drive process did not support either a positive or negative selection model in regard to the kh^{+R} mutation, since the frequency of GFP^{-} black-eyed individuals remained approximately steady (1-3%) over 10 generations (G_{11} to G_{20}), suggesting a negligible fitness difference between that EJ allele and the recoded kh^{Rec+} allele. We further tested the relative fitness of the kh^{Rec+} drive allele in a multigenerational cage experiment where the drive and the functional resistant allele could compete. To do so, we monitored eye fluorescence and pigmentation phenotypes in triplicate cages seeded at equal (1:1) ratios of the two alleles where kh^{Rec+}/kh^{+R} individuals could mate. In these conditions, assuming random mating, phenotypes should stabilize at a 3:1 ratio of GFP+ to GFP- individuals if the two alleles are comparably competitive. We observed that not only did the proportion of GFP^{-}/black-eyed kh^{+R}/kh^{+R} not exceed the 25% expected for Mendelian inheritance, but it decreased over time (Fig. 5) (Supplementary Table 13) suggesting the presence of a fitness load associated with this mutation relative to the drive allele. We found no evidence in these experiments for the resistant allele being cut at low frequency by Cas9 since we did not recover any individual with mosaic or white eyes. In light of these observations, we conclude that the appearance of the kh^{+R} resistant functional allele in the $1{:}3_{B}$ cage is unlikely to have contributed notably to the pause in drive dynamics observed, and moreover that the kh^{Rec+} drive allele is at least as fit, if not more so, than the functional kh^{+R} EJ allele.

Modeling of the Rec gene-drive

We performed mathematical modeling to assess whether the observed experimental drive dynamics in the cages conformed with predictions based on the copying efficiency of Rec in single generation crosses and with genotype-specific loads in females. A model of autosomal Cas9/gRNA-based gene-drive, similar to one used for nRec[9], was fitted to the observed cage data and includes two alternate mutated resistant alleles, functional (kh^{+R}) and non-functional (kh^{-}), maternal deposition of Cas9/gRNA complexes, and genotype-specific loads.

Model fitting was consistent with high (>99%) HDR efficiencies of in males and in females in absence of maternal Cas9/gRNA deposition, and with 17% (95% CrI: 16-18%) of resistant alleles generated being functional, and the remainder being non-functional. Maternal deposition was inferred to result in cleavage of embryonic WT alleles with a frequency of 93.7% (95% CrI: 92.2-95.3%), with cleavage events producing functional or non-functional resistant alleles having the same distribution to preserve identifiability in the model fitting process. Data also are consistent with kh^{-}/kh^{-} females having reproductive load of 99.8% (95% CrI: 99.2-100%), while the drive allele is associated with a negligible load, consistent with laboratory observations. The trajectories of GFP^{+} individuals align well with experimental observations at all release ratios (Fig. 3, Supplementary Fig. 6) and are consistent with a highly efficient gene-drive system.

Functional resistant alleles are generated at a low rate, and although they can persist in the population due to their cut-resistance (GFP^{-}/black in Supplementary Fig. 6), they were not a significant obstacle to the drive at the release ratios analyzed. Non-functional resistant alleles also were generated at a low rate and were strongly selected against in the progeny of females that generated them, while their subsequent elimination was gradual (GFP^{-}/white in Supplementary Fig. 6) due to their viability in males and heterozygotes of both sexes.

Finally, a stochastic model captured the potential role of chance events such as mate choice (multinomial-distributed), egg production (Poisson-distributed), progeny genotype (multinomial-distributed), and finite sampling of the next generation (multivariate hypergeometric-distributed) (Fig. 6). Stochastic model trajectories reflect some of the variability observed in the early stages of spread of the gene-drive allele, with additional transient delays observed in cages $1{:}1_B$ and $1{:}3_B$.

DISCUSSION

Population modification strategies employing gene-drive systems to spread anti-parasite effector molecules through populations of *Anopheles* mosquitoes are gaining momentum in the fight against malaria[10,30,31]. However, the creation of mutated target sequences resistant to the drive, especially those preserving gene function, can limit transgene introduction, particularly if a load is associated with the presence of the drive system[9,13].

Here, we provide the first experimental evidence for a readily generalizable gene-drive rescue system for efficient population modification in *Anopheles* mosquitoes that actively removes non-functional resistant alleles as they arise and rapidly attains >95% introduction in caged populations, despite the creation of rare functional EJ variants. As a result, the Rec system converts a population suppression gene-drive (nRec) to an efficient population modification system in *An. stephensi*. Furthermore, while proof-of-concept for rescue systems that employ recoded sequences has been produced in *D. melanogaster*[20–23], the work presented here represents the first example of a homing-based gene-drive rescue system aimed at ‘global spread’ in mosquitoes.

Assessments of the long-term dynamics of this new system in caged mosquito populations show that Rec spreads quickly (5-11 generations depending on release ratio) and efficiently even when a small percentage of males are released and, after reaching maximum introduction, it persists without an evident impact on the population size. Rec targets the haplosufficient gene *kh*, required for adult female survival and reproduction in *An. stephensi* following a blood meal[9], and provides a partial recoded sequence that rescues gene function. In doing so, individuals that carry a copy of the drive are functionally protected and comparably as fit as their WT counterparts, while non-functional resistant alleles are eliminated owing to the reduced survival and impaired reproductive capacity in white-eyed and mosaic females. We rationalize that such elimination is driven initially by the active process of lethal/sterile mosaicism, which renders recessive non-functional kh^{-} mutations dominant during the drive process, therefore acting as an autocatalytic mechanism that eliminates female progeny of drive mothers from the breeding pool. Mosaicism-mediated elimination is complemented by negative selection of the residual kh^{-} recessive alleles transmitted through male progeny, which acts over many generations to eliminate these costly alleles from the population. Overall, the accelerated elimination of kh^{-} alleles results in an increased apparent HDR-mediated conversion frequency.

Modeling predictions based on transmission frequencies and loads of different allele combinations are consistent with the highly efficient gene-drive outcomes observed in the cage experiments. Simulations are consistent with non-functional kh^{-} resistant alleles, which are generated primarily in females, being eliminated rapidly by lethal/sterile mosaicism and then gradually as standard recessive alleles due to the load associated with bi-allelic *kh* loss-of-function. Consistent with lethal/mosaicism taking place in offspring of gene-drive females, the presence of white-eyed carrying *kh* homozygous mutations in the cage experiments followed a general trend in which they were most abundant at the steepest phase in the drive curve, while the remaining kh^{-} alleles propagating through males were slowly eliminated through selection over time. Potential loads in white-eyed males, such as impaired vision, may have also contributed to the elimination of non-functional resistant alleles. Future recoded drive systems inserted into genes essential for viability of both sexes or required for both male and female fertility could drive even more rapidly.

The lag in drive invasion observed in one of the 1:3 release ratio cages, which deviates from the consistent trends observed in the other 8 cages, remains difficult to explain since it is not fully supported by the predictions of the stochastic model. We exclude this is the result of a sampling effect as a delay on the drive increase was not observed in any other cage, including those seeded with the lowest release ratio. Also, our analysis has excluded the involvement of resistant functional alleles in this observation. Further analysis of these trajectories will be required to ascertain the underlying mechanisms responsible for such outlier events. Nevertheless, the transient delay in drive invasion observed in this cage did not prevent final full introduction of the drive.

A major concern associated with the persistence of gene-drives is the generation of cleavage-resistant sequences that preserve gene function. In population suppression systems, these alleles are positively selected over the drive allele if this causes loss-of-function of the target site resulting in a fitness disadvantage[9,13]. Therefore, choosing a functionally constrained target site should alleviate the issue of resistance and proved successful in

suppression and sex-distorting strategies targeting a highly conversed region of *dsx*[6,7]. This strategy also can mitigate the effect of resistance in population modification systems, where the effect of functional resistant target sequences on the drive dynamics is dependent on their fitness relative to that of the drive. Data from the cage experiments and modeling show that in the Rec system functional resistant alleles are generated at a low rate and do not prevent the drive from reaching full introduction. We attribute this to the high functional constraint of the chosen target site within the *kh* gene that, when mutated, is likely to cause total or partial protein malfunction. This is supported by evidence from the crystal structure of the KH enzyme from *Saccharomyces cerevisiae* where the P326-F327-Y328-G329-Q330 loop, which encompasses the gRNA site in our experiments, plays an essential role in accommodating the rearrangements of the active site of the enzyme during binding[32]. Indeed, this region shows high primary amino acid sequence conservation from insects to humans[28,33]. In line with this, we find multiple examples of in-frame mutations in individuals with white eyes. This is consistent with previous findings from similar cage experiments conducted using the same gRNA where the strong contribution of the Y328 and G329 residues to protein function is highlighted[9]. Here we report evidence for the contribution of the Q330 residue, whose codon forms part of the PAM site. While individuals homozygous for the Q330A substitution display a black WT eye phenotype and the mutation is resistant to Cas9 cleavage, we observed only a modest accumulation of this mutation amongst the non-drive alleles that did not prevent drive invasion. We further explored this in cage experiments were the mutated resistant allele was in direct competition with the drive and found that the mutation was outcompeted by the drive. We therefore conclude that the Q330A mutation likely only partially restores WT levels of KH enzyme and thus does not pose a major obstacle to the drive process. Given the documented functional constraints of multiple residues at the *kh* target site and evidence that the kh^{Rec+} allele does not carry an obvious fitness burden, it is likely that this drive will outcompete the small number of different Cas9-induced functional resistant mutations we have identified. Similarly, while we currently do not have access to genome data on field populations of *An. stephensi*, we do not expect the targeted conserved coding sequence to show high levels of natural polymorphism.

Field performance of population modification drives is not only dependent on the drive copying process as such but also on effects on mosquito fitness produced by sequences encoded in the cargo, such as anti-malarial effectors. The Rec*kh* construct currently lacks anti-malarial molecules as the two effectors m2A10 and m1C3 present in the original prototype were excised due to molecular constraints to allow for *kh* recoding and simultaneous fluorescent marker cassette exchange. However, we do not anticipate major fitness impacts in our drive mosquitoes as our population modification strategy is based on the use of synthetic single-chain antibodies (scFv) specifically directed against *Plasmodium* parasite antigens. Due to their target specificity and tightly regulated blood-meal-induced expression, combinations of these molecules have been shown to not have a major impact on mosquito fitness[12]. In contrast, expression of multiple toxins and synthetic molecules with broader activity can exert undesired impacts on crucial physiological processes[34] or the gut microbiota. Furthermore, we predict that the addition to Rec of genes coding for antimalarial effectors and their regulatory regions will not greatly affect drive copying since the initial exponential growth of Rec and nRec systems were very similar,

supporting the conclusion that the system will tolerate a significant increase in cargo size (i.e., the nRec construct is ~4.6 kb larger than Rec).

We also report the first application to mosquitoes of the highly efficient Swap transgenesis technology, a Cas9/gRNA-driven cassette exchange system[29], to update sequences of previously-integrated gene-drive systems. Swap is a flexible tool that efficiently edits existing gene-drive mosquito lines by using small constructs. Swap also can enable broader genome engineering efforts in mosquitoes. Since it does not require the presence of recombination sites, such as those needed for *φC31* recombinase-mediated cassette-exchange, updating sequences could be inserted anywhere suitable gRNA sites are available. For example, the system could be used to exploit endogenous *cis*-acting elements[35,36] through the seamless integration of desired coding regions. For population modification purposes, a drive line can be envisioned that carries strategically placed gRNA targets to replace anti-parasitic molecule combinations and test their blocking efficacy. Indeed, our next steps include the addition of combinations of anti-malarial scFvs that block parasite development using Swap. While the Rec*kh* line can be used as a classic docking line via the *φC31* attP site introduced along with the recoded *kh* sequence, integration would significantly increase the size of the sequence between the homology arms as well as bringing in additional sequences that might impact drive performance. Nevertheless, this efficient integration strategy can be used to assess blocking capabilities of alternative combinations of antimalarial effectors expressed at the *kh* genomic locus.

Finally, while the Rec system described here is already highly efficient, substituting the current *vasa* promoter with more tightly-regulated control sequences, such as those of the *nanos*[10] or *zpg*[18] genes employed for gene-drive designs in *An. gambiae*, could improve its performance by reducing the fraction of EJ alleles persisting during the drive process.

Overall, the laboratory assessments conducted on this novel system, carried out in line with the recommended phased pathway for testing gene-drive mosquitoes[37–39], show that the characteristics of the Rec gene-drive conform with those defined as part of a proposed Target Product Profile for population modification of mosquito strains[30]. The highly efficient performance of the Rec drive system makes it an excellent candidate for genetic control of an important malaria mosquito, *An. stephensi*, and this technology should be readily adaptable to other mosquitoes as well as other insect disease vectors.

METHODS

Mosquitoes

Anopheles stephensi Indian strain (gift from M. Jacobs-Lorena, Johns Hopkins University) were maintained in insectary conditions (27°C and 77% humidity) with a photoperiod of 12-hour light/dark and 30 minutes of dawn/dusk. Sucrose solutions (10% wt/vol) were provided *ad libitum* and blood meals consisting of defibrinated calf blood (Colorado Serum Co., Denver) were offered to 3-7-day-old adults through the Hemotek® membrane feeding system. Larval stages were reared in distilled water and fed TetraMin® fish food mixed with yeast powder. Gene-drive mosquitoes were contained in ACL-2 insectary facilities at the University of California, Irvine and handled according to recommended safety procedures[40–42].

Plasmids for the Swap strategy

The Swap strategy employed to convert nRec to Rec*kh* uses the three plasmids shown in Fig. 1a: 1) pVG362_Aste-U6A-Swap3-gRNA, to express the gRNA-sw3; 2) pVG363_Aste-U6A-Swap4-gRNA, to express the gRNA-sw4; 3) pVG344_Aste_kh2-MCRv3-vasa-Cas9, to provide the HDR template containing the recoded-*kh* coding fragment and the GFP marker.

To generate plasmids pVG362 and pVG363, a pair of oligonucleotides were synthesized (Integrated DNA Technologies) for each plasmid with 19 (pVG362) or 20 (pVG363) bases of the target sequence chosen for the strategy. These were annealed and ligated with T4 ligase (New England Biolabs) into the pVG145-Aste-U6A-Bbs1 plasmid[8] linearized with *Bbs*I. The cloning strategy was adapted from the work of Port et al.[43]. The oligonucleotides used to construct pVG362 were 1288_Aste-Swap3-Target_F (CTTGTTCTTGGAGGAGCGCACCA) and 1289_Aste-Swap3-Target_R (AAACTGGTGCGCTCCTCCAAGAA). The oligonucleotides used to construct pVG363 were 1290_Aste-Swap4-Target_F (CTTGTTACGttaattaaCGTAGAA) and 1291_Aste-Swap4-Target_R (AAACTTCTACGttaattaaCGTAA).

The pVG344 plasmid was cloned using the NEBuilder HIFI DNA Assembly Cloning Kit (New England Biolabs) to assemble four amplified fragments. Fragment 1 was generated by amplification of the backbone region of plasmid pVG163_pAsMCRkh2[8], fragment 2 was generated by amplification of the *kh* recoded rescue fragment from a plasmid synthesized by GenScript Inc., fragment 3 was amplified from a plasmid containing a 3xP3-GFP cassette commonly used for insect transgenesis, and fragment 4 also was amplified using pVG163_pAsMCRkh2 as a template. Primer pairs used to amplify each fragment were: Fragment 1: 494_pUC19_Backbone_F (GGTATCAGCTCACTCAAAGGCGGTAATACGG) and 1227_As-MCR2_GA_backbone_R (CGTAGAACGGAACCATCGCGTG), Fragment 2: 1231_As-MCR2_GA_RecodedFrag_F (CGCGATGGTTCCGTTCTACGG) and 1232_As-MCR2_GA_RecodedFrag_R (CTACGCCCC,,CAACTGAGAGAACTC), Fragment 3: 1230_As-MCR2_GA_GFP_F (TCTCTCAGTTGGGGGCGTAGCGTACGCGTATCGATAAGCTTTAAGATAC) and 1229_As-

MCR2_GA_GFP_R (CACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCAC, Fragment 4: 1228_As-MCR_GA_backbone_F (CACCATGGTGGCGACCGGTGGATC) and 1241_As_MCR2_GA_HA2_R (CGCCTTTGAGTGAGCTGATACCGTGAGCAAAAGGAGACGG).

Microinjections and establishment of Rec*kh*

Embryos were obtained from heterozygous females of the *An. stephensi* AsMCRkh2 (nRec) gene-drive line[8]. Microinjections were performed as described previously[44] using a plasmid mix containing 600 ng/μL of pRec-*kh* donor (pVG344) and 200 ng/μL of each gRNA-sw3 (pVG362) and gRNA-sw4 (pVG363) plasmids. Surviving G_0 adults were sorted in pools of 2-4 males and 7-10 females and outcrossed to 10x WT females and 1x WT males, respectively. G_1 progeny were screened as larvae for the inheritance of the GFP eye marker and kept as separate lines according to their male (♂4) or female (♀4) founder lineage. The two lines were screened routinely as larvae for the inheritance of the GFP eye marker and as pupae for the eye-color phenotype (black [WT], white or mosaic) and maintained by intercrossing GFP^+ black-eyed individuals. A homozygous drive line was established from the ♀4 intercrossed line.

Molecular confirmation of HDR-mediated target site integration of the Rec*kh* cargo was performed on genomic DNA extracted from single GFP^+ black-eyed individuals using the Wizard® genomic DNA purification kit (Promega). Primers Kh1-ext-fw (CACTGTTGGCACTCCATCTG) and Rec-kh-rv2 (GGGCTTCAACAACTGAAAAG) were used to amplify a 2190bp region spanning the cut site of gRNA-sw4, while primers eGFP-fw (AAGTCGTGCTGCTTCATGTG) and Vasa-rv (GTAAAAGCCGCATTTTCCAA) were used to amplify a 2303bp region across the cut site of gRNA-sw3. Gene amplification reactions were performed using Phusion® High-Fidelity PCR Master Mix (New England Biolabs). Sanger sequencing (Genewiz, San Diego) with primers Rec-kh-rv2 and eGFP-fw was used to confirm the sequence of the integration sites.

Drive transmission assessments

Drive transmission and HDR conversion rates through the male and female lineages were assessed in sequential *en masse* outcrosses of Rec*kh* individuals to WT. Each cross comprised 30 females and 15 males and was performed in three replicate cages. A representative subset of the progeny of each cross was scored for the presence of the GFP fluorescent marker and the eye color phenotype (black, white, or mosaic) in adults. A schematic of the crossing performed is reported in Fig. 2.

Drive transmission is defined as the percentage of individuals inheriting the Rec element. Gene conversion or HDR rate is defined as the percentage of *kh* alleles converted to Rec*kh* by HDR copying and is calculated using the formula $[2(X - 0.5n)/n]$ ('X' is the number of GFP^+ individuals and 'n' the total number of mosquito counted)[8].

Reproductive life-table parameters of Rec*kh* mosquitoes

Female fecundity and fertility

Homozygous Rec*kh* (kh^{Rec+}/kh^{Rec+}), heterozygous Rec*kh* carrying a copy of the drive and a kh^{-} allele (kh^{Rec+}/kh^{-}), WT (kh^{+}/kh^{+}), and white-eye (kh^{-}/kh^{-})[9] females were included in this analysis. Adult females 5-7 day-old were offered a blood meal for 45 minutes over two consecutive days and unfed females removed. After 3 days, single females were set up to lay in 16 oz (~454 cm^3) paper cup containing a plastic oviposition cup lined with damp filter paper. Eggs were counted the next day using a stereomicroscope and transferred to water cups lined with filter paper for hatching. Larvae emerging from single egg batches were counted at the first or second instar (L1-L2). Fecundity refers to the number of eggs laid by a single female and fertility to the proportion of larvae hatching from those single egg batches. A One-Way ANOVA with Tukey's multiple comparison *post-hoc* test was used to assess significant differences (p >0.05) in the performance of females from the four groups tested.

Male contribution to the following generation

Triplicate cages were seeded with 75 Rec*kh* homozygous males, 75 WT males, and 150 WT females. All individuals were added to the cage as 3-7-day old adults and females were offered a blood meal over two consecutive days. Approximately 2000-2500 L4 larvae were selected randomly from the progeny of each replicate cage and scored for the presence of GFP. A two-tail binomial test was used to compare the observed and expected distributions and test for significant (p >0.05) deviation from equal frequency (50%) of GFP^{+} and GFP^{-} individuals.

Cage experiments

Cage trial set up and maintenance

A schematic representation of the cage trial protocol implemented is shown in Supplementary Fig. 2. The trial consisted of 18 non-overlapping generations and was conducted in 5,000 cm^3 cages essentially as described by Pham et al.[9]. Triplicate cages (A, B and C) were seeded with three single release ratios, 1:1, 1:3, 1:9, of 3-5 day old age-matched Rec*kh* heterozygous to WT (Rec*kh*:WT) male adults (100 in total), and 100 WT adult females were added to reach an equal sex ratio for a total of 200 individuals per cage. The number of Rec*kh* males was 50 in the 1:1 release cages, 25 in the 1:3 cages, and 10 in the 1:9 cages. Adults 5-7 days old were offered a blood meal over two consecutive days. Three days later, dead adults were removed from each cage and an egg cup was provided for two days. Of the hatching larvae: 200 L1-L2 were selected at random and reared to adulthood to establish the following generation, 500 L1-L2 were selected randomly to assess the progression of the drive by screening the eye phenotype in L4 larvae and pupae (see Screening of the eye phenotype), and the remainder reared to L4 and stored in ethanol for population counts and molecular analysis. The only exception to the random selection of the 200 L1s to seed the following generation was that, due to the small initial number of transgenics, individuals from generation 1 of the 1:9 cages were all screened for their eye phenotype and new

cages were seeded with the same proportion of drive individuals found. Finally, the screening of cage 1:3_B was carried out for additional two generations for a total of 20 generations.

Screening of the eye phenotype

A sample of 500 randomly-selected L4 larvae were scored at each generation for the presence of GFP fluorescence (GFP^+ and GFP^-) and separated in two corresponding larval trays; pupae emerging from each tray were screened for eye color (black, white, and mosaic). The phenotypes were reported as follows: GFP^+/kh^+ (drive individuals with black eyes); GFP^+/kh^- (drive individuals with white eyes); GFP^+/kh^{mos} (drive individuals with mosaic eyes); GFP^-kh^+ (non-drive individuals with black eyes); GFP^-/kh^- (non-drive individuals with white eyes); GFP^-/kh^{mos} (non-drive individuals with mosaic eyes). Amongst these, individuals with phenotypes GFP^+/kh^- and GFP^-/kh^- were store as adults at -20°C for sequencing.

Population count

L4 larvae collected throughout the experiments were stored in 50 mL conical centrifuge tubes filled with ethanol. Before counting, ethanol was rinsed off and larvae were re-suspended in a fixed volume of deionized water and placed onto a shaker moving at a constant speed. Larvae were collected using a fixed-volume scoop and counted before returning them to the shaker. A total of 6-9 measurements were taken per cage every two generations. The estimated population size was calculated by averaging the number of larvae from replicate measurements and multiplying by the conversion factor (volume of water/scoop volume). The only exception to this method of counting was generation 1 of the 1:9 cages where the whole L4 population was counted.

Sanger sequencing on single mosquitoes

Genomic DNA was extracted from whole single adult mosquitoes using either the Wizard Genomic DNA Purification Kit (Promega) or the DNeasy Blood & Tissue Kit (Qiagen). All gene amplification reactions were performed using the Phusion High Fidelity PCR Master Mix with HF Buffer (New England Biolabs). To analyze the non-drive allele, primers KhE5-4 (GACGGTGACACTGTTCATGC) and KhE5-3 (CAGATGGCATGTGCATCCTC) were used to generate a 372 bp amplicon spanning the gRNA-directed cut site in the *kh* gene. Sanger sequencing (Genewiz, San Diego) of the non-drive amplicons was performed using primer KhE5-4. To analyze the Rec*kh* drive allele, primers KhE4 (CGTTCGAGTAGCACGTTG) and Agam3 rv (CAGGTGTAGAAGAAAACACGTTG) were used to produce a 1287 bp amplicon. Sanger sequencing (Genewiz, San Diego) of the Rec*kh* amplicon was performed using primer KhE4. Sequencing results from mixed traces were resolved using CRISP-ID (http://crispid.gbiomed.kuleuven.be)[45].

Amplicon sequencing of non-drive alleles from pooled mosquito extracts

DNA extraction and amplification

Genomic DNA from individuals used to seed the $1{:}3_B$ cage (generation 0) was extracted from pools of 20 adults (total of ~140); while DNA from individuals from the same cage at generations 8 and 14 was extracted from pools of 50 larvae (total of 300 each). Extractions were performed using the DNeasy Blood & Tissue Kit (Qiagen) according to manufacturer's protocol with an overnight initial lysis step. An equal volume of genomic DNA was pooled from each replicate extraction and used as template for amplification. Gene amplification was performed using the Phusion High Fidelity PCR Master Mix with HF Buffer (New England Biolabs) and primers KhE5-4 (GACGGTGACACTGTTCATGC) and KhE5-3 (CAGATGGCATGTGCATCCTC). Generated amplicons were purified from 1% agarose gels using the Zymoclean Gel DNA Recovery Kit (Zymo Research) before library preparation.

Library preparation and Sequencing

Illumina libraries were prepared for each of three samples (G_0, G_8, and G_{16} from cage $1{:}3_B$) using the NEXTFLEX PCR-free library preparation kit and NEXTFLEX Unique Dual Index Barcodes (BIOO Scientific) following the manufacturer's instructions. The input amount of DNA was 500 ng. The ends of the DNA were repaired and adenylated. The reaction was cleaned using AMPure XP magnetic beads and Illumina barcoded adapters were ligated onto the blunt end adenylated product. The adapter-ligated product was cleaned using AMPure XP beads. DNA quantity was measured by Qubit DNA HS assay and the fragment size assessed by Agilent Bioanalyzer 2100 DNA HS chip assay at the genomics facility of the University of Utah (GNomEx) where the libraries were sequenced on the Illumina NovaSeq with the SP flowcell 2x250 paired end.

Sequencing data analysis

The raw paired-end Illumina reads from the amplified genomic region were cleaned for low quality and trimmed for the presence of adapters using Trimmomatic v0.35[46]. High-quality reads were mapped against the amplicon sequence using BWA-MEM v0.7.8[47] and the alignments sorted using SAMtools v1.9[48]. Mapped paired-end reads were extracted using Picard Tools v1.96 (http://broadinstitute.github.io/picard/), and then joined to reconstruct the complete amplicon sequence using PEAR v0.9.8[49]. Identical amplicon sequences were clustered using module fastx_collapser in FASTX-ToolKit v0.0.14 (http://hannonlab.cshl.edu/fastx_toolkit/). Clustered sequences were aligned to the reference amplicon with MAFFT v7[50] under FFT-NS-2 tree-based progressive method with 1PAM/K=2 scoring matrix, if they were represented by at-least 3 paired-end reads in each dataset. After alignment with the amplicon, the analysis was focused on a 34 bp target sequence including the 23 bp of the gRNA to identify Single Nucleotide Polymorphisms (SNPs) and/or INDELs in this region. The final quantification of mutations at the target site was measured as relative frequency of paired reads in sequence variants represented in at least 100 reads.

Functional resistant allele assessments

Individuals carrying a mutated functional *kh* allele (kh^{+R}) due to the presence of a CAG>GCA-Q330A substitution affecting the PAM site were isolated from non-drive black-eyed (GFP^-/black) individuals from cage $1{:}3_B$ at generation G_{16}. Resistance of the kh^{+R} allele to Cas9-induced cleavage was assessed in the progeny of the cross between males heterozygous for a copy of the Rec*kh* drive allele and the kh^{+R} allele (kh^{Rec+}/kh^{+R}) to WT females by scoring the frequencies of GFP^+ and GFP^- mosquitoes (expected to be ~50% in case of resistance to cleavage).

Allele competition experiments were conducted in four replicate cages (A-D) each seeded with 200 individuals heterozygous for a copy of the Rec*kh* drive allele and a copy of the *kh* functional resistant allele (kh^{Rec+}/kh^{+R}) with a 1:1 sex ratio. Allele competition was inferred from the eye phenotype of the progeny of these crosses by scoring for the presence of the GFP fluorescent marker (GFP^+ or GFP^-) and the eye color (black, white, or mosaics) in adults. This was carried out for six discrete (non-overlapping) generations by screening a representative sample of ~300 adults at each generation and seeding new cages with 200 randomly picked individuals, as described for the gene-drive cage trials. In this set-up, assuming random mating, equally competitive modified *kh* alleles are expected to maintain a phenotypic ratio of 3:1 GFP^+:GFP^- individuals in each generation; deviations from this ratio would signify unequal competitiveness.

Modeling of cage population dynamics

Empirical data from the non-overlapping gene-drive experiments were used to parameterize a model of Cas9/gRNA-based homing gene-drive including resistant allele formation, and a stochastic implementation of the fitted model was used to qualitatively compare the time series of observed genotype frequencies to model-predicted ones. Model fitting was carried out for all nine gene-drive cage experiments using Markov chain Monte Carlo (MCMC) methods in which estimated parameters related to loads, resistant allele generation, and the consequences of maternal deposition of Cas9/gRNA complexes were used.

We considered discrete generations, random mixing, and Mendelian inheritance rules at the gene-drive locus, with the exception that for adults heterozygous for the homing allele (denoted by 'H') and WT allele (denoted by 'W'), a proportion, c, of the W alleles are cleaved, while a proportion, 1-c, remain as W alleles. Of those that are cleaved, a proportion, p_{HDR}, are subject to accurate HDR and become H alleles, while a proportion, (1-p_{HDR}), become resistant alleles. Of those that become resistant alleles, a proportion, p_{RES}, become in-frame, functional, cost-free resistant alleles (denoted by 'R'), while the remainder, (1-p_{RES}), become out-of-frame, non-functional, or otherwise costly resistant alleles (denoted by 'B'). The value of p_{HDR} is allowed to vary depending on whether the HW individual is female or male, and values for female and male specific HDR parameters were estimated based on G_0 crosses that provided direct information on them.

The effects of maternal deposition of Cas9/gRNA complexes were accommodated after computing the gene-drive-modified Mendelian inheritance rules. If offspring having a W allele had a mother having the H allele, then this would lead to Cas9/gRNA complexes being deposited in the embryo by the mother, possibly resulting in cleavage of the W allele. We considered cleavage to occur in a proportion, p_{MC}, of these embryos, with a proportion, p_{MR}, of the cleaved W alleles becoming R alleles, and the remainder, (1-p_{MR}), becoming B alleles. These considerations allow us to calculate expected genotype frequencies in the next generation, and to explore the impacts of loads and maternal deposition parameters that maximize the likelihood of the experimental data. Estimated parameters include loads in females associated with having one or two copies of the H allele or the BB genotype, and p_{RES}, p_{MC} and p_{MR}, as defined earlier. A stochastic version of the fitted model was implemented using a discrete generation version of the Mosquito Gene-drive Explorer (MGDrivE) model[51] with an adult population size of 200. The complete modeling framework is described in the S1 Text section of Pham et al.[9].

DATA AVAILABILITY

The full sequence of the plasmids used in this work will be deposited in GenBank.

Raw sequencing data will be available in the Sequence Read Archive (SRA) database under BioProject PRJNA607757 and accession numbers SAMN14145944 (cage 1:3_B, generation G_0), SAMN14145945 (cage 1:3_B, generation G_8), and SAMN14145946 (cage 1:3_B, generation G_{14}).

All other data are contained within the manuscript main text and supplementary information.

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AUTHOR CONTRIBUTIONS

V.M.G., E.B., A.A.J., and A.A. conceived the experimental approach; A.A., N.J., H-F.L., K.H., E.A.B, and G.T. performed laboratory research; A.R. and J.J.E. performed bioinformatics analysis; J.M.M. and J.B.B. performed modeling; A.A., E.B., J.M.M, and A.A.J. wrote the manuscript draft; V.M.G. prepared figure artwork. All authors contributed to the final version of the manuscript.

COMPETING INTERESTS

V.M.G. and E.B. have an equity interest in Synbal, Inc. and Agragene, Inc., companies that may potentially benefit from the research results, and serve on both companies' Scientific Advisory Board and on the Board of Directors of Synbal, Inc. The terms of this arrangement have been reviewed and approved by the University of California, San Diego in accordance with its conflict-of-interest policies.

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Figure 1

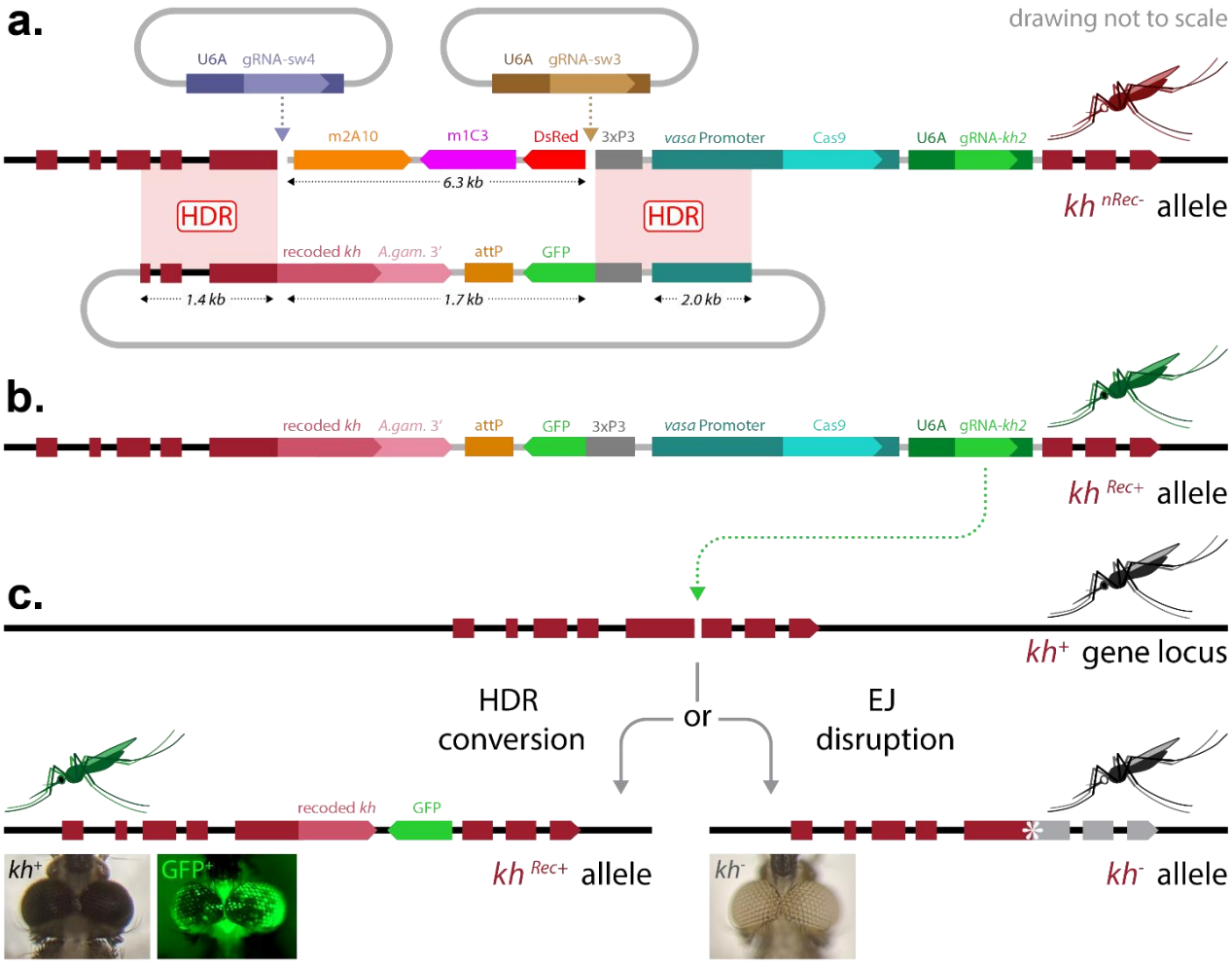

Figure 1. The Rec*kh* gene-drive. a) Swap strategy for Cas9/gRNA-mediated cassette exchange. Two plasmid-encoded gRNAs (top) guide cleavage in the genome of the white-eyed nRec mosquito line (kh^{nRec-})[8] (middle), leading to the excision of a fragment including the DsRed eye (3xP3) marker and the two anti-malarial effectors m2A10 and m1C3[11]. The HDR template plasmid (bottom) carries homology arms flanking either cut site, promoting the insertion of a GFP-marked donor template that carries a recoded portion of the *kh* gene followed by the 3'-end sequence of the *An. gambiae kh* gene including the 3'UTR (A.gam.3') to minimize homology. **b)** The insertion of this unit restores *kh* gene function while creating a sequence (kh^{Rec+}) that is uncleavable by the endogenous drive components. **c)** The Rec*kh* gene-drive includes an *An. stephensi* codon-optimized Cas9 driven by the germline-specific *vasa* promoter from *An. stephensi* and a gRNA (gRNA-kh2) directed to the fifth exon of the unmodified kh^{+} gene (top) regulated by the ubiquitous promoter of the *An. stephensi U6A* gene. The cut in the *kh* gene of the Rec*kh* mosquito germline can be repaired by drive integration via HDR (homology-directed repair) or by the less desirable EJ (end-joining) pathway (bottom). HDR results in the integration of the drive cassette that maintains *kh* gene function at the integration site (kh^{Rec+}); while EJ usually causes the formation of loss-of-function alleles (kh^{-}). When function is lost in both copies of the gene, individuals with white eyes are produced. *kh*: *kynurenine hydroxylase* gene. attP: *φC31* recombination site. 3xP3: eye-marker promoter.

Figure 2

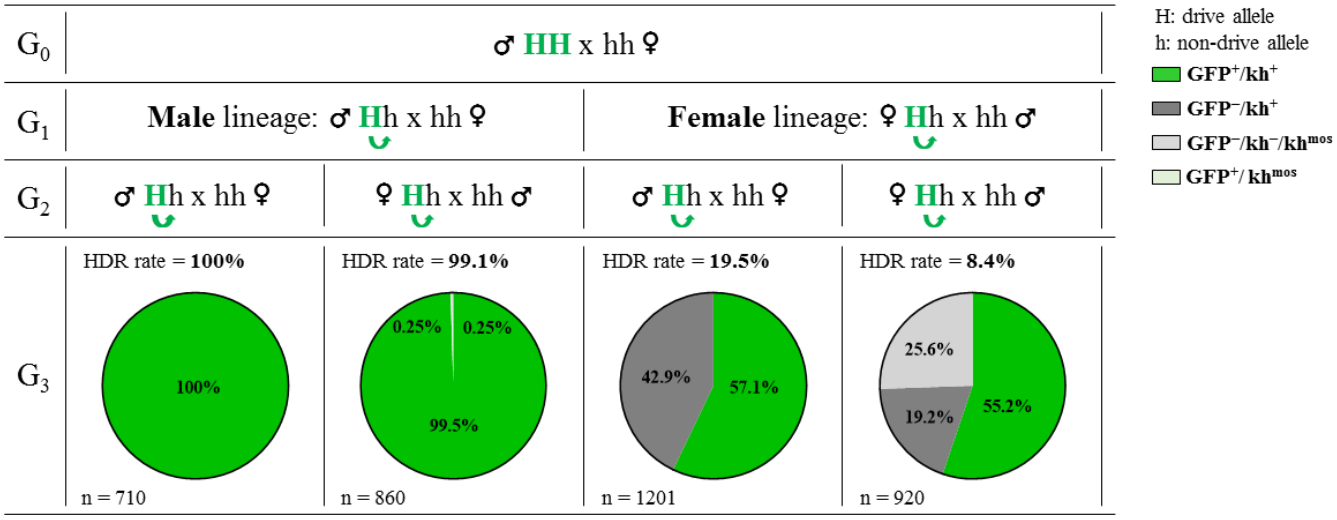

Figure 2. Inheritance of Rec*kh* through paternal and maternal lineages. Charts represent the proportion of individuals inheriting the Rec*kh* drive element (GFP$^+$, in green) from heterozygous parents originated from drive males or drive females. The proportions of individuals that have not inherited the drive (GFP$^–$) element and have WT black eyes (*kh*$^+$) (dark grey) and those with white (*kh*$^–$) or mosaic (*kh*^{mos}) eyes (light grey) are also shown. Rare (0.25%) drive individuals with mosaic eyes (GFP$^+$/*kh*^{mos}) are depicted in light green. 'H' and 'h' refer to the mosquito genome at the *kh* locus, where 'H' is the Rec*kh* drive allele and 'h' is a non-drive allele. The green arrows show the potential for conversion of the h allele in the germline. The corresponding HDR rate, i.e. the proportion of h alleles converted to H alleles is reported. Each cross was performed *en masse* (30 females and 15 males) in triplicate cages using drive individuals mated to WT and by screening a representative subset of individuals (n) generated in the progeny. The numbers reported are the mean from the three replicates. Raw data for these crosses are reported in Supplementary Table 2.

Figure 3

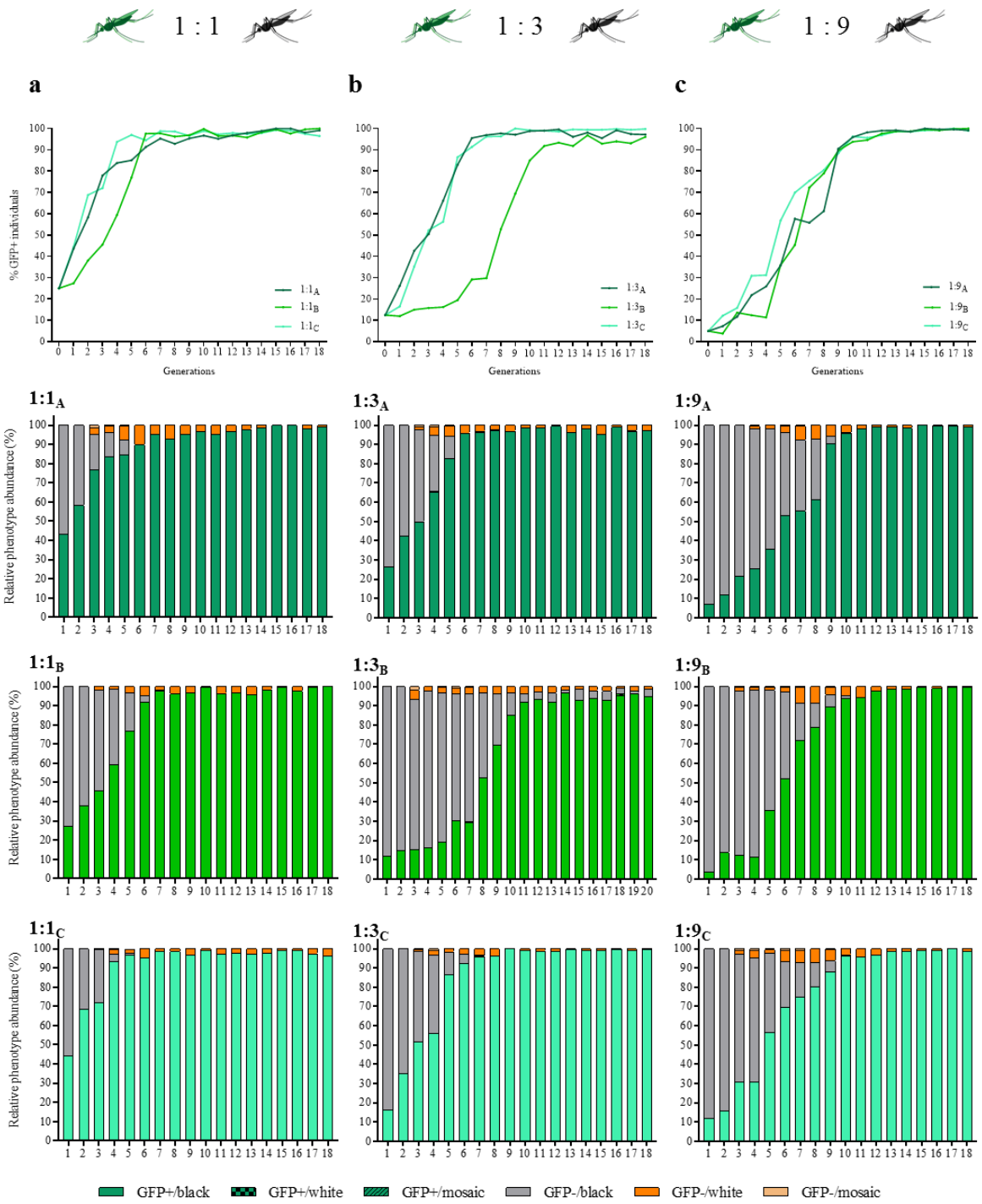

Figure 3. Dynamics of Rec*kh* over 18 discrete generations in caged populations seeded with three release ratios of Rec*kh*:WT males. Top row: drive efficiency shown as percentage of GFP$^+$ individuals (Y axes) at each generation (X axes) in triplicate cages seeded with 1:1 (**a**), 1:3 (**b**) and 1:9 (**c**) Rec*kh*:WT male ratios. Bottom three rows: relative proportion of eye phenotypes (Y axes) observed in a sample of ~500 individuals reported for each generation (X axes) for all cages. Individuals containing the drive are shown in green, those with wild-type phenotype in grey, and non-drive individuals with white or mosaic eyes in dark and light orange, respectively. A schematic of the protocol used is reported in Supplementary Fig. 2 and raw data for each cage in Supplementary Tables 6-8.

Figure 4

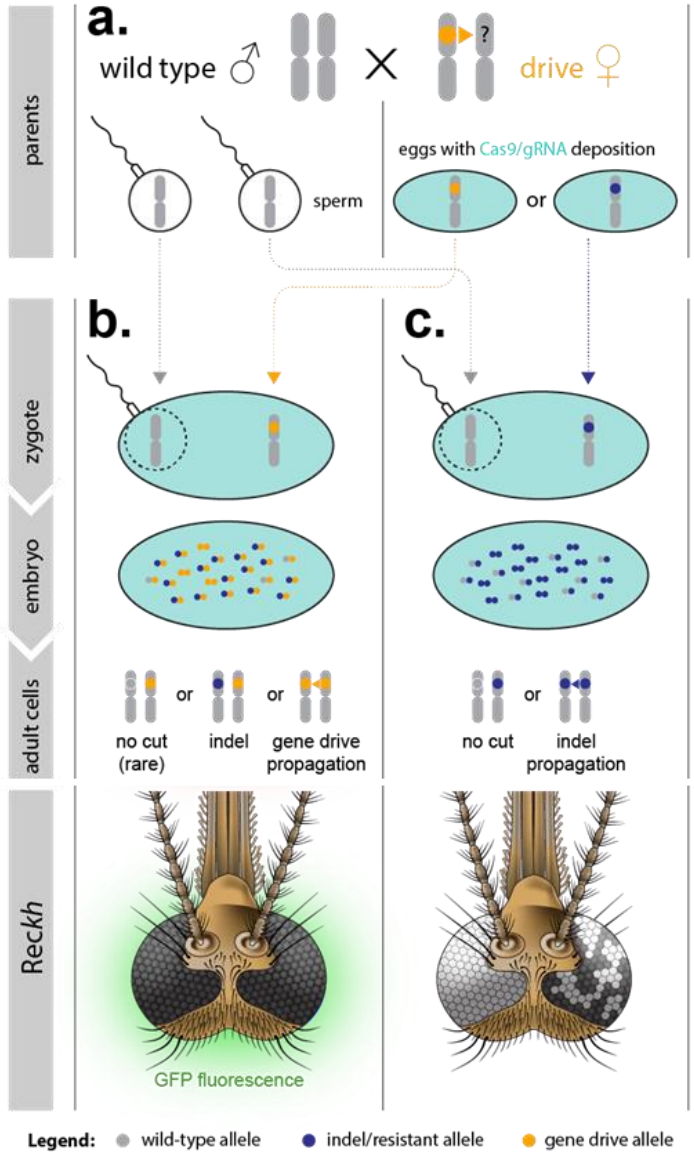

Figure 4. Effects of lethal/sterile mosaicism on the Rec gene-drive system. a) A female heterozygous for the drive can produce eggs carrying a copy of the drive (●, kh^{Rec+}) or eggs carrying an EJ-induced non-functional resistant allele (●, kh^{-}). Both types of eggs carry maternally deposited cytoplasmic Cas9/gRNA complexes (light blue filling) that can act on the incoming WT paternal allele (●, kh^{+}). **b**) The soma of individuals inheriting a copy of the drive from their mothers is a mosaic of cells with varying proportions of genotypes kh^{Rec+}/kh^{-}, kh^{Rec+}/kh^{+}, and kh^{Rec+}/kh^{Rec+}. Rec*kh* individuals emerging from such embryos have at least one functional copy of *kh* provided by the drive system (kh^{Rec+}), therefore have GFP^{+}/black eyes and females are fit for reproduction. **c**) The soma of individuals inheriting an EJ non-functional mutation from their drive mothers is a mosaic of cells with genotypes kh^{-}/kh^{-} or kh^{-}/kh^{+}. The ability of females emerging from such embryos to reproduce depends on the proportion of somatic cells with genotype kh^{-}/kh^{-}. These individuals may display mosaic or white eye phenotype if mutations affect the cells forming the eyes. Diploid cells in (b) and (c) that become germline progenitors also may be affected by mosaicism, which can affect drive capabilities.

Figure 5

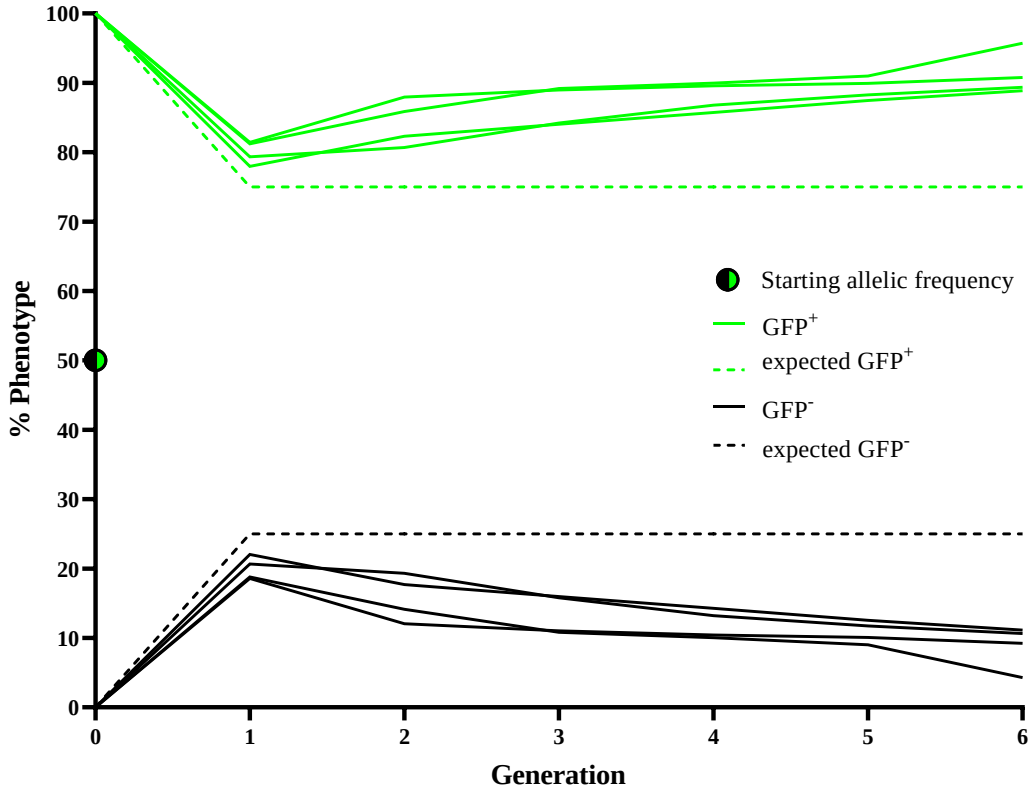

Figure 5. Competition between the drive *kh*$^{Rec+}$ and the resistant functional *kh*$^{+R}$ alleles in caged populations. Four independent cages were set up using 100 male and 100 female *kh*$^{Rec+}$/*kh*$^{+R}$ mosquitoes each, which corresponds to an initial allelic frequency of 50%, marked using a half green-half black dot at generation G_0. Eye fluorescence (GFP$^+$ or GFP$^-$) and color (black, white, or mosaic) frequencies associated with each modified *kh* allele were scored at every generation for six consecutive non-overlapping generations. The proportion of GFP$^+$ individuals (genotype *kh*$^{Rec+}$/*kh*$^{Rec+}$ or *kh*$^{Rec+}$/*kh*$^{+R}$) in the replicate cages is depicted by green lines and its expected frequency in the presence of equal competition between the two alleles (75%) as a dashed green line. The proportion of GFP$^-$ individuals (genotype *kh*$^{+R}$/*kh*$^{+R}$) is depicted as black lines and its expected frequency in the presence of equal competition between the two alleles (25%) as a dashed black line. All individuals screened presented a fully intact WT black eye.

Figure 6

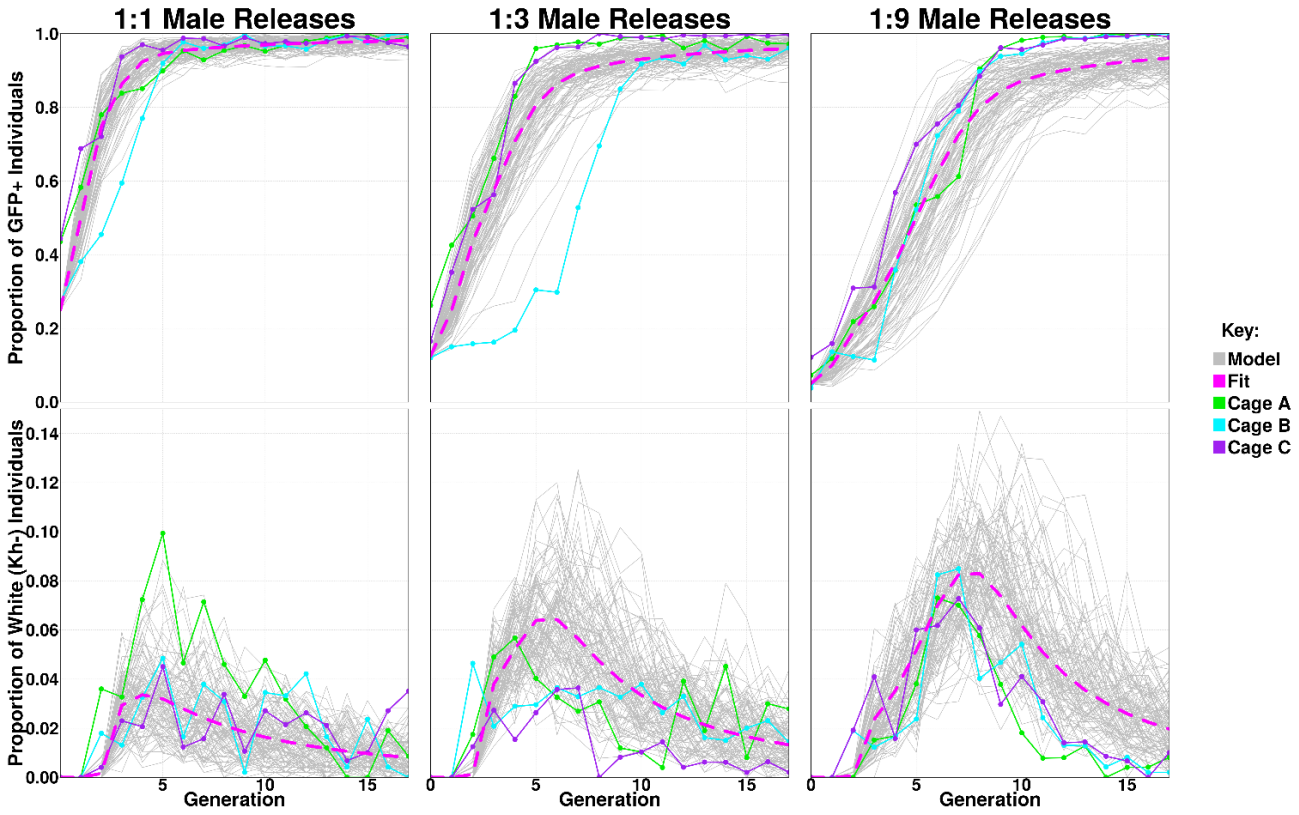

Figure 6. Observed and model-predicted dynamics of GFP$^+$ and *kh*$^-$ phenotypes in the Rec*kh* cage experiments. Solid green, blue, and purple lines represent the experimental data over 18 generations observed in three replicates (Cages A, B, C) with release ratios of Rec*kh*:WT males of 1:1, 1:3, and 1:9. Dotted pink lines represent the fitted deterministic model (Fit), and grey lines are 100 stochastic realizations of the fitted model for each release ratio (Model). X axes report the generation number after release and Y axes the proportion of each eye-phenotype. The GFP$^+$ phenotype results from having at least one copy of the drive allele and hence reflects the spread of the gene-drive system to full or near-full introduction for all experiments. The *kh*$^-$ phenotype is associated with having no copies of the WT, Rec*kh*, or functional resistant alleles (i.e. having two copies of the non-functional resistant allele) and reflects the low-level emergence and gradual elimination of this allele from the population due to its load in homozygous females. The stochastic model captures the variability inherent in the experimental process and reflects some of the variability observed in the early stages of the spread of the gene-drive allele.