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Adaptive Evolution under Extreme Genetic Drift in Oxidatively Stressed Caenorhabditis elegans

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Abstract

A mutation-accumulation (MA) experiment with Caenorhabditis elegans nematodes was conducted in which replicate, independently evolving lines were initiated from a low-fitness mitochondrial electron transport chain mutant, gas-1. The original intent of the study was to assess the effect of electron transport chain dysfunction involving elevated reactive oxygen species production on patterns of spontaneous germline mutation. In contrast to results of standard MA experiments, gas-1 MA lines evolved slightly higher mean fitness alongside reduced among-line genetic variance compared with their ancestor. Likewise, the gas-1 MA lines experienced partial recovery to wildtype reactive oxygen species levels. Whole-genome sequencing and analysis revealed that the molecular spectrum but not the overall rate of nuclear DNA mutation differed from wildtype patterns. Further analysis revealed an enrichment of mutations in loci that occur in a gas-1-centric region of the C. elegans interactome, and could be classified into a small number of functional-genomic categories. Characterization of a backcrossed four-mutation set isolated from one gas-1 MA line revealed this combination to be beneficial on both gas-1 mutant and wildtype genetic backgrounds. Our combined results suggest that selection favoring beneficial mutations can be powerful even under unfavorable population genetic conditions, and agree with fitness landscape theory predicting an inverse relationship between population fitness and the likelihood of adaptation.

Key words: adaptation, complex I, electron transport chain, mitochondrial dysfunction, mutation accumulation, sign epistasis.

Introduction

In agreement with predictions of Fisher’s geometric model of adaptation (Fisher 1930), experimental evidence confirms that new mutations with measurable effects reduce the fitness of well-adapted genotypes (Lynch et al. 1999; Kondrashov and Kondrashov 2010). Original theoretical treatments of the threat to population survival posed by such mutations assumed that they affected fitness independently of genetic or environmental background and that little or no opportunity for reversion or other types of beneficial mutations existed (Lynch et al. 1993, 1995; Lande 1994). Empirical study suggests that both assumptions were wrong: beneficial mutations arise more frequently than originally appreciated (Joseph and Hall 2004; Hall et al. 2008; Achaz et al. 2014) and the most readily harmful mutations—those with moderate fitness effects—may be rare (Estes et al. 2004; Katju et al. 2015). Furthermore, individual mutational effects can be highly dependent upon their environmental and genomic contexts (Lenski and Travisano 1994; Burch and Chao 1999; Elena and Lenski 2001; Mainsnier-Patin et al. 2002; Rokyta et al. 2002; Estes and Lynch 2003; Remold and Lenski 2004; Wang et al. 2009, 2013), with a potentially large supply of compensatory epistatic mutations available to partially ameliorate the effects of previously acquired deleterious mutations. Indeed, adaptive landscape theory predicts that the probability of improvement increases with the distance...
of a population’s mean fitness from a theoretical optimum, and that maladapted populations can access a greater fraction of beneficial mutations than well-adapted ones (Fisher 1930; Whitlock and Otto 1999; Poon and Otto 2000; Tenaillon 2014). In other words, the mutational distribution of fitness effects will depend upon how well adapted a population is (Martin and Lenormand 2006, 2015; Chevin et al. 2010). Another prediction is that small-effect beneficial mutations exist in greater supply than mutations of larger effect (Orr 1998); it follows that adaptive evolution in small populations (with fewer genomes available for mutation) will primarily be driven by fixation of small-effect mutations, whereas larger populations can adapt more quickly by fixing fewer large-effect mutations. These predictions have largely been borne out by data from studies with microbes (Burch and Chao 1999; Sanjuan et al. 2004; Perfeito et al. 2007; Silander et al. 2007; Barrick et al. 2010; Hietpas et al. 2013; Wang et al. 2013), although important exceptions exist (Miller et al. 2011). Studies in complex eukaryotes are still lacking (but see Steams and Fenster 2016), which is problematic given the potential importance of organismal complexity and pleiotropy in determining real evolutionary outcomes (Orr 2000).

Laboratory mutation-accumulation (MA) experiments allow the impact of mutation to be distinguished from that of other evolutionary forces affecting rates of molecular evolution. Selection is rendered inefficient to the maximum extent possible by maintaining replicate lineages derived from a common ancestral genotype by clonal reproduction, self-fertilization, or extreme inbreeding across many generations, during which time MA lines accumulate and fix independent sets of mutations (Halligan and Keightley 2009; Teotónio et al. 2017). The vast majority of these experiments have initiated MA lines from wildtype ancestral strains that have undergone a period of laboratory domestication and are thus well adapted to laboratory conditions. Although we are aware of no MA experiments using extremely low-fitness ancestors, modifications to the standard MA design have included initiating MA lines from moderately low-fitness ancestors (Sharp and Agrawal 2012) and specific mutant genotypes for the purpose of revealing the effects of deficiencies in DNA repair pathways (Estes et al. 2004; Denyer et al. 2006) and mitochondrial functioning (Joyner-Matos et al. 2011). Several MA experiments have now been combined with high-throughput sequencing to provide direct estimates of the average per-generation rate of mutations arising in nuclear genomes along with detailed analyses of their molecular spectra and patterns of bias (Lynch et al. 2008; Denyer et al. 2009, 2012; Keightley et al. 2009; Ossovski et al. 2010; Lee et al. 2012; Saxer et al. 2012; Heilbron et al. 2014). When MA line fitness is evaluated, the near universal outcome is one of reduced mean fitness and increased among-line variance for fitness, consistent with mutations having predominantly deleterious effects. A notable exception is the study of Shaw et al. (2000, 2002), which estimated that half of the mutations accumulated in MA lines of Arabidopsis thaliana were beneficial (Shaw et al. 2002)—a result later supported by Rutter et al. (2010, 2012). Shaw et al. (2000) originally suggested that intraindividual selection (e.g., differential cell lineage growth) may have contributed to this result. It would of course be difficult to experimentally minimize or control selection at this level, but by confining our attention to individual-level selection, we may underestimate the power of beneficial mutation to sustain the genetic health and fitness of populations.

The mitochondrial electron transport chain (ETC) offers a compelling framework for studying the endogenous factors that influence mutation. Because the mitochondrial ETC is vital for energy metabolism in all complex life and is thus highly conserved, it is an ideal system for studying the impact of deleterious mutation. Since proper ETC functioning relies on the maintenance of favorable mitonuclear epistatic interactions (Blair et al. 2001; Dowling et al. 2008), it is also an excellent system for addressing the role of epistasis in maintaining population fitness. The mitochondrial ETC also generates reactive oxygen species (ROS) as a byproduct of cellular metabolism (Murphy 2009). ROS are important cell signaling molecules (Mittler et al. 2011), but high ROS levels (e.g., resulting from mitochondrial dysfunction) have long been hypothesized to be mutagenic, especially for mtDNA genomes owing to their proximity to the site of production (Hsie et al. 1986; Demple and Harrison 1994; Cooke et al. 2003). Recent work fails to implicate oxidative stress in somatic mtDNA mutation (Ameur et al. 2011; Yu et al. 2013; Itsara et al. 2014); however, the question of whether ROS are an important contributor to heritable germline mutation remains understudied.

Here, we build upon our previous work to provide a comprehensive, integrative assessment of the impact of mitochondrial dysfunction on nuclear DNA (nDNA) variation and phenotypes related to fitness and physiology. As described in Wernick et al. (2016), which reported on mitochondrial DNA mutation processes, we performed a MA experiment using a mitochondrial ETC-deficient genotype of C. elegans, gas-1(fc21), as the ancestor. We phenotyped replicate MA lines initiated from this mutant and applied Illumina MiSeq technology to analyze the nuclear genomes of a subset of these lines. As before, we compare our findings to those from a previous MA study initiated from a wildtype C. elegans ancestor (Baer et al. 2005). Bioinformatic approaches identified novel, putatively beneficial mutations fixed within MA lines; a subset of these was characterized to determine the contribution to surprising patterns of fitness and phenotypic evolution observed here.

Materials and Methods

Strains

This study utilized MA lines generated from a gas-1 mutant strain of C. elegans. The gas-1(fc21) allele is a single basepair
missense mutation (Kayser et al. 1999) associated with deleterious phenotypes including: reduced fecundity, reduced complex I-dependent metabolism (Kayser et al. 2004), hypersensitivity to oxidative stress owing to increased ROS production (Kayser et al. 2001, 2004), and low ATP levels relative to wildtype (Hartman et al. 2001; Kayser et al. 2001, 2004; Lenaz et al. 2006). The gas-1 mutant, derived from ethyl methanesulfonate (EMS) mutagenesis (Kayser et al. 1999), was obtained from the Caenorhabditis Genetics Center (University of Minnesota) and repeatedly backcrossed to N2 in an attempt to create an isogenic mutant strain. As detailed in Wernick et al. (2016), which reported on the mitochondrial DNA mutation processes within the same MA lines, offspring of a single gas-1 (fc21) hermaphrodite were then used to initiate 48 MA lines, maintained for an average of 43 generations (range: 35–47). Failed bottlenecks occasionally resulted from hermaphrodite sterility or death prior to reproduction; in this event, a sibling from the same generation was chosen from a backup plate to initiate the next generation. An MA line was considered extinct when it could not be reconstituted in this way. A subset of five gas-1 MA lines was selected at random for whole-genome sequencing and additional phenotypic analyses. We also utilized data from a previous analysis of MA lines generated from a wildtype N2 strain, which were evolved in the manner described earlier for a maximum of 250 generations (Baer et al. 2005). Namely, gas-1 MA results were compared with those from a subset of five N2 MA lines for which genome sequence (Denver et al. 2009, 2012) and phenotypic data (Denver et al. 2009; Joyner-Matos et al. 2013; Andrew et al. 2015) were available.

Life History Assays and Data Analysis

We assayed nematode life-history and analyzed the resulting data following established methods (Joyner-Matos et al. 2011). Owing to difficulty in working with the poorly performing gas-1 MA lines, life-history assays were conducted in four blocks in which different subsets of gas-1 MA lines were assessed alongside N2 and gas-1 ancestral (hereafter “gas-1 G0” for generation 0) controls. A fifth and sixth block were conducted to increase the sample size of the five gas-1 MA lines selected for whole genome sequencing (below). Specifically, we measured daily offspring production for the gas-1 MA lines, gas-1 G0 and N2 strains; we also recorded the number of unhatched and presumably unviable eggs, easily distinguished from unfertilized eggs under a light microscope. Data were used to calculate mean absolute (total reproductive output, W) and relative fitness (w) of the gas-1 mutant compared with N2, and of each gas-1 MA line compared with the gas-1 G0 ancestor. Relative fitness of each individual was computed as: \( w = \frac{\sum_{x} l(x) m(x)}{l(x)} \), where \( l(x) \) is the number of worms surviving to day \( x \), \( m(x) \) is the fecundity at day \( x \), and \( r \) is the mean intrinsic population growth rate of the assay-specific N2 or gas-1 G0 control as appropriate. The latter was calculated by solving Euler’s equation for \( r \) from the equation \( w = e^{-\Delta \epsilon} \frac{m(x)}{l(x)} = \frac{m(x)}{l(x)} \). We used \( \Delta \epsilon = 4.75 \) on the first reproductive day (c.f., Vassilieva et al. 2000).

To determine the impact of MA on evolution of the above phenotypes, the per generation change in the mean, \( \Delta M \), of each trait was estimated as the generalized linear regression coefficient of trait value scaled as a fraction of the block-specific gas-1 G0 mean on line-specific MA generation number. For the MA lines, within- and among-line components of variance were calculated using restricted maximum likelihood (REML) with variance estimates constrained to be nonnegative (except for when calculating confidence intervals). We tested the model \( trait = mean = \mu + block + MA \ line(block) + parent \ line(block) \) + error, wherein all effects are random—and MA line(block) represents among-line (genetic) variance and \( \epsilon \) represents the within-line (environmental) component of variance, \( V_e \). A frequency distribution of gas-1 MA line fitness relative to gas-1 G0 was created using least squares means for the gas-1 MA lines derived from the MA line(block) term using the expected mean squares (EMS) method as applied in JMP12 (SAS). For N2 and gas-1 G0 control lines, we tested the model \( trait = mean = \mu + block + parent(block) + error \), wherein all effects are random and parent(block) represents among-line (or pseudoline) variance. Second, the per-generation change in genetic variance owing to MA, the mutational variance \( V_M \), was calculated for each trait as the difference in the among-line components of variance of the gas-1 G0 control and the MA lines divided by \( 2t \), where \( t \) is the maximal number of MA generations. The per generation change in among-line variance, \( V_{ab} \), was calculated for the gas-1 MA lines by dividing the among line variance for each line by the average number of generations, 42.8.

Steady-State ROS and ATP Levels

Prior to all experiments, strains were allowed to recover from freezing for two generations at 20 °C on Nematode Growth Medium-Lite (NGML) plates containing 20 μg/ml streptomycin and seeded with Escherichia coli OP50-1. Lines were age synchronized by standard bleach treatment prior to each assay. We quantified in vivo steady-state ROS levels of the five gas-1 MA lines compared with N2 and gas-1 G0 strains using established fluorescence microscopy methods (Hicks et al. 2012; Joyner-Matos et al. 2013; Smith et al. 2014). ROS levels of the five sequenced N2 MA lines were previously reported (Joyner-Matos et al. 2013). We quantified ATP content for four to five independent samples from each of the five N2 and gas-1 MA lines compared with N2 and gas-1 G0 strains following methods adapted from Van Raamsdonk et al. (2010) and Yang and Hekimi (2010). For each sample, roughly 200 age-synchronized young adult worms were washed and worm cuticles were broken via successive freeze-thaw cycles. Samples were boiled for 15 min, sonified (20% amplitude,
twice for 12 s), and centrifuged at 10,000×g for 12 min. About 90 μl of supernatant was used to quantify ATP levels with a luminescence ATP detection kit (Invitrogen, Carlsbad, CA) and a Tecan Infinite M200 Pro plate reader (Tecan, Männedorf, Switzerland). ATP measurements were normalized by protein content measured with a Pierce BCA Protein Assay Kit (Thermo Fisher Scientific, Waltham, MA).

Illumina MiSeq Read Mappings and Analyses
Whole-genome sequencing was conducted for five randomly chosen gas-1 MA lines, N2 and the backcrossed gas-1 G0. Samples were prepared from first larval (L1) stage nematodes as described in (Wernick et al. 2016). Following each Illumina MiSeq run, reads were aligned to the C. elegans genome (version WS242) using CLC Genomics Workbench (CLC Bio-Qiagen, Aarhus, Denmark). All reads were paired-end (2×150 bp) and mapped using the following parameters: no masking, mismatch cost = 2, insertion cost = 3, deletion cost = 3, length fraction = 0.98, read fraction = 0.98, global alignment = no, nonspecific match handling = map randomly. Illumina data were deposited in the SRA database under accession number SRP069774.

Characterization of gas-1 G0 Genetic Background
Two potential sources of genetic difference between the gas-1 G0 and N2 progenitor strains are: (1) mutations resulting from the EMS mutagenesis employed to create the original gas-1 mutant, and (2) spontaneous mutations fixed during the ten generations of backcrossing. The majority of mutations from the first source should have been eliminated during the ten generations of backcrossing gas-1 to N2 males, but some EMS-induced mutations, particularly those closely linked to the gas-1 locus, may have remained. C. elegans experiences base substitutions at the rate of approximately two per generation (Denver et al. 2004), meaning that roughly 20 mutations were expected to have accumulated during the backcrossing process. All single-basepair mutations in gas-1 G0 were identified as sites that differed from the C. elegans reference genome (WS242) and were not present in our N2 lab strain. Each MA line was also surveyed for retention or loss of SNPs identified in gas-1 G0. To eliminate false positives, we applied the aforementioned criteria and required at least 5-fold coverage. Lastly, we only considered mutations found in one line to eliminate false positives associated with cryptic heterozygosity or paralogy following our previous approaches (Denver et al. 2009, 2012).

Mutation Rate Analysis
The nuclear mutation rate was calculated as previously described (Denver et al. 2009) from pooled gas-1 MA lines using the equation \( \mu bs = \frac{m}{L nT} \) where \( \mu bs \) is the base substitution rate (per nucleotide site per generation), \( m \) is the number of observed mutations, \( L \) is the number of MA lines, \( n \) is the number of nucleotide sites, and \( T \) is the time in generations. Values for \( n \) reflect the total number of base pairs surveyed that met the criteria for consideration of a possible mutation site. Conditional rate estimates for the six possible mutation types (A: T → G; C: G → A; T: A → C; G: C → T; A: T → A; and G: C → C) were also determined in a non-strand specific manner using the pooled gas-1 MA line muta-
tions. Standard errors for these estimates were approximated as \( \sqrt{\frac{\mu bs}{nT}} \). We compared observed conditional rate estimates in the gas-1 MA lines to published values for N2 MA lines (Denver et al. 2012).

Gene Ontology Enrichments
We used GoMiner (Zeeberg et al. 2003, application build 457) and the GO MySQL Database (MySQL 3.7.13, Oracle Corporation, Cupertino, CA; GO database build 2016-06-07, geneontology.org) to calculate gene ontology (GO) enrichments for genes in the gas-1 interactome and all nDNA SNPS that arose within protein coding regions of gas-1 MA and the N2 MA lines within three functional domains—biological process, cellular component, and molecular function. GoMiner reports a two-sided Fisher's exact P value based upon the number of genes in a category and a false discovery rate (FDR)-corrected P value for multiple testing (Zeeberg et al. 2005); however, the FDR can be overly conservative when the sample size or number of discoveries is small; that is, <100 (Zeeberg et al. 2005; Tong and Zhao 2008), so we based interpretations on results of the Fisher's exact tests with \( x = 0.05 \). We then determined which broader-level functional “GO slim” categories, as defined by the GO Consortium (Version 1.2, 2012-09-21, geneontology.org), were enriched using CateGORizer (Hu et al. 2008), which classifies enriched GO terms into their respective GO slim categories, giving a coarser-scale overview of enrichment
patterns. GO slim categories were then checked against the GoMiner output to assess statistical significance.

Interactome Analysis of gas-1 and N2 MA Line Mutations

Following our previous approach (Denver et al. 2010), GeneOrienteer version 2.25 (Zhong and Sternberg 2006) was used to construct an interactome, a list of genes predicted to interact with a gene of interest (gas-1), and determine the extent to which mutated MA line genes showed membership within this network. We first queried the entire C. elegans interactome to determine the interactions involving gas-1. The query returned 181 genes predicted to “directly” interact with gas-1 within one degree. We then queried this smaller interactome to identify genes predicted to interact within two degrees of gas-1. We refer to the comprehensive list of first- and second-degree gas-1 interacting genes, totaling 4,189, as the “gas-1 centric interactome.” We next identified all genic mutations within the gas-1 and N2 MA line sets that were members of the gas-1-centric interactome and used Monte Carlo Maximum Likelihood simulations to assess the probability of observing the results by chance. Twenty-three mutations (the number of genic mutations discovered in gas-1 MA lines) were randomly generated using a simulation written in Python. This simulation was repeated for 1,000 iterations, and the average and standard deviation of the number of mutations occurring within the gas-1 centric interactome were calculated. This simulation was repeated for N2 with the exception that 59 mutations, the number of genic mutations discovered within N2 MA lines (Denver et al. 2012), were randomly generated.

Isolation and Characterization of Candidate Beneficial Mutations from MA431

Because results of the above analyses indicated that some degree of adaptive evolution had occurred in the gas-1 MA lines, we aimed to characterize candidate beneficial or compensatory SNPs that arose within one particular line. Line MA431 was chosen for analysis as it was found to contain the genes identified by the GO and interactome analyses and/or with known function—namely, *rheb-1*, *daf-2*, and *sel-2*, all of which reside on chromosome III. Toward this goal, MA431 was backcrossed to N2 following the same approach used to generate the gas-1 G0 strain. At each generation, DNA was extracted from the parental MA431 hermaphrodite (n = 30–44) for PCR and Sanger DNA sequencing at three SNP locations within the *rheb-1*, *daf-2*, and *sel-2* genes. Offspring from hermaphrodites retaining at least one of these SNPs were used in the next round of crossing. Although our aim was to isolate each chromosome III SNP individually, we were unsuccessful at maintaining strains that did not contain all three (see Results for MA431 SNP linkage).

After seven rounds of backcrossing, hermaphrodites containing MA431 mutations were allowed to self and tested to find homozygotes, resulting in a strain referred to hereafter as N2*MA431*. Finally, the MA431 chromosome III homozygous mutant lines were crossed with our near-isogenic gas-1 G0 strain and offspring allowed to self to produce a strain that contained only the chromosome III SNP mutations on the gas-1 background, gas-1*MA431*.

We performed a life-history assay as previously described for the N2*MA431* and gas-1*MA431* strains alongside N2 and gas-1 G0 controls, which included 40 replicates of each strain. Selection coefficients of the MA431 SNPs on each genetic background were calculated as the difference in relative fitness between N2*MA431* and N2 and between gas-1*MA431* and gas-1 G0. A Cox proportional hazards method was used to compare age-specific mortality of the N2*MA431* and gas-1*MA431* strains and their N2 and gas-1 G0 controls, with strain and parent(strain) as main effects. Lastly, we quantified in vivo steady-state ROS and ATP levels of the N2*MA431* and gas-1*MA431* lines compared with N2 and gas-1 G0 strains as previously described.

Results

Characterization of gas-1 G0 Genetic Background

Bioinformatic analysis of the gas-1 G0 strain identified 76 genetic differences relative to our N2 strain (supplementary fig. S1 and table S1, Supplementary Material online). The X-chromosome (where gas-1 is located) harbored the majority, ~62%, of these mutations compared with 15.7% of the total mutations identified in the N2 MA lines (Denver et al. 2012)—a highly significant difference (P < 0.00001, χ² test). The gas-1 G0 X-chromosome also experienced an increased proportion of G: C → A: T mutations compared with the published N2 value (80.9% vs. 23.5%; P < 0.00001, χ² test). Genome-wide, the gas-1 G0 strain also showed a much higher proportion of G: C → A: T mutations compared with the published N2 value (61.8% vs. 33.3%; P < 0.00001, χ² test). All 76 background mutations present within gas-1 G0 were retained within the sequenced MA lines (below).

gas-1 G0 Phenotypes

There were no significant effects of assay block on any life-history trait (not shown). As expected based on previous studies of the CGC gas-1 strain (Morgan and Sedensky 1994; Kayser et al. 1999), our backcrossed gas-1 G0 strain produced far fewer offspring than N2 (fig. 1 and table 1; supplementary table S2, Supplementary Material online), resulting in lower relative fitness (t148 = 9.954, P < 0.0001; table 1). gas-1 G0 reproductive maturity and peak reproductive output were also delayed by a full day compared with N2 (fig. 1).
Potential for Selection during gas-1 MA

Eight of the original 48 gas-1 MA lines (16.7%) went extinct prior to the 50 generation cut-off, as compared with only one extinction among 48 MA lines initiated from N2 (2%) during 125 generations of evolution (Joyner-Matos et al. 2011). The frequency of failed bottlenecks occurring during the gas-1 MA experiment, 14.2%, was twice that reported for the N2/MA experiment, 7.1% (Joyner-Matos et al. 2011). Additionally, gas-1 MA lines laid an increased number of fertilized but ultimately unhatched eggs compared with ancestral controls. The difference in unhatched egg counts among N2, gas-1 G0 and MA groups ($F_2, 677 = 8.9345, P < 0.0001$) was due to the gas-1 MA line group having a small but significantly greater number of unhatched eggs ($3.68 \pm 0.31$) than either gas-1 G0 ($1.51 \pm 0.41$) or N2 ($1.09 \pm 0.18$) (Tukey HSD; $\alpha = 0.05, P < 0.01$). In contrast, the prevalence of “bagging” (where internal hatching of eggs kill the parent) in the MA lines (8.2%) was indistinguishable from that in N2 (12.4%) or gas-1 G0 (10.2%) ($\chi^2$ test), and thus did not significantly impact MA line fitness.

gas-1 MA Life-History Evolution

gas-1 lines evolved higher average absolute and relative fitness during the MA process, leading to positive values for $\Delta M$, the per generation change in mean phenotype (table 1). These differences were due to MA lines producing, on an average, significantly more offspring on days 1, 3, 4, and 5 of their reproductive period (fig. 1 and supplementary table S2, Supplementary Material online). Eighteen MA lines were the major contributors to this pattern; of the remaining 30 MA lines, 8 went extinct (above) and 22 exhibited unchanged or slightly reduced fitness relative to gas-1 G0 (fig. 2).

As expected, phenotypic variance among ancestral N2 or gas-1 G0 control lines did not differ from zero for absolute or relative fitness (table 1); within-line (environmental) variance estimates are shown in supplementary table S3, Supplementary Material online. Significant per-generation changes in among-line (genetic) variance, $V_{g}$, were detected for both fitness metrics in gas-1 MA lines (table 1). However, point estimates for $V_{g}$ were uniformly lower for gas-1 MA lines compared with those for the gas-1 G0 ancestor for both traits (table 1). If we had corrected for the (nonsignificant) among-(pseudo)line variance observed for the gas-1 G0 control (c.f., Joyner-Matos et al. 2011), we would have detected no genetic variance for the MA lines. Accordingly, mutational variance, $V_{m}$, estimates are low and slightly negative for both traits (table 1). Finally, a roughly similar pattern of reduced variance was observed for $V_{p}$, the per-generation within-line variance, meaning that average MA line performance became more uniform compared with that of its ancestor.

gas-1 MA ROS and ATP

No significant block or interaction effects for either ROS or ATP were found when N2 and gas-1 G0 control performance was modeled as a two-way ANOVA: $y = \mu + strain + block + strain^{*} block + \epsilon$, where block and strain* block are random effects (not shown). gas-1 G0 exhibited significantly higher ROS (supplementary fig. S2A, Supplementary Material online) and lower ATP (supplementary fig. S2B, Supplementary Material online) than N2. gas-1 MA line ROS levels were significantly reduced compared with gas-1 G0 and statistically indistinguishable (although higher) than wildtype levels (supplementary fig. S2A, Supplementary Material online). gas-1 MA lines also exhibited lower amounts of within-line variance than gas-1 G0, approaching levels observed for N2 (not shown). Average steady-state ATP levels in the gas-1 MA lines were unchanged compared with gas-1 G0; both gas-1 G0 and its MA lines had significantly reduced

Table 1
Summary Statistics for Fitness Traits

|            | $W$     | $\omega$ |
|------------|---------|----------|
| N2         | 151.6±10.03 | 1.000±0.053 |
| gas-1 G0   | 38.40±3.277 | 0.225±0.057 |
| gas-1 G0*  | 38.40±3.277 | 1.000±0.085 |
| gas-1 MA*  | 50.58±1.647 | 1.260±0.058 |
| $\Delta M$ (x $10^{-6}$) | 127.9±38.20 | 5.757±1.317 |
| $V_{g}$ gas-1 G0 | 76.74±84.81 | 0.054±0.059 |
| $V_{g}$ gas-1 MA | 5.191±1.824 | 0.010±0.004 |
| $V_{g}$ gas-1 G0 | 628.6±105.7 | 0.014±0.002 |
| $V_{g}$ gas-1 MA | 20.58±1.439 | 0.017±0.001 |
| $V_{m}$    | −1.547   | −0.004   |

Note.—All values are means ± 1 SEM.
*Fitness relative to gas-1 G0; fitness is otherwise reported relative to N2.
$W$, absolute fitness; $\omega$, relative fitness.

FIG. 1.—Reproductive schedules. Daily offspring production of N2 (solid line), gas-1 G0 (dashed line, squares), and the combined gas-1 MA lines (dashed line, triangles). Error bars are 1 SEM. Summary statistics are reported in supplementary table S2, Supplementary Material online.
Rates and Spectra of gas-1 MA Line Mutations
Forty novel mutations were detected across the five sequenced gas-1 MA lines (table 2); additionally, all 76 background mutations detected within gas-1 G0 were retained by each MA line. Considering only the novel mutations that arose during MA, MA-line specific mutation numbers ranged from 5 to 11. The per-generation base-substitution mutation rate, 2.13 (±0.34)×10^{-9}, was statistically indistinguishable (within two SEM) from that previously reported for N2, 2.7 (±0.40)×10^{-9} (Denver et al. 2009). The largest mutation class (16/40) was composed of G: C → A: T transition events. Compared with estimates published for N2 MA lines (Denver et al. 2012), these events alone were substantially elevated in the gas-1 MA lines (SEM values for N2 and gas-1 MA G: C → A: T conditional rates did not overlap; supplementary fig. S3, Supplementary Material online). There was no significant difference between the proportion of synonymous to nonsynonymous mutations between the gas-1 MA and N2 MA values (P = 0.92, χ² test).

GO Term Enrichment
Supplementary file S1, Supplementary Material online, gives a complete accounting of GO enrichment results. No significantly enriched GO slims were shared between the gas-1 MA and N2 MA line groups (supplementary file S1, Supplementary Material online and fig. 3A and B). For gas-1 MA lines, two categories were significantly enriched: the biological process of transport and the cellular component of plasma membrane (fig. 3A). Four gas-1 MA line genetic mutations were classified under both transport and plasma membrane; those in: smf-3, daf-2, tkw-3, and rheb-1 genes. In contrast, 12 GO slims were enriched in the N2 MA lines (fig. 3B). In addition to the lack of overlap between enriched gas-1 and N2 MA line GO slims (fig. 3A and B), we found that all 12 GO slim categories enriched among N2 MA lines were also enriched in the entire gas-1 interactome set (see below), which contained 80 significantly enriched GO slim categories. Conversely, transport was the only term enriched among both the gas-1 MA line and gas-1 interactome gene sets.

gas-1 Interactions
Of the 23 genic mutations (i.e., those discovered within exons or introns; table 2) found within sequenced gas-1 MA lines, 8 were predicted to interact within 2-degrees of the gas-1 gene (fig. 3C); 1 of these, alh-2—encoding a mitochondrial aldehyde dehydrogenase—was a direct interactor with gas-1. Simulations revealed that this number (eight) was higher than that expected by chance, 3.3 (P = 0.005, χ² test; supplementary fig. S4, Supplementary Material online), and in only 6 of the 1,000 iterations did eight or more mutations reside within this network. None of the 76 gas-1 G0 background mutations was found within the interactome. Of the 59 genic mutations found within sequenced N2 MA lines, 12 were located within the gas-1-centric interactome. In contrast to the gas-1 MA line result, this number was no different than that expected by chance, 8.4 (P = 0.177, χ² test; supplementary fig. S5, Supplementary Material online); 131/1,000 iterations saw at least 12 mutations located in genes predicted to interact within 2-degrees of gas-1.

MA431 SNP Linkage and Characterization
The above analyses revealed several notable SNPs to be contained within one gas-1 MA line, MA431; we therefore sought to isolate and individually characterize these mutations on both gas-1 G0 and wildtype N2 backgrounds. Among the nine total SNPs discovered within MA431, three affected genes within the gas-1-centric interactome: rheb-1, daf-2, and sel-2. All reside on chromosome III separated by approximately: 8.5 cM (rheb-1 and daf-2), 3.5 cM (rheb-1 and sel-2), and 11.0 cM (daf-2 and sel-2) (Wormbase, version WS254), meaning we could expect ~8.5%, 3.5%, and 11% of chromatids from each cross to be recombinant for each pair, respectively. Contrary to this expectation, we observed no recombinant genotypes over the course of the seven-generation backcrossing experiment, but our power to detect such genotypes was limited by the small number of offspring (n = 30–44) we could practically sample and genotype at each generation. We were, however, successful in separating this group of SNPs from all others except one; a fourth SNP on chromosome V remained linked to the chromosome III set. This SNP resided within C04E12.10 (Wormbase, version WS254), an orthologue of human NGLY1 (N-glycanase 1).
Non, synonymous or nonsynonymous mutation.

resulted from a translocation event occurring within asparagine with a histidine. (Camon 2003; Mulder 2003), resulting in replacement of an MA431 and not the result of a translocation, the BLAST type that, if the chromosome V SNP was both specific to the N2 reference genome (WS242) with the expected from each BLAST search were then used as a BLAST query against both custom BLAST databases. Finally, the SNP (V: 3,379,000–3,379,499 bp) was then used as the BLAST query against both custom BLAST databases. Finally, the top contigs—with 6-kb flanking sequences—returned from each BLAST search were then used as a BLAST query against the N2 reference genome (WS242) with the expectation that, if the chromosome V SNP was both specific to MA431 and not the result of a translocation, the BLAST searches would return only chromosome V sequences. A caveat is that if a segment of highly repetitive DNA joined an asparagine with a histidine.

We found no evidence that the latter observation resulted from a translocation event occurring within either gas-1 G0 or MA431. To investigate this possibility, de novo assemblies of both the gas-1 progenitor strain and gas-1 MA431 were conducted using CLC Genomics Workbench and used to create custom BLAST databases. A 500-bp section of the MA431 chromosome V containing the SNP (V: 3,379,000–3,379,499 bp) was then used as the BLAST query against both custom BLAST databases. Finally, the top contigs—with 6-kb flanking sequences—returned from each BLAST search were then used as a BLAST query against the N2 reference genome (WS242) with the expectation that, if the chromosome V SNP was both specific to MA431 and not the result of a translocation, the BLAST searches would return only chromosome V sequences. A caveat is that if a segment of highly repetitive DNA joined

Table 2
gas-1 MA Line Mutations

| gas-1 MA Line | Position | Type Conversion | Mutation Type | Gene | Classification | Ref Codon | Ref AA | Var Codon | Var AA | Syn or Non |
|---------------|----------|-----------------|---------------|------|----------------|-----------|-------|-----------|--------|------------|
| MA412         | II: 11,182,784 | A: T → C: G | A → C | F37H8.3 | Exon | CCA | Pro | CCC | Pro | Syn |
| MA412         | II: 13,912,231 | G: C → A: T | G → A | W02B8.2 | Exon | GAG | Glu | AAG | Lys | Non |
| MA412         | V: 11,394,089 | A: T → G: C | A → G | Intergenic |
| MA412         | V: 12,318,251 | A: T → C: G | T → G | Intergenic |
| MA412         | V: 19,920,250 | A: T → G: C | A → G | Intergenic |
| MA412         | V: 20,674,727 | G: C → T: A | G → T | mlt-1 | Exon | TCG | Ser | TCT | Ser | Non |
| MA412         | X: 5,107,789 | A: T → G: C | T → C | Intergenic |
| MA412         | X: 6,529,937 | A: T → C: G | T → C | Intergenic |
| MA412         | X: 10,265,781 | G: C → T: C | G → C | Intergenic |
| MA419         | III: 896,522 | G: C → T: A | G → T | F23H11.2 | Exon | TGC | Cys | TTC | Phe | Non |
| MA419         | V: 3,152,259 | A: T → T: A | T → A | Intergenic |
| MA419         | X: 10,274,961 | G: C → A: T | C → T | F41E7.2 | Intron |
| MA419         | X: 4,975,182 | G: C → C: G | G → C | ZC8.6 | Exon | TTC | Phe | TTG | Phe | Syn |
| MA419         | X: 10,368,359 | G: C → T: A | G → T | Intergenic |
| MA419         | X: 12,384,471 | G: C → A: T | C → T | Intergenic |
| MA429         | I: 12,870,206 | G: C → A: T | C → T | Intergenic |
| MA429         | II: 4,663,692 | G: C → A: T | C → T | T50A7.11 | Exon | GCA | Ala | ACA | Thr | Non |
| MA429         | IV: 3,470,137 | G: C → A: T | G → A | F58E2.2 | Exon | AAG | Lys | AAA | Lys | Syn |
| MA429         | X: 17,132,019 | A: T → G: C | T → C | K09E3.7 | Exon | GTG | Vak | ATG | Met | Non |
| MA431         | I: 10,724,831 | A: T → G: C | A → G | srz-85 | Exon | CAT | His | CAC | His | Syn |
| MA431         | III: 9,455,062 | A: T → T: A | A → T | rheb-1 | Intron |
| MA431         | III: 3,002,544 | G: C → A: T | G → T | daf-2 | Intron |
| MA431         | III: 4,598,014 | G: C → A: T | C → T | sel-2 | Exon | CGT | Arg | CAT | His | Non |
| MA431         | IV: 12,986,492 | G: C → A: T | C → T | Intergenic |
| MA431         | IV: 14,058,054 | A: T → T: A | T → A | Intergenic |
| MA431         | IV: 17,181,972 | G: C → A: T | G → A | C52D10.3 | Intron |
| MA431         | V: 3,379,498 | G: C → C: G | G → C | C04E12.10 | Exon | GAT | Asp | CAT | His | Non |
| MA431         | X: 5,964,400 | A: T → T: A | T → A | R07E4.1 | Intron |
| MA438         | I: 8,987,554 | G: C → A: T | G → A | Intergenic |
| MA438         | II: 13,977,594 | G: C → A: T | G → A | sre-48 | Intron |
| MA438         | III: 2,792,754 | G: C → T: A | G → T | Y71H2AM.24 | Intron |
| MA438         | III: 11,412,255 | A: T → C: G | A → C | twk-31 | Intron |
| MA438         | IV: 2,620,955 | G: C → A: T | G → A | smf-3 | Intron |
| MA438         | IV: 7,452,889 | G: C → A: T | G → A | Intergenic |
| MA438         | V: 14,423,155 | G: C → A: T | C → T | Intergenic |
| MA438         | V: 1,646,965 | A: T → C: G | A → C | alh-2 | Exon | TGA | Trp | TGC | Cys | Non |
| MA438         | V: 18,784,124 | A: T → G: C | T → C | Y17D7B.10 | Intron |
| MA438         | X: 9,580,008 | A: T → T: A | A → T | Intergenic |
| MA438         | X: 17,456,803 | G: C → A: T | G → A | Intergenic |

Ref Allele, reference allele; Var allele, variant allele; Ref Codon, Reference Codon; Ref AA, reference amino acid; Var Codon, variant codon; Var AA, variant amino acid; Syn or Non, synonymous or nonsynonymous mutation.

(Camon 2003; Mulder 2003), resulting in replacement of an asparagine with a histidine.

We found no evidence that the latter observation resulted from a translocation event occurring within either gas-1 G0 or MA431. To investigate this possibility, de novo assemblies of both the gas-1 progenitor strain and gas-1 MA431 were conducted using CLC Genomics Workbench and used to create custom BLAST databases. A 500-bp section of the MA431 chromosome V containing the SNP (V: 3,379,000–3,379,499 bp) was then used as the BLAST query against both custom BLAST databases. Finally, the top contigs—with 6-kb flanking sequences—returned from each BLAST search were then used as a BLAST query against the N2 reference genome (WS242) with the expectation that, if the chromosome V SNP was both specific to MA431 and not the result of a translocation, the BLAST searches would return only chromosome V sequences. A caveat is that if a segment of highly repetitive DNA joined...
the translocated region, the de novo assembly would be unable to construct a contig across that region.

The four isolated MA431 SNPs increased relative fitness on both gas-1 G0 and wildtype N2 backgrounds (fig. 4), exhibiting a slightly greater selective benefit on the N2 (s = 0.065; fig. 4A) compared with the gas-1 G0 background (s = 0.029; fig. 4B). Fitness of the gas-1 G0 and gas-1 MA431 pair of strains was dramatically reduced compared with the N2 and N2MA431 pair (Tukey HSD, α = 0.05). This between-pair difference overshadowed the small but significant differences within each pair (fig. 4). The improved fitness of MA431-SNP containing strains was mainly due to increased early life (but not total) reproduction compared with gas-1 G0 or N2 (supplementary fig. S6 and table S4, Supplementary Material online). Note that N2 “catches up” on the second reproductive day, producing significantly more offspring than N2MA431.

Strains also varied with respect to age-specific survival (supplementary fig. S7, Supplementary Material online) and mortality risk (log-rank $\chi^2 = 19.29$, $P < 0.0001$) such that gas-1 MA431 mortality was reduced compared with gas-1 G0 (risk ratio: 0.546, 95% C.I. = 0.347–0.856, $P < 0.008$), but N2MA431 mortality was indistinguishable from that of N2. No differences in average lifespan (mean number of days ± SEM) were detected among gas-1 MA431 (14.67 ± 0.773), gas-1 G0 (12.29 ± 0.613), N2MA431 (15.80 ± 0.673), or N2 (17.53 ± 0.586).

ROS levels differed among the four experimental strains (supplementary fig. S8, Supplementary Material online; $F_3$, $166 = 20.95$, $P < 0.0001$), such that gas-1 MA431 ROS was reduced compared with gas-1 G0, and both gas-1 (fc21)-containing strains exhibited higher ROS levels than N2 and N2MA431 at $P < 0.01$ (Tukey’s HSD, α = 0.05). Strains also
varied in their ATP content (supplementary fig. S9, Supplementary Material online; $F_{16,97} = 9.781$, $P = 0.0007$), such that N2 had significantly higher ATP levels than either of the gas-1 (fc21)-containing strains at $P < 0.01$, and marginally higher levels than $N_2^{MA431}$ at $P = 0.0695$ (Tukey’s HSD, $a = 0.05$). $N_2^{MA431}$, gas-1 G0 and gas-1 $^{MA431}$ ATP levels were statistically indistinguishable.

Discussion

We reported on phenotypic and nuclear genome evolution of *C. elegans* MA lines initiated from a mitochondrial ETC mutant (gas-1) compared with previously studied lines initiated from a wildtype (N2) ancestor (Baer et al. 2005). We also functionally characterized a set of mutations that arose during controlled laboratory evolution—the first *C. elegans* experiment to do so.

Genetic Analysis of gas-1 G0 Reveals Residual Mutations Consistent with EMS Generation

Ideally, MA lines initiated from isogenic strains of gas-1 (fc21) and N2 would be compared with determine how gas-1 (fc21) affects evolution under drift. Because the gas-1 strain resulted from EMS mutagenesis, we backcrossed it to our laboratory N2 to eliminate extraneous mutations resulting from this treatment, ~99% of which were expected to be G: C → A: T transitions (Greene et al. 2003; Kim et al. 2006). Our results were consistent with a swath of EMS-generated mutations having been maintained even after backcrossing due to linkage with the selected gas-1 (fc21) mutation. The original gas-1 (fc21) strain was not sequenced, but we speculate that it contained vastly more EMS-induced mutations than our backcrossed strain. These findings are concerning considering the large number of previous studies employing the CGC gas-1 (fc21)-containing strain and others derived from chemical mutagenesis. In any case, whereas we can safely compare gas-1 G0 with its resulting MA lines, comparisons of gas-1 G0 with N2 and between MA lines generated from each strain must be viewed with some caution because we failed to eliminate all genetic differences between the two ancestral strains. Future work targeting single SNPs using CRISPR-Cas9 gene editing can avoid these potential problems.

Fig. 4.—Relative fitnesses for MA431 SNP-containing lines and ancestral controls. Fitness of MA431 backcrossed lines relative to N2 reported (mean ± 1 SEM); note the different y-axis scales in each panel: Wilcoxon rank sums tests showed that $N_2^{MA431}$ had improved fitness compared with N2 ($\chi^2 = 5.16$, $P < 0.02$) and that gas-1 $^{MA431}$ had improved fitness compared with gas-1 G0 ($\chi^2 = 7.34$, $P < 0.01$). (A) Wildtype N2 (1.000 ± 0.021) and $N_2^{MA431}$ (1.065 ± 0.033) and (B) gas-1 G0 (0.068 ± 0.005) and gas-1 $^{MA431}$ (0.097 ± 0.008). * and ** denote statistical significance at $P < 0.01$ and $P < 0.05$ levels, respectively.

gas-1 G0 Exhibits Elevated ROS and a “Slow-Living” Phenotype

Keeping the above caveat in mind, gas-1 G0 was substantially less fit than N2 owing to reduced reproductive output along-side delayed reproductive maturity. As in previous studies (Kayser et al. 2001, 2004), gas-1 G0 exhibited increased ROS and depressed ATP levels relative to wildtype. We also previously found that pharyngeal pumping rates, a biomarker of age in *C. elegans* (Collins et al. 2008), were much lower in gas-1 G0 than in N2 and failed to show the typical pattern of age-correlated decline (Lue 2015). These phenotypes make sense in light of previous work showing that, whereas the CGC gas-1 (fc21) mutant exhibits elevated ROS and oxidative stress, it also upregulates expression of numerous metabolic and cellular defence pathways (Falk et al. 2008). The latter is consistent with the fact that DAF-16, the single FOXO transcription factor present in *C. elegans*, is constitutively translocated to nuclei in this mutant, an event that normally occurs only under conditions of starvation, oxidative, and other forms of stress in wildtype nematodes (Kondo et al. 2005). daf-16 is negatively regulated by the insulin/insulin-like growth factor (IGF) signaling pathway and, in response to environmental stimuli, regulates ~100 genes encoding protective products such as heat shock proteins and antioxidants (Hu 2007). The presence of DAF-16 in the nuclei of gas-1 mutants could result from either or both its high intracellular ROS levels or reduced rates of pharyngeal pumping if the latter leads to dietary restriction, and account for its “slow-living” phenotype (c.f.
Feng et al. 2001). The former scenario seems more likely since gas-1 worms did not have noticeable frequencies of Dauer larva (personal observation), which might be expected under diet restriction (Hu 2007).

**gas-1 nDNA Mutation Spectrum but Not Per-Generation Rate Differs from Wildtype**

Oxidative stress is associated with two major base-substitution types; G: C → A: T transitions and G: C → T: A transversions, caused by 5-hydroxyuracil and 8-oxo-dG lesions, respectively (Wiseman and Halliwell 1996; Cooke et al. 2003; Cooke and Evans 2007). Both types were found to predominate the nDNA mutational spectrum in N2 MA lines (Denver et al. 2009); conversely, the gas-1 mutational spectrum was dominated by G: C → A: T transitions alone. Although this difference could indicate different underlying mechanisms of mutation, considerable evidence from this study indicates that gas-1 MA line mutations had been filtered by selection. G: C → T: A transversions may therefore have been selectively removed in gas-1 MA lines. Similarly, our previous analysis of mtDNA mutation within the same lines found that, whereas rates of heritable mtDNA mutation in gas-1 MA lines were indistinguishable from wildtype, the molecular spectrum of mutations was skewed—in that case toward an increased frequency of single nucleotide substitutions and a reduced frequency of indels compared with wildtype (Wernick et al. 2016). The potentially biased sample of mutations, combined with the downward evolution of ROS levels during gas-1 MA, makes it impossible to test for a relationship between endogenous ROS and germline mutation rate in this system. Our results make it impossible to test for a relationship between endogenous ROS and germline mutation rate in this system. Our results indicate that a different form of intraindividual selection that yielded a similar outcome.

Results of our bioinformatics analyses also bore the signature of selection and were consistent with the idea that some gas-1 MA line mutations conferred beneficial or compensatory effects. First, fewer GO slim categories were significantly enriched in the gas-1 MA line mutated gene set compared with that of the N2 MA lines. The GoMiner enrichment algorithm takes the total number of altered genes into account when calculating enrichment scores, so this pattern is not a consequence of N2 MA lines having more mutations and is instead consistent with a weaker role for genetic drift in gas-1 MA versus N2 MA line molecular evolution. Second, four genetic categories in the gas-1 MA lines—daf-2, rheb-1, twk-31, and smf-3—had membership in the same GO slim categories—transport, plasma membrane, and cell (the latter not significantly enriched)—suggesting or confirming known overlap in their function. For instance, daf-2 (the C. elegans insulin/IGF-1 receptor) and rheb-1 (a GTPase) are known members of the nutrient-sensing target of rapamycin, TOR, pathway that affects growth and longevity; reviewed in Lapierre and Hansen (2012). It may be that altering the transport of nutrients, signaling molecules, or other proteins and ions across membranes counterbalances gas-1-associated mitochondrial dysfunction. Given these genes’ membership in important metabolic pathways (insulin signaling; mitochondrial unfolded protein response; K⁺ transport), it is possible that any ameliorating effects act by altering flux in these pathways at plasma membrane junctions. Third, the number of gas-1 MA line mutations occurring within gas-1 interactome genes was higher than expected by chance, suggesting that some gas-1 MA line mutations were fixed in response to the gas-1 mutation rather than resulting from drift. Finally, four of G0 background mutations was observed in any MA line, their fitness gains were necessarily fuelled by fixation of de novo beneficial or compensatory epistatic mutations. The most likely fate of such mutations arising in this unfavorable population genetic environment would be loss by drift, but the high numbers of failed bottlenecks and gas-1 MA line extinctions is consistent with selection operating at individual and/or intra-individual (e.g., gametic) levels. Additionally, the increased numbers of nonviable eggs is indicative of purifying selection (e.g., at zygotic or postzygotic levels) against new deleterious mutations, and suggests that an increased fraction of mutations was lethal on the gas-1 genetic background compared with N2. More work would be required to identify the mechanism(s) of selection in the gas-1 MA lines, but our findings recall those of the *Arabidopsis thaliana* MA experiments of Shaw and colleagues (Shaw et al. 2000, 2002; Rutter et al. 2010) where mean fitness of wildtype MA lines remained unchanged over generations of inbreeding, a pattern that may have resulted from the action of somatic cell lineage selection occurring in the meristem prior to formation of germ cells (Otto and Orive 1995). Our gas-1 MA lines may have benefitted from a different form of intraindividual selection that yielded a similar outcome.

Life History and Bioinformatic Results Signal Positive and Purifying Selection in gas-1 MA Lines

Contrary to results of standard MA studies, after fewer than 50 generations of single-individual bottlenecking, mean absolute, and relative fitness of gas-1 MA lines improved slightly beyond that of their ancestral gas-1 G0 control, whereas among-line variance in these traits declined. For comparison, the mutational variance, \( \sigma^2_M \), for absolute fitness (W) was 5.77 for the N2 MA lines (Baer et al. 2005) compared with a negative estimate, \( -1.547 \), for the gas-1 MA lines. Improved gas-1 MA line fitness was entirely due to improvements in early life reproduction beyond that of gas-1 G0. Because gas-1 MA lines were initiated from a genetically homogeneous ancestral population and evolved by strict selfing, and since neither reversion of the gas-1 mutant allele nor loss of the gas-1
the mutated genes—daf-2, rheb-1, smf-3, and sel-2—with membership in the enriched gas-1 MA GO slim categories (plasma membrane and transport) were also members of the gas-1 interactome. Interestingly, the plasma membrane category was not significantly enriched among gas-1 interactome genes, yet they may have been an important target for compensatory or beneficial mutation in the gas-1 MA lines.

Potential for Protective Metabolic Shift in gas-1 MA Lines

The evolution of gas-1 MA ROS levels toward lower, wildtype levels contrasts with the elevated ROS levels we previously observed among N2 MA lines (Joyner-Matos et al. 2013). Conversely, the MA process had little impact on steady-state ATP levels in gas-1 MA lines—the same was true for pharyngeal pumping (Lue 2015). A potential explanation for these combined results is that the gas-1 MA lines benefitted from a metabolic shift toward increased reliance upon fermentation and away from oxidative phosphorylation—a phenomenon known to occur in certain cancer cells (the Warburg effect, Warburg 1956). By utilizing one or more of their diverse fermentation pathways (Holt and Riddle 2003; Hulme and Whitesides 2011), C. elegans could reduce mitochondrial ROS production, perhaps offsetting the cost of the strain’s already low ATP (Tielens et al. 2002), preventing apoptosis (Ruckenstuhl et al. 2009), or increasing mtDNA genome stability (Ericson et al. 2012). In the absence of gene expression or other supporting data, we do not know whether such a shift, if one occurred, resulted from fixation of beneficial mutations and/or a stress response to deleterious MA in gas-1 MA lines.

Beneficial Haplotype Characterization Indicates Role for Epistasis

Although we were unable to isolate single, candidate beneficial gas-1 MA431 SNPs to ascertain their individual contributions to the line’s slight fitness recovery, this failure revealed a potentially large role for epistasis in gas-1 MA line fitness evolution. Our inability to break up the three chromosome III SNPs may have been due to their strong linkage and our limited power to detect recombinant genotypes. But failure to isolate the chromosome V SNP from the chromosome III group is consistent with some form of epistasis operating between this SNP and one or more on chromosome III. Interestingly, the four-SNP combination proved to be slightly more advantageous on its nonnative N2 background, and thus did not appear to specifically compensate for the gas-1 (fc21) mutation. This result was somewhat surprising given the interactome results and the reasonable expectation that N2 had achieved maximal laboratory adaptation, and is consistent with the existence of a rugged genetic landscape in which a new local fitness peak was opened to N2 by addition of the MA431 SNP set (c.f., Poelwijk et al. 2007). Two genetic explanations for this outcome include one of strong positive epistasis operating between some combination of MA431 SNPs, which would be neutral or beneficial on their own but advantageous in combination (Phillips 2008); in this scenario, the MA431 SNPs could have conferred a greater advantage on the N2 background simply because they did not have to contend with the 76 background mutations present within gas-1 G0. A second possibility is one of reciprocal sign epistasis (Kvitek and Sherlock 2011; Poelwijk et al. 2011), in this case involving individually deleterious mutations conferring a beneficial effect in combination. As previously noted, when any one of four MA431 SNPs was lost during the back-crossing phase, all others would be lost in the following generation—an outcome consistent with this form of epistasis operating between some combination of SNPs. If true, the mutational route to this beneficial SNP combination may have been complex given the likely existence of low-fitness intermediate genotypes; a transgenerational analysis of gas-1 MA431 mutational dynamics would be necessary to distinguish among these possibilities.

In contrast to the similar fitness effects of the MA431 SNPs in the gas-1 G0 versus N2 strains, their physiological effects were strongly strain-dependent. The four SNPs’ gas-1 G0-specific consequences (reduced ROS levels with no effect on ATP levels) are consistent with our metabolic shift hypothesis (above), whereas the consequences for N2 (reduced ATP levels with no effect on ROS levels) are more mysterious. Clearly, more work would be required to fully characterize the MA431 SNP set, but these results reveal strong context dependency in its effects at the physiological level. Finally, we note that the above interpretations ignore the possibility of epistatic interactions between the MA431 SNP set and mtDNA variants and/or nDNA mutation types not considered here. The former at least seems unlikely since, although we previously identified four heteroplasmic mtDNA variants segregating within the MA431 line, none were detected at levels exceeding ~4% in the sampled population (table 4 in Wernick et al. 2016).

Conclusion

Our study indicates that, even under conditions of extreme genetic drift, low-fitness populations can maintain or slightly improve their fitness through both selective elimination of deleterious mutations and fixation of novel beneficial mutations or allelic combinations. These unusual results are consistent with predictions of adaptive landscape theory—namely, with the existence of an inverse relationship between a population’s fitness and its likelihood of adaptation, and considerable context dependency of the mutational distribution of fitness effects. A greater fraction of new mutations may confer beneficial and lethal effects in populations existing at low-fitness extremes, simultaneously opening more mutational routes to both fitness maintenance/recovery and extinction. In addition, the fact that we observed only minor fitness
improvements—nothing approaching complete recovery of ancestral fitness levels—in gas-1 MA lines is consistent with the prediction that most advantageous mutations confer only small fitness benefits; however, the individual effects of any medium- or large-effect beneficial mutations acquired by the gas-1 MA lines were likely muted by deleterious mutations present in the same genomes. The above interpretation was supported by our bioinformatic analyses, which revealed highly nonrandom patterns of genetic network location and functional annotation among gas-1 versus N2 MA line mutations. Interestingly, these analyses implicated some of the same pathways known to be upregulated in the gas-1 mutant ancestor (Falk et al. 2008), suggesting that both genetic and nongenetic responses may tend to occur via similar or overlapping pathways. This study also revealed the capacity of ETC-deficient populations experiencing relaxed selection to rapidly recover near-wildtype levels of ROS—a pattern that may have been at least partly due to nongenetic mechanisms (i.e., compensatory transcriptional upregulation of metabolic and damage response pathways, Falk et al. 2008), which were further activated in response to deleterious MA in the gas-1 background. The downward evolution of ROS levels was accompanied by maintenance of a wildtype mutation rate but an altered mutational spectrum—a result similar to that of our previous analysis of mtDNA mutation processes in the same lines (Wernick et al. 2016). Understanding the extent to which this pattern may be due to selection favoring or eradicating particular base-substitution types would require further study. Lastly, our characterization of a SNP combination fixed within one gas-1 MA line was consistent with a role for reciprocal sign epistasis in fitness evolution in our system, and adds to the growing body of evidence that fitness landscapes are rugged and, whereas possibly dominated by genetic constraint, can provide routes to adaptation and “accessible innovation” (c.f., fig. 3 in Barrick and Lenski 2013).

**Supplementary Material**

Supplementary data are available at Genome Biology and Evolution online.

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