Received: 2 May 2022
Accepted: 24 May 2022
Published: 26 May 2022

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1. Introduction

Microbes live and evolve in dynamic ecosystems that differ widely in temperature, pH, osmotic stress and the availability of carbon sources [1,2]. These environmental changes can often occur at regular intervals or can have a predefined course of changes, providing an opportunity for a microbe to adapt and anticipate the upcoming condition based on the preceding signal or condition. An anticipatory response can help an organism make pertinent adaptive changes in advance to efficiently survive in a dynamic environment and hence may provide evolutionary and fitness advantages over organisms with a lower capability for adaptation. Several studies have demonstrated that bacteria have the potential to adapt and compete in dynamic and carbon source limited environments [3–5].
The mammalian digestive system, which has been inhabited by thousands of bacterial species for millions of years, is a perfect example of a dynamic ecosystem with spatial changes in stress, pH and metabolizable carbon sources. Recent studies suggest that the composition of gut microbiota influences the risk of several diseases in humans, including colorectal cancer, obesity, inflammatory bowel disease and type 2 diabetes. Moreover, it is now evident that dietary nutrients, including the nature and the availability of carbon sources for bacteria, have a significant impact on the composition and colonization of the gut microbiome [6,7].

Several carbon sources present in the diet have predefined spatial abundance in the intestine. According to the nutrient-niche theory, first developed by Freter [3,8], the nutrient landscape dictates which organisms can successfully colonize and persist in the gut [9]. Hence, it can be argued that the spatial abundance of different carbon sources in the human intestine provides an optimal platform for microbes, such as *Escherichia coli*, to develop correlative responses or even anticipate the upcoming environmental cue. *E. coli* is a well-studied model bacterium that travels back and forth between the mammalian intestine and the environment. Usually, *E. coli* is one of the first species to colonize the human intestine and inhabit there throughout human life [10]. In addition to the dynamic environment of the intestine, *E. coli* also faces competition from other bacterial species that inhabit the intestine [11]. Interestingly, only a handful of previous studies have suggested that *E. coli* has the potential to learn and anticipate the future environment. For example, anticipatory behavior in *E. coli* was first reported between the temperature upshift and changes in the oxygen level in the gut [12], and another study showed that D-lactose grown *E. coli* can anticipate the maltose [13]. More generally, the association between carbon sources and the genome-wide expression profile they induce has been investigated before in isolation [14]. It is still unknown how the correlation structure of the environment may be influencing anticipatory responses and the molecular mechanisms that facilitate these transitions.

Here, we explored whether cross-dependencies and anticipatory responses exist in the expression profiles of *E. coli* cells exposed to the seven carbon sources (D-galactose, D-glucose, D-maltose, D-trehalose, D-fructose, D-lactose and Oleic acid) that have previously been reported to have concentration gradients in the mammalian intestine. *E. coli* was transcriptionally profiled after growth in these seven carbon sources, and differential expressions of the catabolic genes related to these seven carbon sources were calculated. We found 67% agreement between the measured anticipatory responses and what we would expect theoretically, while 83% and 0% of cases were in agreement with the homeostatic and random responses, respectively. To understand the genetic and phenotypic basis of the discrepancies between the expected and measured anticipatory responses, and to demonstrate if anticipatory responses can be rewired, as a case study, we thoroughly investigated the discrepancy in the D-galactose treatment and the expression of the maltose operon gene in *E. coli* through whole genome random mutagenesis, the screening of desired phenotypes, sequencing, and a cost-benefit analysis (Figure 1).
which has an inherent capability to adapt to new conditions, may learn and anticipate the availability of upcoming carbon sources, such as D-maltose, when it encounters an abundance of a particular carbon source. Based on these assumptions and the current knowledge, we created a map of the expected anticipation, demonstrating the presence of a carbon source and the expression of catabolic genes of relevant carbon sources (Figure 2b, top left slice). Subsequent transcriptome profiling and RT-PCR measurements were performed to check the validity of the expected anticipations.

2. Results

2.1. Identification of Carbon Sources with Spatial Concentration Gradients in the Mammalian Intestine

A literature survey was performed to identify the carbon sources that have spatial abundances in the mammalian intestine. We were able to find a limited number of studies focusing on identifying the concentration gradients of carbon sources [15–18]. Based on these studies, we selected seven carbon sources (D-galactose, D-glucose, D-maltose, D-trehalose, D-fructose, D-lactose and Oleic acid) that have been reported to have spatial concentration gradients in the mammalian intestine and can be metabolized by E. coli (Figure 2a and Figure S1) in order to explore the existence of anticipatory responses in E. coli [15–18]. Since the data were collected from different sources, they had heterogeneity in the data points—hence, the reported concentrations of carbon sources and the length of the intestine were locally normalized from 0 to 1, and 1000 fitted data points for each carbon source were generated by Loess regression to obtain a better picture of spatial abundances (Figure 2a) [19]. In some cases, actual concentrations of the carbon sources were not reported in the literature; in such cases, either activities or concentrations of enzymes were used as proxies of the carbon source concentrations (Supplementary file 2). Figure 2a demonstrates the spatial concentration gradients of seven carbon sources across the mammalian intestine. For example, the concentration of D-lactose is high at the front end of the intestine, while that of D-maltose is high at the distal end of the intestine. As we mentioned earlier, bacteria such as E. coli have been passing through the mammalian intestine for millions of years and, in the standard case, will repeatedly experience a similar kind of spatial abundance as these seven carbon sources. So, we hypothesize that E. coli, which has an inherent capability to adapt to new conditions, may learn and anticipate the upcoming carbon sources, such as D-maltose, when it encounters an abundance of a particular carbon source, such as D-lactose, at the front end of the intestine. Based on these assumptions and the current knowledge, we created a map of the expected anticipation, demonstrating the presence of a carbon source and the expression of catabolic genes of relevant carbon sources (Figure 2b, top left slice). Subsequent transcriptome profiling and RT-PCR measurements were performed to check the validity of the expected anticipations.
RT-PCR measurements were performed to check the validity of the expected anticipatory profiles matched with the experimental anticipatory profiles obtained from the transcriptome profiling, while 83% and 0% agreed with the homeostatic and random response, respectively. We defined homeostatic response as when cells growing in a sugar induce or repress the carbon catabolic genes of sugars with a similar pattern of a concentration gradient in the intestine. We identified 18 such cases, and there were three differences between the expected response and the response measured using RNA-Seq. In random response, cells randomly induce the carbon catabolic genes of sugar with a similar pattern of a concentration gradient in the intestine. We identified 18 such cases, and there were three differences between the expected response and the response measured using RNA-Seq. 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There was 89% agreement between the findings of the transcriptome profiling and those of
the RT-PCR.

2.3. Anticipatory Responses in E. coli Are Re-Programmable

Next, we attempted to understand the mechanism of the formation of anticipatory
behavior in E. coli. We picked up the case where D-galactose negatively regulates the
expression of maltose operons and attempted to neutralize or reverse the association to
understand the feasibility of reprogramming and the associated genetic and phenotypic
consequences. The case of the negative anticipation of D-maltose once E. coli has encoun-
tered D-galactose is interesting, as it is the opposite of what E. coli should have evolved to
do naturally in the intestine. In the mammalian intestine, the concentration of D-galactose
is high at the front portion of the intestine, while D-maltose is high at the end of the intes-
tine; hence, we can anticipate positive anticipation between D-galactose treatment and the
expression of maltose operons because of millions of years of the adaptation of E. coli in
the gut, but experimental observations indicate that E. coli shuts the expression of maltose
operons when it encounters the D-galactose. To quantitate the expression of the maltose
operon, we constructed gfp:kanR cassette and integrated that to downstream of the malP
gene (maltose operon) in E. coli MG1655, generating the strain E. coli MING (Figure S3). We
performed whole genome random mutagenesis in MING using ethyl methanesulfonate
(EMS) to evolve the potential phenotypes demonstrating the induction of maltose operons
(malP:gfp) in D-galactose supplemented growth media. EMS has been used widely for
whole genome random mutagenesis to create the desired phenotypes in a short dura-
tion [25]. D-galactose and D-maltose inducible colonies were identified by measuring the
malP:gfp expression separately in these carbon sources, as described in Section 4. Briefly,
455 colonies were screened (Figure 3a,b), and 31 colonies demonstrated a >1-fold increase
in GFP fluorescence upon treatment with 10 mM D-galactose against the colonies grown in
0.1% glycerol. A total of 20 colonies demonstrating maximum fold change were further
validated by characterizing them at least in triplicate in 10 mM D-galactose (Figure 3c). The
colonies showing a positive response to the D-galactose treatment were Sanger sequenced.
The potential genes and promoters that possibly influence the dose–response curve of the
maltose operon (mal)—specifically the genes malP, crP, DNA pol III, galR and malT and the
promoter regions of malt—were sequenced. The majority of mutants responding positively
to D-galactose treatment did not have mutations in these genes, but we identified two
E. coli mutants, EGK5_A8 and EGK8_A7, with unique mutations in the crP gene and one
mutant, EGK6_D3, with the mutation in the promoter region of malT (Figure 4a). These
observations indicate that the genetic networks of E. coli have the capability to create a
positive association between D-galactose treatment and the expression of maltose operon.

Repair Mutants Reverse the Response to D-Galactose

To establish that the observed mutations in the EGK5_A8, EGK8_A7 and EGK6_D3
mutations are indeed responsible for the development of positive anticipatory responses
between D-galactose treatment and the expression of malP gene (maltose operon), the
mutations were fixed using the λ-red recombinase system [26] to generate the strains MING_crP2,
MING_crP1 and MING_pmalT1, respectively. Sanger sequencing was performed to val-
idate the fixation of the mutations. The responses of the repair mutants were measured
in D-galactose by the flow cytometer, and, surprisingly, the repair mutants responded
similarly to the parental E. coli strain MING, where the expression from the maltose operon
(malP:gfp) was repressed in the 10 mM D-galactose supplemented M9 (Figure 4b).
Figure 3. Screening of *E. coli* MG1655 mutants demonstrating a positive association between D-galactose treatment and the expression of *malP* (a gene of the maltose operon). (a,b) Screening of D-galactose and D-maltose responsive *E. coli* strains; (c) Further characterization of demonstrating a positive association between D-galactose treatment and the expression of *malP*, at least in triplicate. The responses reported in plot A were measured in a plate reader, and the rest of the measurements were taken using a flow cytometer. * indicates significant differences (*p*-value < 0.05), and ns indicates no significant differences (*p*-value > 0.05). The *p* values were calculated by the two-sample *t*-test. Error bars indicate the standard error of the mean (±).
Figure 4. Identification of mutations and characterization of repair mutants. (a) Mutations in strains demonstrating the upregulation of $\text{malP}$ expression in D-galactose supplemented media. EGK5_A8 and EGK8_A7 had point mutations in the coding region of $\text{crP}$, while EGK6_D3 had a point mutation in the promoter region of the $\text{malt}$ gene; (b,c) Responses of repair mutants in 0.1% glycerol M9 and 0.1% glycerol M9 supplemented with 10 mM D-galactose. Fold repression was calculated by dividing the $\text{gfp}$ ($\text{malP}$) levels in 0.1% glycerol M9 supplemented with 10 mM D-galactose with the $\text{gfp}$ ($\text{malP}$) levels in 0.1% glycerol M9. Point mutations in EGK5_A8, EGK8_A7 and EGK6_D3 were repaired to generate the repair mutants MING_crP2, MING_crP1 and MING_pmalT1, respectively. * indicates significant differences ($p$-value < 0.05). The $p$ values were calculated by the two-sample t-test. Error bars indicate the standard error of the mean ($\pm$).

2.4. Expression of Maltose Operons in D-Galactose Is Costly

We further investigated, given the feasibility of the emergence of a positive anticipatory response between D-galactose treatment and the expression of maltose operon, why the genetic networks of $E.\ coli$ have not evolved to exhibit such phenotype, despite millions of years of encounters with high D-galactose at the top section and with high D-maltose at the bottom section of the intestine. To solve this puzzle, we first created the $\text{lacZ}$ deleted strains of EGK5_A8, EGK8_A7 and EGK6_D3 (coined as EGK5_A8x, EGK8_A7x and EGK6_D3x), which competed against the parental strain MING in 0.1% glycerol M9 media, where either 10 mM each of D-galactose and D-maltose was provided simultaneously or where D-maltose was provided 1 h after D-galactose treatment (Figure 5a). These two time points were chosen between D-galactose and D-maltose treatment to determine the best time to see the conditioning effect of D-galactose. The quantification of the competition assay was conducted by growing treated cultures on LB agar plates supplemented with the IPTG and X-gal and then counting the blue/white colonies. It was observed that the fitness of the evolved mutant strains was 12% to 20% lower compared to that of the wild type strain when conditioned in the D-galactose, and the simultaneous experiments and those after 1 h of treatment with D-maltose showed similar responses (Figure 5b). These observations indicate that the cost of expressing maltose operons in D-galactose growth media is higher compared to the benefit; hence, $E.\ coli$ has not evolved a positive association between D-galactose treatment and the expression of maltose operons.
we found only a limited number of studies demonstrating the concentration gradients of carbon sources. Based on evolutionary training and the current knowledge, a map of cross carbon source anticipatory behavior was created and validated experimentally, which was agreed upon at a rate of 67%. Different factors can contribute to the discrepancies, such as inaccuracies in our limited knowledge of the concentration gradients of carbon sources and the high cost of expressing catabolic genes for a second carbon source in advance. In one of the cases of disagreement, as per the expectation based on evolutionary training, there should be a positive correlation between the presence of D-galactose and the expression of maltose operons, but a negative correlation was observed. Whole genome random mutagenesis and selected screening demonstrated that E. coli has the capacity to upregulate the expression of maltose operons in D-galactose. The subsequent investigation revealed that, though E. coli has the capacity to upregulate maltose operons in D-galactose, due to the high cost of expression, it does not do so. These findings indicate that E. coli can anticipate the subsequent environmental conditions, and based on appropriateness, it can either create a positive or negative anticipatory response. This work can be further extended to study the existence and dynamics of anticipatory responses in the gut microbiota by performing metatranscriptomics in different carbon sources. Additionally, the selected microbial species can be trained to perform a specific task. For example, E. coli can be

Figure 5. Competition assays to measure the fitness of lacZ deleted mutant strains showing a positive association between D-galactose treatment and malP expression. (a) Experimental strategy; (b) Fitness of lacZ deleted mutant strains against wild type strain MING.

3. Discussion

Environmental conditions are dynamic, and, in several instances, these conditions follow a specific course where, based on the current condition, the upcoming condition can be anticipated. An organism with the capability of learning and anticipation can prepare itself in advance to cope with the upcoming condition and hence will have the advantage of survival and growth over other organisms. Learning and anticipatory behaviors in mammals are well-studied phenomena, by which they are capable of associating two different environmental signals after repeated training. Pavlovian conditioning is a well-known example. Mammalian systems learn and anticipate primarily by making appropriate changes in the interconnections of neurons [27], but in microbes, such as E. coli, neurons are lacking, so any adaptive response generating anticipation should happen preferably through genetic and/or epigenetic modifications.

The environmental conditions of the mammalian intestine, though dynamic, harbor a sequential presence of predefined environmental composition. E. coli has been passing through the intestine for millions of years and hence has been trained indirectly to associate and anticipate the future environment based on the preceding environment. Only two studies have reported the existence of anticipatory behavior in E. coli [12,13]. Here, we explored the existence of anticipatory behavior in E. coli for seven carbon sources that have been reported to have spatial concentration gradients across the intestine. Surprisingly, we found only a limited number of studies demonstrating the concentration gradients of carbon sources. Based on evolutionary training and the current knowledge, a map of cross carbon source anticipatory behavior was created and validated experimentally, which was agreed upon at a rate of 67%. Different factors can contribute to the discrepancies, such as inaccuracies in our limited knowledge of the concentration gradients of carbon sources and the high cost of expressing catabolic genes for a second carbon source in advance.

In one of the cases of disagreement, as per the expectation based on evolutionary training, there should be a positive correlation between the presence of D-galactose and the expression of maltose operons, but a negative correlation was observed. Whole genome random mutagenesis and selected screening demonstrated that E. coli have the capacity to upregulate the expression of maltose operons in D-galactose. The subsequent investigation revealed that, though E. coli has the capacity to upregulate maltose operons in D-galactose, due to the high cost of expression, it does not do so. These findings indicate that E. coli can anticipate the subsequent environmental conditions, and based on appropriateness, it can either create a positive or negative anticipatory response. This work can be further extended to study the existence and dynamics of anticipatory responses in the gut microbiota by performing metatranscriptomics in different carbon sources. Additionally, the selected microbial species can be trained to perform a specific task. For example, E. coli can be
evolved and trained to secrete species-specific toxins when it encounters the targeted pathogenic bacteria in the intestine.

4. Materials and Methods

4.1. Strains and Media

*E. coli* MG1655 [28] was used as a parental strain, and the strains derived from the parental strain are mentioned in Table 1. All *E. coli* strains were maintained at 4 °C on LB agar plates supplemented with the required antibiotic. For all the quantitative measurements, the cells were first grown overnight in LB broth. A fraction of the cells were transferred to a fresh M9 salt medium supplemented with 0.1% glycerol (Affymetrix) and grown for 8 h at 37 °C in an incubator shaker. Later, a fraction of the cells were transferred to the required media for either growth measurements or fluorescence measurements. All experiments were performed in three biological replicates unless otherwise indicated.

Table 1. Strains used in this study.

| Strain            | Description                                      | Reference         |
|-------------------|--------------------------------------------------|-------------------|
| *E. coli* MG1655  | Wild-type                                        | Laboratory stock  |
| MING              | MG1655 (*malP:gfp:kan^R* )                       | This study        |
| EGK5_A8           | MING with a point mutation in the coding region of *crP* | This study        |
| EGK8_A7           | MING with a point mutation in the coding region of *crP* | This study        |
| EGK6_D3           | MING with a point mutation in the promoter region of *malT* | This study        |
| MING_crp1         | EGK8_A7 with a repaired point mutation in the coding region of *crP* | This study        |
| MING_crp2         | EGK5_A8 with a repaired point mutation in the coding region of *crP* | This study        |
| MING_pmalT1       | EG6_D3 with a repaired point mutation in the promoter region of *malT*. | This study        |
| EGK5_A8x          | EGK5_A8 (ΔlacZ)                                  | This study        |
| EGK8_A7x          | EGK8_A7x (ΔlacZ)                                 | This study        |
| EGK6_D3x          | EGK6_D3x (ΔlacZ)                                 | This study        |

4.2. Growth Measurements at Different Concentrations of Carbon Sources

Fresh colonies of *E. coli* MG1655 were transferred to 1 mL LB broth media and grown for 8 h at 37 °C in an incubator shaker. After 8 h, 5 µL of grown cultures were transferred to 96 well plates (Costar) containing 195 µL of 0.1% glycerol M9 media supplemented with 5, 10, and 20 mM of carbon sources: D-galactose (Acros Organics, Geel, Belgium), D-Glucose (Acros Organics), D-maltose (Acros Organics), D-Trehalose (Fisher Scientific, Waltham, MA, USA), Oleic acid (Fisher Scientific) and D-Fructose (Acros Organics). Cell density (OD_{600}) was measured every 15 min using a plate reader (BioTek HTX) at 37 °C for 24 h. The maximum growth rate (µ_{max}) was calculated using the custom program in MATLAB^{TM}. A total of 500 mM of a stock solution of oleic acid was prepared using water, Brij35 (Sigma, Burlington, MA, USA) and ethanol, while 500 mM of the stock solutions of the other five carbon sources was prepared in water. The stock solutions were filter sterilized using 0.22 µm PVDF filters (Olympus plastics).

4.3. Treatment of *E. coli* MG1655 with Carbon Sources, RNA Isolation and Transcriptome Profiling

Fresh colonies of *E. coli* were grown overnight in 0.1% glycerol M9. The next day, 50 µL of cells were transferred to 3 mL 0.1% glycerol M9 supplemented with or without 10 mM of each carbon source mentioned earlier and was grown and harvested in a mid log phase at 8 h. Then, 1 mL of the growing culture was mixed with the chilled 0.5 mL 5% phenol/ethanol (v/v), and the cells were subsequently pelleted down at 13,200 rpm at 4 °C. The supernatant was discarded carefully, and the cell pellets were stored immediately at −80 °C until use. RNA was extracted from the frozen cell pellet using a RNeasy kit (Qiagen,
Hilden, Germany). The traces of any leftover genomic DNA were cured using an RNase-Free DNase Set (Qiagen). The concentration of total RNA was measured using a NanoDrop spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA). The quality of the isolated total RNA was checked by running 2 to 3 µg of total RNA on 1.5% denaturing agarose gel. For transcriptome profiling, 5 µg of total mRNA was taken, and mRNA enrichment was performed using a MICROBExpress™ Bacterial mRNA Enrichment Kit (Thermo Fisher Scientific). The libraries from the mRNA enriched samples were prepared using the KAPA standard RNA-Seq library preparation kit (Kapa Biosystems, Wilmington, MA, USA). Double size selections (200 to 500 bp) of the libraries were performed using Agencourt AMPure XP (Beckman Coulter, Brea, CA, USA) beads. The quantification of the libraries was performed using a Qubit fluorometer (Thermo Fisher Scientific). The quality of the individual library was checked on a Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA). The concentrations of all the libraries were normalized, and the libraries were pooled together and sequenced by an Illumina Hiseq 2500 system running in high throughput mode (Single end, 50 cycles). Since the minimum lengths of the RNA-Seq libraries were 200 bp, most of the tRNAs that are less than 100 nucleotides long [29] were lost during the fragmentation and size selection steps of the library preparation; hence, the tRNAs were excluded in the subsequent analysis. Please refer to Supplementary File 1 for a detailed analysis of the RNA-Seq data and the differentially expressed genes (DEGs).

4.4. Real-Time Reverse Transcription PCR (RT-PCR)

The cell growth, the treatment with specific carbon sources, the total RNA isolation and removal of genomic DNA were performed as described in the previous section. The quality of the isolated RNA was checked on 1.5% denaturing agarose gel. The first strand of cDNA was synthesized from 1 µg of RNA using a RevertAid™ First Strand cDNA Synthesis Kit (Thermo Scientific). The supplied random hexamers were used as primers. Gene expression was measured using the VeriQuest SYBR Green qPCR Master Mix on the ABI Viia 7 RT PCR platform (Thermo Scientific). A total of 2 µL of cDNA was mixed with 1 µL each of the required forward and reverse primers (10 µM; Table S1). The other components of the reaction mixtures were added as per the manufacturer’s instructions. The total reaction volume was made to 20 µL in 396 well plates. The following program was used for the amplification and quantification: 95 °C for 2 min, 40 cycles of 94 °C at 15 s, 60 °C for 1 min, 72 °C for 30 s, final annealing at 72 °C for 1 min, and melt curve from 55 °C to 95 °C for 20 min. The constitutive transcript ihfb was used as an internal control to normalize the expression [30].

4.5. Chromosomal Integration of gfp:kanR Cassette at the Downstream of malP

To directly measure the expression of the malP promoter, the gfp:kanR polycistronic cassette was integrated downstream of the chromosomal malP gene of E. coli. The gfp was amplified from BioBrick BBa_E0020 (parts.igem.org/Part:BBa_E0020) using the primers Gfp_in_fw and Gfpkan_rv1, while kanamycin was amplified from the plasmid psb3k3 (parts.igem.org/Part:psb3k3) using the primers Kan_in_fw and Kan_gfp_rv (Table S2). Phusion polymerase (Thermo Fisher Scientific) was used for the error free PCR. The 3’ end of the primers Gfpkan_rv1 and Kan_in_fw had the restriction site for the XbaI. Kan_in_fw also had the ribosome binding site (BioBrick B0030) downstream of the XbaI site. After PCR amplification, the fragments were gel purified using a gel extraction kit (Thermo Fisher Scientific). Subsequently, the fragments were digested with XbaI for 3 h at 37 °C and later column purified. The purified fragments were ligated overnight at 16 °C using T4 ligase (NEB). A total of 5 µL of the ligated product was enriched by performing PCR using the primers Gfp_in_fw, Kan_gfp_rv, and Phusion polymerase. The PCR amplified products were gel eluted. The PCR amplified product was inserted downstream of the malP gene using the lambda red recombinase system, as described elsewhere [26]. The screening of the successful strain was performed by performing selection on LB agar plates containing
50 µg/mL kanamycin, and, later, the sequences and the site of insertion were verified by the Sanger sequencing of the gfp:kanR cassette and flanking regions.

4.6. Ethyl Methanesulfonate (EMS) Driven Random Mutagenesis and Screening of the Desired Mutant

A fresh colony of E. coli-MING was grown overnight at 37 °C in 20 mL LB broth supplemented with 50 µg/mL kanamycin. E. coli culture was washed with PBS (Phosphate Buffered Saline; 137.93 mM NaCl, 2.67 mM KCl, 1.47 mM KH₂PO₄, 8.1 mM Na₂HPO₄; pH of 7.4) at 8000 rpm for 2 min; then, the pellet was resuspended in PBS to the original volume. A total of 40 µL of EMS (ACROS Organics) was added to 2 mL of E. coli suspension, and the cells were incubated for 30, 60 and 120 min at 37 °C in an incubator shaker. After incubation, the cells were washed twice with PBS at 8000 rpm for 2 min. Then, they were resuspended in 2 mL of LB broth, grown for 1 h at 37 °C, serially diluted, and plated on LB agar plates. The LB agar plates were incubated overnight at 37 °C, and the grown colonies were used to screen the desired mutants. Individual bacterial colonies were grown overnight in 200 µL LB broth supplemented with 50 µg/mL kanamycin in 96 well plates at 37 °C in a plate reader cum shaker operating at 37 °C. The next day, 5 µL of grown culture was transferred to 195 µL of an M9 salt medium supplemented with 0.1% glycerol and 0.1% glycerol plus 10 mm D-maltose in 96 well plates. The cells were grown for 12 h in a plate reader at 37 °C, and the cell density (OD₆₀₀) and GFP fluorescence (excitation: 485/20 nm, emission: 528/20 nm) were measured. After 12 h, 10 µL of the cultures grown only in 0.1% glycerol M9 was transferred to 190 µL of the M9 salt medium supplemented with 0.1% glycerol and both with 0.1% glycerol and 10 mM D-galactose. The cells were grown for 10 h in a plate reader at 37 °C. Later, the expressions of gfp in the individual cells were measured using a BD Accuri™ C6 cytometer (BD Biosciences). At least 20,000 events were recorded for each sample. For each event, forward- and side-scatter, as well as GFP levels (488 nm excitation laser; FL1 filter set), were recorded. The cells were selected from a tight forward and side-scatter gate to calculate the levels of GFP.

4.7. Mutation Repair

The repairs of the mutants were performed in two steps using the lambda red recombination system, as described in the above section. In the first step, the mutant genes were replaced by a spectinomycin resistance expressing cassette, and the subsequently integrated spectinomycin cassette was replaced with a cassette comprised of the wild type gene and the autonomously expressing chloramphenicol resistance gene. The integration was confirmed by Sanger sequencing. The spectinomycin cassette was amplified from the genomic DNA of E. coli MG1655Z1 [31] using the following primer sets: (i) SP7.2_FW and SPU_Rv to integrate the purified PCR product at the crp site of E. coli MING_crp1; (ii) SP7.4_FW and SPU_Rv to integrate the purified PCR product at the crp site of E. coli MING_crp2; (iii) MT1S_Fw and MT1S_Rv to integrate the purified PCR product at the malT site of E. coli MING_malT (Table S3). All the primers had a 5’ 36- to 50-nucleotide region with perfect homology with their respective chromosomal integration sites. To facilitate the chromosomal integration, the E. coli strains MING_crp1, MING_crp2 and MING_malT were transformed with ampicillin resistance and the temperature sensitive plasmid pKD46 using the CaCl₂ mediated heat shock method. The successful transformants were selected on an LB agar plate supplemented with 100 µg/mL ampicillin at 30 °C. The cells with plasmid pKD46 were made electrocompetent and transformed with respective spectinomycin cassettes using the BioRad electroporator using a 1mm cuvette at 1.75 KV. The successful transformants were selected on kanamycin (50 µg/mL) and spectinomycin (50 µg/mL) LB agar plates at 37 °C. Later, the integration was confirmed with PCR and Sanger sequencing. The primers used during various steps of the integration are mentioned in Supplementary Table S3.
4.8. Competition Assays

First, the lacZ gene of the mutant strains EGK5_A8, EGK8_A7 and EGK6_D3 was replaced by the spectinomycin resistance gene using the lambda red recombination system, as mentioned in the above sections, to generate the following ΔlacZ strains: EGK5_A8, EGK8_A7 and EGK6_D3, respectively. The competition assay was performed between wild type E. coli MG1655 and EGK5_A8, EGK8_A7 and EGK6_D3. All the E. coli strains were grown for 8 h in 3 mL LB broth at 37 °C in an incubator shaker; then, 50 µL of grown cultures were transferred to 2 mL of an M9 medium supplemented with 0.1% glycerol and was grown overnight at 37 °C in an incubator shaker. The cells were pelleted by centrifuging at 6000 rpm for 3 min. The supernatant was discarded, and the pellets were dissolved in 2 mL of the M9 salt medium. The OD_{600} was measured and normalized to the identical cell density using the M9 salt medium. The MG1655 was mixed separately with EGK5_A8, EGK8_A7, and EGK6_D3 in equal volume. Then, the competition assay was performed using two different protocols (Figure 5a): (i) 5 µL of the individual mixture of cultures was transferred to 195 µL of M9 media containing 0.1% glycerol, 10 mM D-galactose and 10 mM D-galactose in 96 well plates, and (ii) 5 µL of the individual mixture of cultures was transferred to 195 µL of M9 media containing 0.1% glycerol and 10 mM D-galactose in 96 well plates. The cells were grown for 1 h and then 10 mM D-maltose was added. The cells were grown, in total, for 12 h at 37 °C in a plate reader (BioTek HTX). The samples were collected at time 0 (start of plate reader) and at 12 h (completion of plate reader). The competition assay was performed with at least four biological replicates. The counting of the blue and white colonies was performed by growing the cells on LB agar plates containing 0.25 mM IPTG (Isopropyl-β-d-1-thiogalactopyranoside) and 40 mg/mL X-gal (bromo-chloro-indolylgalactopyranoside). The plates were incubated overnight at 37 °C and subsequently, the blue and white colonies were counted. The percentage loss in the fitness of the mutant strains against the wild type strain was calculated using the following equation:

\[ x = \left( \frac{\text{blue cfu}}{\text{white cfu}} \right)_{t=0}, \quad y = \left( \frac{\text{blue cfu}}{\text{white cfu}} \right)_{t=12}, \quad \text{Percentage loss in fitness} = \left( \frac{y - x}{x} \right) \times 100 \]

4.9. Statistical Analysis

All the data have been reported as the mean with the standard error. The values of the mean and standard errors were calculated from at least three separate experiments using the OriginPro software (OriginLab Corporation). The p-values were calculated by the two-sample t-test using the OriginPro software. The statistical analysis used in the analysis of the RNA-Seq data has been described in Supplementary File 1 (section, “Transcriptome analysis of RNA-Seq experiments” and “DEG (Differentially Expressed Gene) analysis”).

Supplementary Materials: The following are available online at https://www.mdpi.com/article/10.3390/ijms2315985/s1.

Author Contributions: I.T. conceived and supervised all aspects of the project. N.R. performed all experiments and analyzed the data. M.K. analyzed the RNA-Seq raw data. I.T. and N.R. wrote the paper. All authors have read and agreed to the published version of the manuscript.

Funding: This work was supported by AFRI Competitive Grant no. 2020-67021-32855/project accession no. 1,024,262 from the USDA National Institute of Food and Agriculture. This grant is being administered through the USDA-NIFA/NSF AI Institute for Next Generation Food Systems (AIFS) https://aifs.ucdavis.edu (accessed on 25 April 2022).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: Data used to generate Figure 2a are available in the article (Supplementary file 2). Other data presented in this study are available on request from the corresponding author.
Conflicts of Interest: The authors declare no conflict of interest. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript; or in the decision to publish the results.

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