

Research



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Natural alleles at the *Doa* locus underpin evolutionary changes in *Drosophila* lifespan and fecundity

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‘Evolve and resequence’ (E&R) studies in *Drosophila melanogaster* have identified many candidate loci underlying the evolution of ageing and life history, but experiments that validate the effects of such candidates remain rare. In a recent E&R study we have identified several alleles of the LAMMER kinase *Darkener of apricot* (*Doa*) as candidates for evolutionary changes in lifespan and fecundity. Here, we use two complementary approaches to confirm a functional role of *Doa* in life-history evolution. First, we used transgenic RNAi to study the effects of *Doa* at the whole-gene level. Ubiquitous silencing of expression in adult flies reduced both lifespan and fecundity, indicating pleiotropic effects. Second, to characterize segregating variation at *Doa*, we examined four candidate single nucleotide polymorphisms (SNPs; *Doa-1*, *-2*, *-3*, *-4*) using a genetic association approach. Three candidate SNPs had effects that were qualitatively consistent with expectations based on our E&R study: *Doa-2* pleiotropically affected both lifespan and late-life fecundity; *Doa-1* affected lifespan (but not fecundity); and *Doa-4* affected late-life fecundity (but not lifespan). Finally, the last candidate allele (*Doa-3*) also affected lifespan, but in the opposite direction from predicted.

1. Background

‘Evolve & resequence’ (E&R) studies, combining experimental evolution experiments with whole-genome sequencing, have emerged as a powerful method for identifying the genetic basis of evolutionary change [1–5]. In the *Drosophila melanogaster* model, for example, E&R studies have been successfully used to identify candidate loci underlying thermal adaptation [6,7], the evolution of developmental rate [8], body size [9], hypoxia tolerance [10,11], courtship song [12], lifespan and late-life fertility [13–15], dietary metabolism [16], pathogen resistance [17,18], egg size [19], desiccation resistance [20], starvation resistance [21] and factorial selection on multiple life-history traits [22], among others.

Despite the identification of many putatively adaptive loci in such E&R studies, experimental assays that validate the presumed functional effects of such candidates are rare, which remains a major challenge for current tests of adaptation at the genetic level [1–3,23]. Here, we examine the putative life-history effects of a candidate locus, *Darkener of apricot* (*Doa*), and associated candidate alleles that we have previously identified in an E&R experiment on longevity and late-life fertility in *D. melanogaster* [22]. *Doa*, a member of the LAMMER kinases, is known to phosphorylate a wide range of substrates and to be involved in many biological functions, such as embryonic development, oocyte formation, somatic sex determination, courtship behaviour and oxidative stress resistance (see Supplementary file 1 for additional information) [24–30]. Interestingly, *Doa* has been identified as a promising life-history candidate locus in several independent E&R experiments and genome-wide association studies (GWAS) on lifespan and late-life fertility, egg volume and ovariole number [15,19,22,31–33]. These

findings make *Doa* a prime candidate locus for further study. Importantly, while several gene functions of *Doa* have been well established in molecular genetics studies (see above), the putative effects upon fitness components of naturally occurring polymorphisms at *Doa* have not yet been assessed.

In our experiments, we used two complementary approaches to investigate the functional role of *Doa* in affecting two major fitness components that had evolved in our E&R study: lifespan and fecundity [22,34]. First, we used ubiquitous adult-specific RNAi silencing to examine the overall effects of *Doa* on lifespan and fecundity. Similar to using null mutants (amorphic mutations), this type of functional test is aimed at understanding function at the level of the whole gene; it can potentially reveal the complete phenotypic effects of a candidate gene, including any pleiotropic (and potentially deleterious) functions that it might have (e.g. [35,36]). However, given that specific alleles or mutations of a pleiotropic gene may differ in the functions they affect (see [35–37]), we next investigated segregating variation at *Doa* by examining four candidate single nucleotide polymorphisms (SNPs) using a genetic association approach based on ‘Mendelian randomization’. Beyond confirming a role of the *Doa* locus in life-history adaptation, our results illustrate key differences in the effects of the four investigated SNPs on fecundity and longevity.

2. Material and methods

(a) Transgenic RNAi

Transgenic *in vivo* RNAi was performed using the mifepristone (RU486)-inducible GeneSwitch(GS)-GAL4 system in combination with *Doa* UAS-RNAi constructs [38]. The GS system allows us to drive the expression of *Doa* UAS-RNAi during the adult stage only, thereby avoiding potential developmental carry-over effects. Importantly, this system makes it possible to compare the effects of RNAi (i.e. the application of the drug, resulting in RNAi-mediated knockdown) with negative control (i.e. no application of the drug) within the same transgenic genotype, thus providing the most robust control possible with regard to genotype. We used the ubiquitously expressing *daughterless* (*da*)-GeneSwitch(GS)-GAL4 construct [39] (courtesy of Véronique Monnier, Paris) to drive the expression of two independent *Doa* UAS-RNAi lines, obtained from the Vienna *Drosophila* RNAi Center (VDRC) (#19066 [D19]; #102520 [D10]), with construct insertions on chromosomes 3 and 2, respectively, thus controlling for potentially confounding effects of insertion position. These constructs target the catalytic domain of *Doa* that is shared by all isoforms.

All lines were kept and assays were performed at 25°C, 65% humidity and 12h : 12h light : dark cycle, on a cornmeal–yeast–sucrose–agar medium (per 1 L of food: 7 g agar, 50 g sucrose, 50 g cornmeal, 50 g yeast, 6 ml propionic acid, 10 ml of a 20% nipagin stock solution). After emergence, flies were kept on medium containing either 100 or 200 µg ml⁻¹ mifepristone (233 or 466 µM, respectively) dissolved in ethanol, or on control medium (i.e. containing ethanol without mifepristone). Note that increasing levels of mifepristone can induce higher levels of gene knockdown, in a dose-dependent fashion. We confirmed that both RNAi lines resulted in a significant knockdown of *Doa* expression using quantitative real-time PCR (qRT-PCR) (see electronic supplementary material, File S2 for details).

Mifepristone concentrations of up to 200 µg ml⁻¹ have previously been used without detrimental effects on survival of adult flies [15,39,40]. To confirm this, we tested the effect of 100 and 200 µg ml⁻¹ mifepristone on lifespan and fecundity of F1 flies of a cross of *da*-GS-GAL4 females with males of the

isogenic progenitor strain for the VDRC (GD) RNAi library strains, *w*¹¹¹⁸ (#60000). We did not observe any confounding deleterious effects of these concentrations on the phenotypes of interest (electronic supplementary material, File S3).

To assess the effect of RNAi directed against on *Doa* on lifespan, cohorts of F1 offspring between crosses of *da*-GS-GAL4 virgin females and males carrying one of the two UAS-RNAi constructs or the isogenic control strain were collected within a 24 h window. Flies were sexed under mild CO₂ exposure and transferred to 1 L demography cages with food vials (with 0, 100 or 200 µg ml⁻¹ mifepristone) attached to the cages. For each genotype and mifepristone concentration, we set up three replicate cages, each containing 75 flies per sex. Dead flies were scored and fresh food was provided every two days. Differences in lifespan between mifepristone-induced RNAi and uninduced controls were analysed in *R* (v. 3.3.1) using mixed-effects Cox (proportional hazards) regression with mifepristone concentration, sex and their interaction as fixed effects and with ‘replicate cage’ as a random effect, using the *R* package *coxme* (v. 2.2-5).

The effect of *Doa* RNAi on fecundity was assessed by measuring daily egg production of females. Virgin females were collected from the F1 offspring of *da*-GS-GAL4 females and males carrying one of the two UAS-RNAi constructs or the isogenic control strain. After 24 h, two virgin females and two *w*¹¹¹⁸ males were placed together in vials with either 0 (i.e. control) or 200 µg ml⁻¹ mifepristone. Ten replicate vials were prepared per genotype and mifepristone concentration. Flies were left for 48 h to ensure mating and consumption of mifepristone before the start of the experiment; after this period, they were transferred to fresh vials with food (with 0 or 200 µg ml⁻¹ mifepristone, respectively) to lay eggs for 24 h. The numbers of eggs laid by each pair of females were counted under a dissecting microscope; daily egg production was measured for nine consecutive days. We calculated average fecundity per female over 3 days in order to average out day-to-day variation in egg laying. Fecundity data were analysed in *R* (v. 3.3.1) using generalized linear mixed models with a Poisson distribution and with mifepristone concentration, with day and their interaction as fixed effects and with ‘replicate vial’ as a random effect using the *R* package *lme4* (v. 1.1-13). Exposure to mifepristone of the control line did not cause adverse (and thus confounding) effects on lifespan and fecundity (see electronic supplementary material, File S3).

(b) SNP association study

To examine whether the four experimentally candidate SNPs at *Doa* affect lifespan and fecundity (see below for details of SNP identification), we performed a genetic (SNP) association study, based on ‘Mendelian randomization’ [41–43]. Mendelian randomization (MR) approaches aim to identify putative causal effects of candidate loci by testing the alternative allelic states in a genetically diverse background to limit the impact of potentially confounding (epistatic) factors in the genetic background. A critical factor for the reliability of MR approaches is the lack of linkage disequilibrium (LD) between the focal locus and other loci in the genetic background. Here, we used strains from the *Drosophila* Genetic Reference Panel (DGRP [44]; obtained from the Bloomington *Drosophila* Stock Center [BDSC]), which provides ample natural genetic variation for MR. As LD typically decays very rapidly in *D. melanogaster*, within a few hundred base pairs or so [44], the MR approach is expected to provide information on the functional impact of an individual candidate SNP, with little or no confounding effects of other (*Doa*) SNPs. To confirm this, we analysed LD (measured by pairwise *r*²) among all polymorphic *Doa* SNPs (minor allele frequency ≥ 0.1) in the complete panel of DGRP lines, as done by [43] before (see electronic supplementary material, File S4).

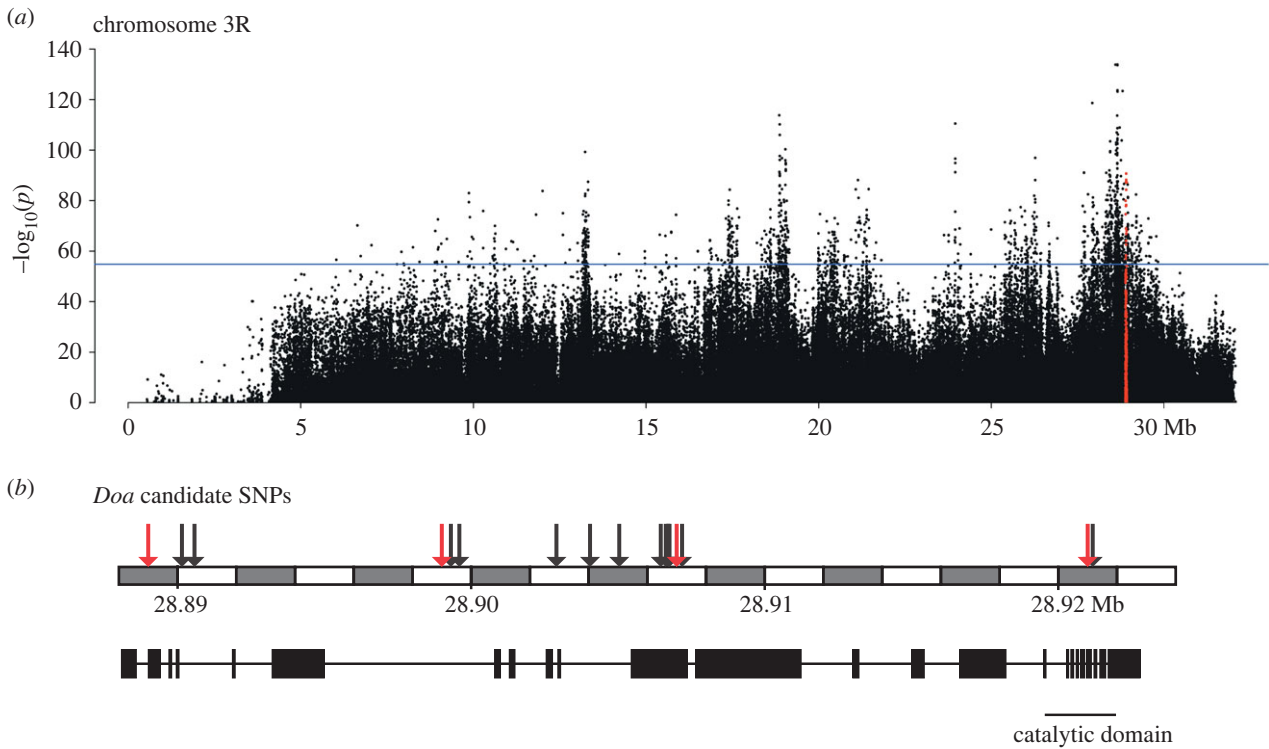


Figure 1. Overview of the experimentally evolved *Doa* SNPs. (a) The Manhattan plot demonstrates the position of *Doa* on chromosome 3R in the Evolve and resequence study by Hoedjes *et al.* [22]. *Doa* (all SNPs within the gene are highlighted) is located within a relatively large region at the end of chromosome 3 that had been under selection. The horizontal line (at $-\log_{10}(54.9)$) indicates the threshold for significant candidate SNPs (false discovery rate (FDR) = 0.0005). (b) The gene structure of *Doa* with the 16 significant candidate SNPs (at FDR < 0.0005; indicated with arrows) that were identified as candidates for ageing and reproduction. Arrows that have been highlighted indicate the four SNPs that have been investigated functionally in this study. Coordinates according to reference genome v6.

For each of the four candidate nucleotide positions at *Doa*, we randomly selected 20 distinct DGRP lines that were fixed for the SNP allele that was previously identified as being the major allele in the short-lived, early reproduction experimental evolution lines (control lines; see [22]). Similarly, we randomly selected 20 lines fixed for the SNP allele that was found to be the major allele in the long-lived, late-reproduction experimental evolution lines (see electronic supplementary material, table S3 for details of the crosses). SNP genotypes were confirmed by sequencing a small genomic region surrounding each SNP using Sanger sequencing. For each allelic state ('short-lived' versus 'long-lived') and nucleotide position, we generated 10 unique F1 crosses, each cross being made from a different pair of distinct DGRP lines sharing the same SNP state (i.e. virgin females of one strain crossed to males from the other strain); because the DGRP lines are inbred, this was done to minimize potentially confounding homozygous effects at non-candidate loci in the genomic background. Thus, for each of the four candidate nucleotide positions and for each alternative allele ('short-lived' versus 'long-lived') we had a 10-fold replicated panel of independent F1 genotypes fixed for a given SNP allele but maximally heterozygous at other genomic positions (for details see the overview in electronic supplementary material, table S3). In the end, due to the low viability of some DGRP lines and F1 crosses, we phenotyped between 8–10 F1 crosses per candidate SNP and allelic state. To evaluate whether any other positions in the genome, besides the candidate SNP allele, were highly differentiated between the four pairs of panels, we calculated SNP-wise F_{ST} based on the method of Weir and Cockerham [45], using the pooled genome sequence information per panel [42] (electronic supplementary material, File S5).

F1 crosses were reared and assays performed at 25°C, 65% humidity and 12 h : 12 h light : dark cycle, on a cornmeal–yeast–sucrose–agar medium, as described above. Lifespan was measured using demography cages, as above. Flies that had emerged within a 24 h window were collected, and for each F1

cross 75 males and 75 females were placed in a single demography cage. Differences in lifespan between the two allelic states of each SNP were analysed in *R* (v. 3.3.1) using mixed-effects Cox (proportional hazards) regression with allele, sex and their interaction as fixed effects and with 'F1 cross' as a random effect using the *R* package *coxme* (v. 2.2-5).

Fecundity was measured over a period of 30 days after eclosion in order to provide insight into early (peak) and late (post-peak) fecundity. Flies that had eclosed within a 24-h window were collected for crosses; for each F1 cross, two females and two males were placed in a vial containing regular medium, with three replicate vials per F1 cross. Every third day (i.e. on days 3, 6, 9, 12, 15, 18, 21, 24, 27 and 30), the number of eggs laid by each pair of females during a 24-h period was determined using a dissecting microscope. Fecundity was analysed using generalized linear mixed models with a Poisson distribution in *R* (v. 3.3.1), with allelic state, day and their interaction as fixed effects and 'replicate vial' as a random effect using the *R* package *lme4* (v. 1.1-13).

3. Results and discussion

(a) Evolutionary changes at *Doa* might underpin life-history evolution

We previously identified *Doa* as a life-history candidate locus in an E&R experiment in which fruit flies were selected for late-life fecundity and where a longer lifespan evolved as a correlated response [22]. In that study, *Doa* was identified as one of multiple candidate loci under selection (figure 1a). Genetic tests of candidate genes and SNPs are critical to distinguish the putative causal loci from false positive signals and to determine if they have an effect on either one or

Table 1. Details on the *Doa* candidate SNPs. The genomic location of the four *Doa* SNPs that were investigated functionally is shown. For each SNP, a significant difference in allele frequencies was observed between lines selected for early age-at-reproduction (control) versus lines selected for late-life (postponed) reproduction (which associated with an evolutionary increase in lifespan: 'long-lived').

| name | location | feature | allele frequency | | control allele | 'long-lived' allele |
|--------------|---------------|------------|------------------|------------|----------------|---------------------|
| | | | control | long-lived | | |
| <i>Doa-1</i> | 3R:28'888'916 | intronic | 0.18 | 0.52 | C | T |
| <i>Doa-2</i> | 3R:28'898'997 | intronic | 0.43 | 0.80 | A | G |
| <i>Doa-3</i> | 3R:28'907'179 | missense | 0.55 | 0.90 | A | G |
| <i>Doa-4</i> | 3R:28'921'024 | synonymous | 0.40 | 0.78 | C | T |

Table 2. Statistical tests of the effects of *Doa* RNAi on lifespan and fecundity (egg-laying rate). Two independent RNAi constructs (D19 and D10) that both target the catalytic domain of *Doa* were used in combination with the mifepristone-inducible GeneSwitch-GAL4 > UAS system. A strain with the same genetic background as the two constructs (*w¹¹¹⁸*) was used as control for adverse effects of mifepristone application. Significant effects are indicated in bold.

| | longevity | | fecundity | |
|--|-----------|-----------------------------------|--|----------|
| | χ^2 | <i>p</i> | χ^2 | <i>p</i> |
| <i>w¹¹¹⁸</i> (control) | | | <i>w¹¹¹⁸</i> (control) | |
| mifepristone | 8.64 | 0.071 | mifepristone | 7.31 |
| sex | 95.68 | <2.2 × 10⁻¹⁶ | day | 50.83 |
| interaction | 3.63 | 0.163 | interaction | 3.59 |
| D10 | | | D10 | |
| mifepristone | 51.53 | 1.7 × 10⁻¹⁰ | mifepristone | 1.64 |
| sex | 83.56 | <2.2 × 10⁻¹⁶ | day | 34.12 |
| interaction | 37.29 | 8.0 × 10⁻⁹ | interaction | 1.61 |
| D19 | | | D19 | |
| mifepristone | 317.24 | <2.2 × 10⁻¹⁶ | mifepristone | 320.54 |
| sex | 383.21 | <2.2 × 10⁻¹⁶ | day | 508.72 |
| interaction | 284.46 | <2.2 × 10⁻¹⁶ | interaction | 307.51 |

both of the evolved traits. *Doa* is a very large gene, spanning 34.7 kb, and encodes at least 6 protein isoforms that are expressed in an age- and tissue-specific manner from alternative promoters and which have different, non-redundant functions [25,26]. SNPs located at different positions within the *Doa* gene might thus have different functions.

In total, we identified 16 biallelic SNPs (either intronic or in the coding region) having highly significant allele frequency differentiation (FDR < 0.0005) between the early-reproduction and late-reproduction (and hence increased lifespan) selection regimes in our E&R study [22] (figure 1*b*, electronic supplementary material, table S1). We chose four of these SNPs, based on their allele frequencies' differentiation between the selection regimes and their distribution across the length of the gene, for functional assays (figure 1, red arrows, and table 1; see below). As these SNPs were identified in an E&R study performed in a controlled laboratory setting, we first compared their allele frequencies to those in natural populations, using data from the DEST database [46] (see electronic supplementary material, File S6 for approach). These analyses showed that

all four SNPs are polymorphic in European populations and that the allele frequencies observed in the E&R study fall within the range of frequencies in natural populations (*Doa-1*: 0.16–0.57, *Doa-2*: 0.34–0.72, *Doa-3*: 0.65–0.98, *Doa-4*: 0.51–0.95, see electronic supplementary material, File S6 and table S2). Moreover, there was a significant latitudinal cline in allele frequency at *Doa-4* ($\chi^2 = 174.3$, $P_{\text{corrected}} = 0.0069$) and a significant longitudinal cline at *Doa-3* ($\chi^2 = 222.9$, $P_{\text{corrected}} = 0.037$) across European populations (electronic supplementary material, table S4). This is notable because numerous life-history traits in *D. melanogaster*, including fecundity and lifespan, exhibit a clinal distribution, presumably due to spatially varying selection [3,42,43,47–50]. These population genetic observations thus lend further support to the idea that *Doa* potentially represents a target of selection on life-history traits.

(b) *Doa* has pleiotropic life-history effects

To functionally validate the role of *Doa* in longevity and fecundity at the level of the whole gene we knocked down

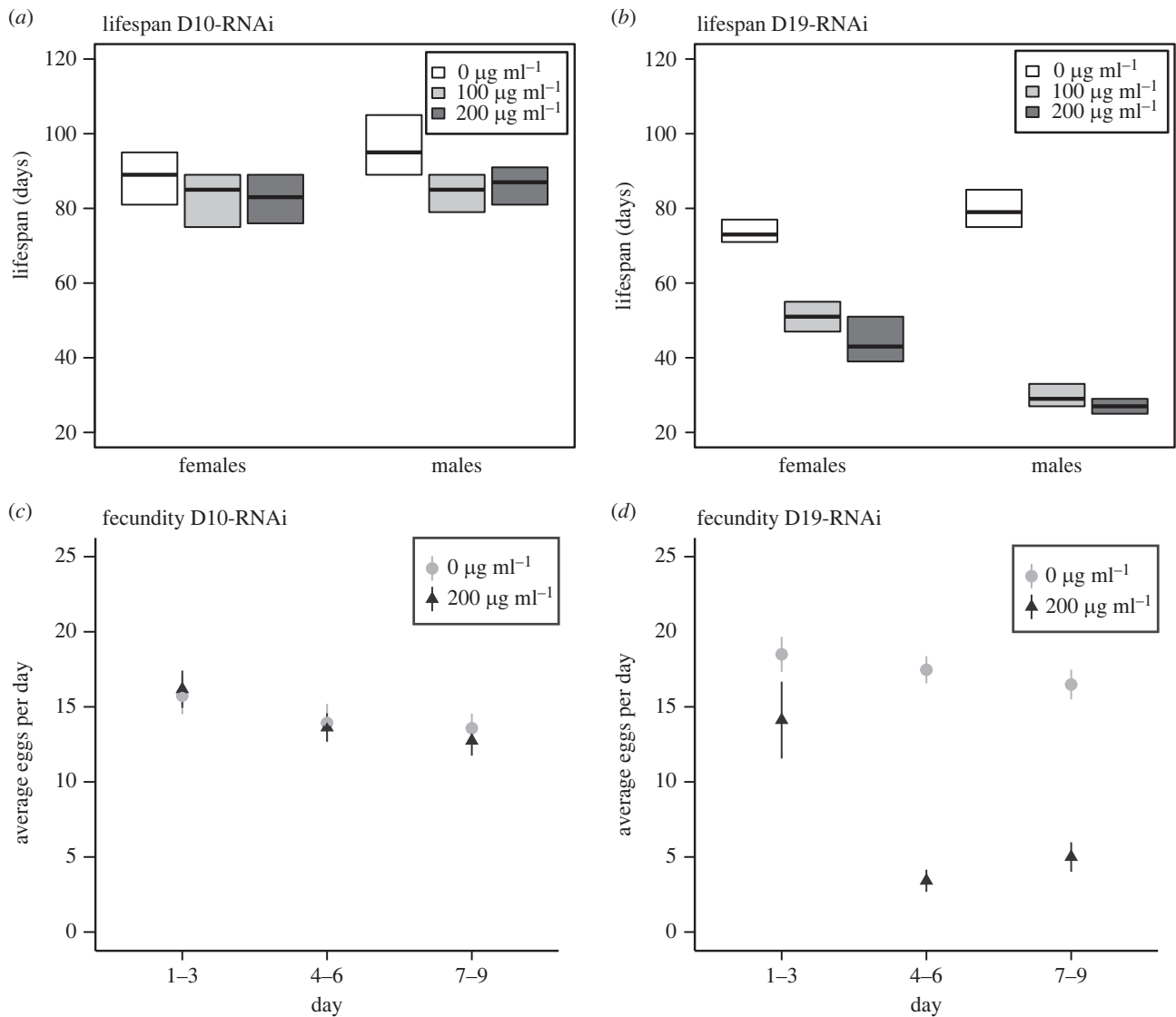


Figure 2. Knockdown of *Doa* using transgenic RNAi demonstrates significant effects on lifespan and fecundity. Two independent RNAi constructs (D19 and D10) that both target the catalytic domain of *Doa* were used in combination with the mifepristone-inducible GeneSwitch-GAL4 > UAS system. Concentrations refer to the concentrations of mifepristone (RU-486) used to induce RNAi. A significant reduction of adult lifespan was observed with both constructs ((a) construct D10, (b) construct D19), whereas a reduction in female fecundity was observed for construct D19 only ((c) construct D10, (d) construct D19; see table 2 for statistics).

all transcript variants by targeting the common, catalytic domain of *Doa* with ubiquitous (i.e. non-tissue-specific) transgenic RNAi. We employed two different RNAi constructs (i.e. two independent chromosomal insertions) to control for confounding effects of insertion position. To exclude potentially detrimental developmental carry-over effects of *Doa* knockdown on adult fitness, we reduced *Doa* expression levels in the adult stage only, by driving RNAi with the mifepristone-inducible GeneSwitch-GAL4 system [38]. For both *Doa*-RNAi constructs, we observed a significant reduction in lifespan in both sexes with increasing levels of mifepristone (figure 1*a,b*, table 2, electronic supplementary material, S2). Overall, the effect on lifespan was strongest for the D19 construct, which also achieved a stronger knockdown of *Doa* as determined by qRT-PCR as compared to construct D10. For both constructs, there was a significant interaction between sex and mifepristone concentration, which reflects the overall stronger effects of *Doa* RNAi on male than female lifespan. These findings agree with the observation of Huang *et al.* [31] that weak, constitutive knockdown of *Doa* (also using construct D10, VDRC #102520) affects lifespan in males, but

not females; however, in their study, the direction of the effect depended on assay temperature. Sexual dimorphism in longevity is not uncommon among organisms, including fruit flies [51,52]. In terms of fecundity, we observed a strong, significant reduction in egg-laying rate for construct D19 but not for D10 (figure 2*c,d*, table 2).

These findings show that the *Doa* gene has pleiotropic effects on lifespan and reproduction [22] and demonstrate that modifying expression in the adult stage is sufficient to mediate these effects. Moreover, the magnitude and the direction of these effects depend on the strength of the knockdown (also see [31]). To obtain a better understanding of the role of *Doa* in evolving populations we next studied the effects of the four candidate SNPs identified in the E&R study on fecundity and longevity (see above and [22]).

(c) *Doa* natural alleles have pleiotropic and non-pleiotropic effects

The four candidate SNPs that were functionally characterized were located both in coding and non-coding regions; *Doa-4* is

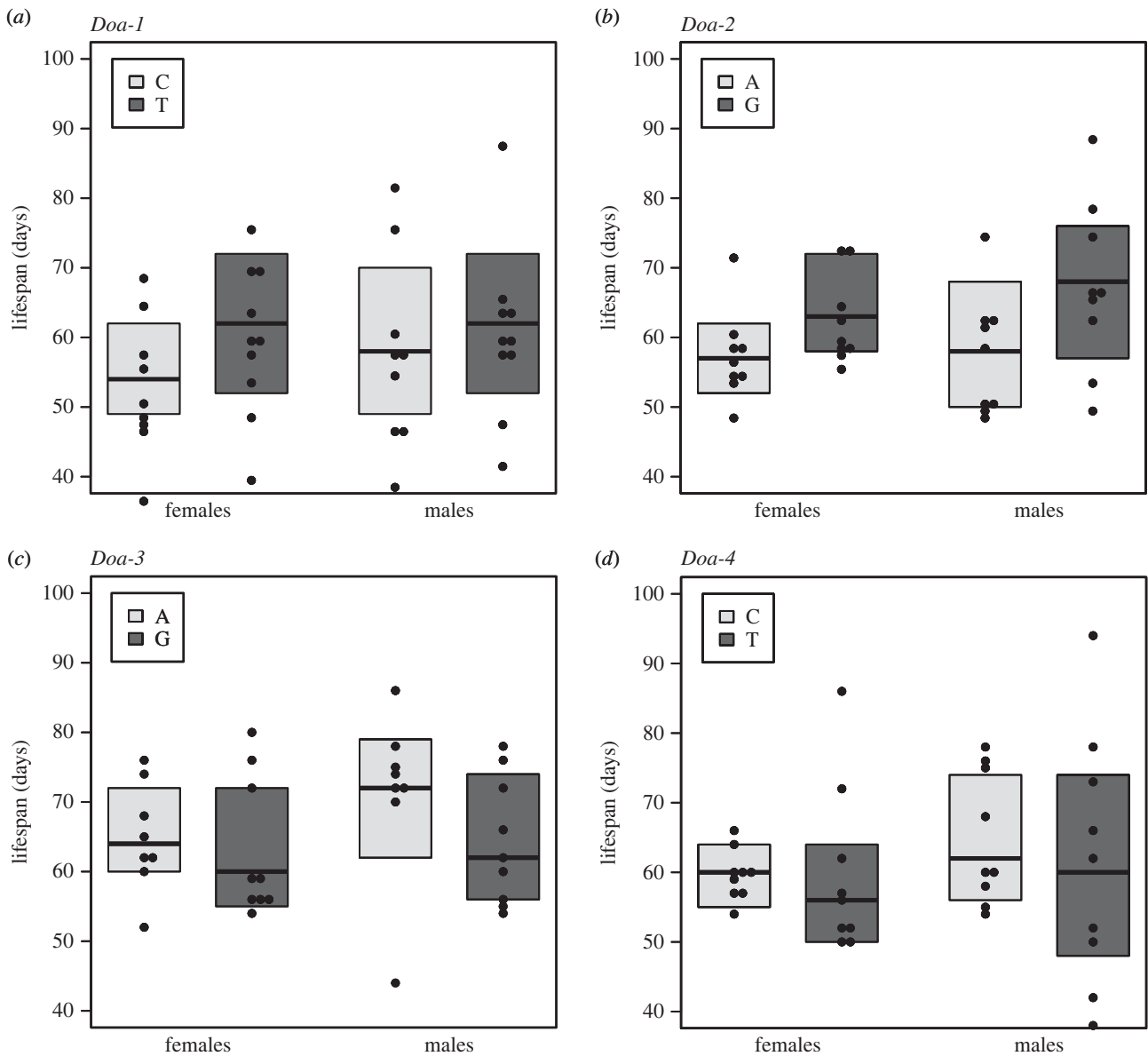


Figure 3. Association between candidate SNPs at *Doa* and lifespan. F1 crosses of the genetically diverse *Drosophila* Genetic Reference Panel with different allelic states were assessed to test the association of the candidate SNPs with lifespan. The graphs show the average lifespans of the F1 crosses for each allelic state at the four candidate *Doa* SNP positions investigated. The allele that is predominantly found in long-lived, late-reproducing EE populations, as identified by Hoedjes *et al.* [22], is indicated by the darker shade. Significant differences in lifespan between the two allelic states were observed for *Doa-1*, *Doa-2* and *Doa-3* (see table 3 for statistics).

a synonymous SNP located in the catalytic domain that is shared by all isoforms; *Doa-1* and *Doa-2* are intronic SNPs and may have regulatory functions; and *Doa-3* is a missense SNP located in exon N8 (N-terminal variable region), which encodes part of the 227 kD protein isoform [26]. To study the effects of these SNPs on fitness components we used a SNP association approach based on Mendelian randomization using lines of the *Drosophila* Genetic Reference Panel (DGRP) (see above, §2) (figure 2).

For three of the *Doa* SNPs we found a significant correlation between allelic state and median lifespan (figure 3, table 3). For *Doa-1* and *Doa-2*, the correlation was in the predicted direction (i.e. increased median longevity of lines carrying the allele that was enriched in the long-lived E&R populations). Interestingly, there was also a significant correlation between lifespan and allelic state for *Doa-3*, but the direction was opposite to what we had hypothesized: although the 'G' variant was the major allele in the long-

lived experimental evolution lines [22], this allele was associated with lower median lifespan in our functional assays (figure 3, table 3).

In terms of effects on fecundity, we observed a significant correlation between allelic state and egg-laying rates for two of the *Doa* SNPs, *Doa-2* and *Doa-4*. Moreover, in both cases, there was also a significant interaction between allelic state and age, indicating that the effect on fecundity was age-specific (figure 4, table 3). The difference in egg-laying rate became visible starting from 18–24 days after eclosion, with a higher fecundity of the crosses carrying the alleles associated with selection for postponed reproduction in the E&R study [22].

To rule out potentially confounding effects of linked causal SNPs in the genetic background, we analysed LD (measured by pairwise r^2) among *Doa* SNPs in the DGRP, which indicated very low levels of LD across the gene, as well as among the four candidate SNPs (see electronic supplementary material, File

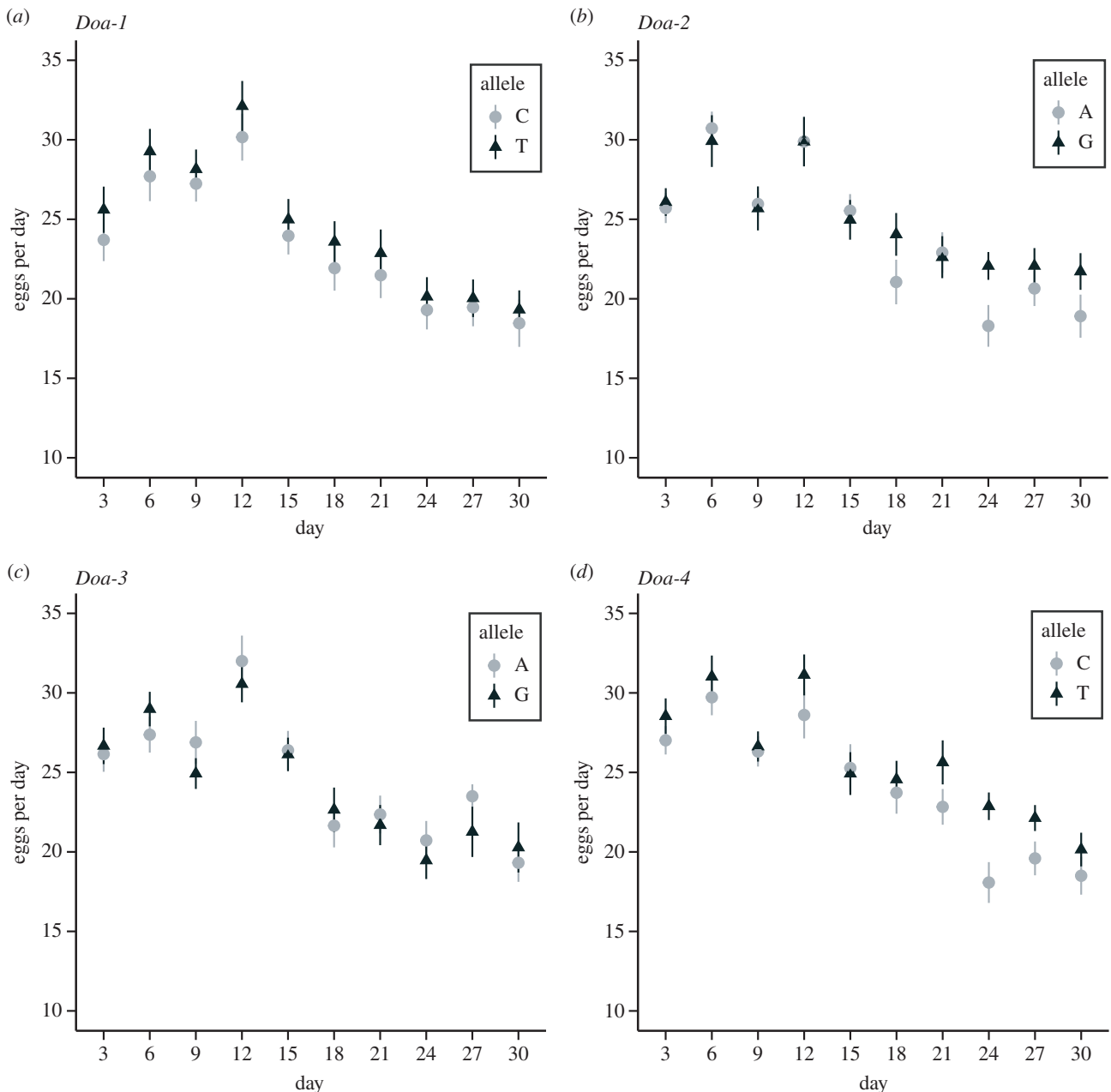


Figure 4. Association between candidate SNPs at *Doa* and fecundity. Shown are average egg-laying rates over a period of 30 days after emergence of F1 crosses for each allelic state at the four *Doa* candidate SNP positions investigated. The allele that is pre-dominantly found in long-lived, late-reproducing EE populations, as identified by Hoedjes *et al.* [22], is indicated by the darker shade and triangles. Significant differences in lifespan between the two allelic states were observed for *Doa-2* and *Doa-4* (see table 3 for statistics).

S4). In addition, analyses of genetic differentiation (SNP-wise F_{ST}) among lines with alternative allelic states demonstrated that only the focal SNP was fixed ($F_{ST}=1$) for each of the four panels of lines (electronic supplementary material, File S5). None of the other SNPs, both within *Doa* or elsewhere in the genome, were fixed between two panels of lines, and the number of strongly differentiated SNPs ($F_{ST}>0.5$) was very low as well. These analyses strongly suggest that our findings are very unlikely to be confounded by LD or due to effects in the genetic background of the candidate SNPs tested.

4. Conclusion

Our study provides strong support for a role of *Doa* in the evolution of lifespan and fecundity in the fruit fly, as expected

based on our previous E&R study [22]. Ubiquitous gene silencing of *Doa* using transgenic RNAi in adult flies reduced both lifespan and fecundity, indicating positive pleiotropy. In addition, each of the four candidate *Doa* SNPs tested had a significant effect on either lifespan and/or fecundity. The exact effects depended on the specific SNP, however, indicating that functional characterization of individual polymorphisms is essential for identifying the loci underlying adaptation. Three polymorphisms had effects on lifespan and/or fecundity that agree qualitatively well with predictions [22]. One of these SNPs, *Doa-2*, affected both lifespan and late-life fecundity, illustrating that even single nucleotide changes can have pleiotropic effects on complex traits (for other examples see [37,42,43]). However, one of the four SNPs, *Doa-3*, affected lifespan in the opposite direction than predicted. A possible explanation for this surprising result

Table 3. Statistical tests of the effects of alternative alleles at the four *Doa* SNP positions on lifespan and fecundity (egg-laying rate). F1 crosses of the genetically diverse *Drosophila* Genetic Reference Panel with different allelic states were set up and tested for lifespan and fecundity in order to assess the association of the candidate *Doa* SNPs with lifespan. Asterisks indicate significant results. *** $p < 0.001$, ** $0.001 < p < 0.01$, * $0.01 < p < 0.05$.

| lifespan | | | fecundity | | |
|---------------------|----------|----------------------------|---------------------|----------|----------------------------|
| | χ^2 | p | | χ^2 | p |
| <i>Doa-1</i> | | | <i>Doa-1</i> | | |
| allele | 43.27 | 4.02×10^{-10} *** | allele | 0.83 | 0.66 |
| sex | 137.99 | $<2.2 \times 10^{-16}$ *** | day | 477.8 | $<2.2 \times 10^{-16}$ *** |
| allele \times sex | 41.42 | 1.23×10^{-10} *** | allele \times day | 0.24 | 0.6224 |
| <i>Doa-2</i> | | | <i>Doa-2</i> | | |
| allele | 7.62 | 0.022 * | allele | 16.23 | 0.0003 *** |
| sex | 79.22 | $<2.2 \times 10^{-16}$ *** | day | 394.66 | $<2.2 \times 10^{-16}$ *** |
| allele \times sex | 3.35 | 0.067 | allele \times day | 15.84 | 6.90×10^{-5} *** |
| <i>Doa-3</i> | | | <i>Doa-3</i> | | |
| allele | 12.02 | 0.0025 ** | allele | 1.20 | 0.55 |
| sex | 228.45 | $<2.2 \times 10^{-16}$ *** | day | 348.77 | $<2.2 \times 10^{-16}$ *** |
| allele \times sex | 11.46 | 0.00071 *** | allele \times day | 1.13 | 0.28 |
| <i>Doa-4</i> | | | <i>Doa-4</i> | | |
| allele | 3.78 | 0.15 | allele | 9.42 | 0.009 * |
| sex | 141.33 | $<2.2 \times 10^{-16}$ *** | day | 486.4 | $<2.2 \times 10^{-16}$ *** |
| allele \times sex | 3.17 | 0.075 | allele \times day | 7.68 | 0.0056 * |

might be that this SNP, and potentially other SNPs at *Doa*, are part of functionally and evolutionarily important haplotypes subject to linkage disequilibrium and/or epistasis. Similar analyses of other candidate loci, both within *Doa* and elsewhere in the genome, could resolve these questions and provide a more comprehensive overview of the polygenic regulation of these traits. Together, our results illustrate that it is important to go beyond traditional gene knockdown or knockout analyses and to perform functional tests of putatively adaptive candidate loci in order to understand the genetic basis of evolutionary change.

Data accessibility. The raw data for this paper are available from the Dryad Digital Repository: <https://doi.org/10.5061/dryad.0gb5mkm4t> [53].

Supplementary material is available online [54]. This manuscript is available as a pre-print in BioRxiv at <https://doi.org/10.1101/2022.10.14.512079> [55].

Authors' contributions. K.H.: conceptualization, data curation, formal analysis, funding acquisition, investigation, methodology, project

administration, resources, software, supervision, validation, visualization, writing—original draft, writing—review and editing; H.K.: investigation, writing—review and editing; L.K.: conceptualization, funding acquisition, project administration, resources, supervision, writing—review and editing; T.F.: conceptualization, resources, supervision, writing—review and editing.

All authors gave final approval for publication and agreed to be held accountable for the work performed therein.

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