Selection of Bacterial Mutants in Late Infections: When Vector Transmission Trades Off against Growth Advantage in Stationary Phase

Marine Cambon, Nathalie Parthuisot, Sylvie Pages, Anne Lanois, Alain Givaudan, Jean-Baptiste Ferdy

To cite this version:
Marine Cambon, Nathalie Parthuisot, Sylvie Pages, Anne Lanois, Alain Givaudan, et al.. Selection of Bacterial Mutants in Late Infections: When Vector Transmission Trades Off against Growth Advantage in Stationary Phase. mBio, American Society for Microbiology, 2019, 10 (5), 14 p. 10.1128/mBio.01437-19. hal-02336483

HAL Id: hal-02336483
https://hal.archives-ouvertes.fr/hal-02336483
Submitted on 28 Oct 2019

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Distributed under a Creative Commons Attribution 4.0 International License
Selection of Bacterial Mutants in Late Infections: When Vector Transmission Trades Off against Growth Advantage in Stationary Phase

Marine C. Cambon,a,b* Nathalie Parthuisot,a Sylvie Pagès,b Anne Lanois,b Alain Givaudan,b Jean-Baptiste Ferdya

aÉvolution et Diversité Biologique, CNRS–Université Paul Sabatier, Toulouse, France
bDiversité, Génome et Interactions Microorganismes Insectes, INRA–Université Montpellier, Montpellier, France

ABSTRACT Bacterial infections are often composed of cells with distinct phenotypes that can be produced by genetic or epigenetic mechanisms. This phenotypic heterogeneity has proved to be important in many pathogens, because it can alter both pathogenicity and transmission. We studied how and why it can emerge during infection in the bacterium Xenorhabdus nematophila, a pathogen that kills insects and multiplies in the cadaver before being transmitted by the soil nematode vector Steinernema carpocapsae. We found that phenotypic variants cluster in three groups, one of which is composed of lrp defective mutants. These mutants, together with variants of another group, have in common that they maintain high survival during late stationary phase. This probably explains why they increase in frequency: variants of X. nematophila with a growth advantage in stationary phase (GASP) are under strong positive selection both in prolonged culture and in late infections. We also found that the within-host advantage of these variants seems to trade off against transmission by nematode vectors: the variants that reach the highest load in insects are those that are the least transmitted.

IMPORTANCE Pathogens can evolve inside their host, and the importance of this mutation-fueled process is increasingly recognized. A disease outcome may indeed depend in part on pathogen adaptations that emerge during infection. It is therefore important to document these adaptations and the conditions that drive them. In our study, we took advantage of the possibility to monitor within-host evolution in the insect pathogen X. nematophila. We demonstrated that selection occurring in aged infection favors lrp defective mutants, because these metabolic mutants benefit from a growth advantage in stationary phase (GASP). We also demonstrated that these mutants have reduced virulence and impaired transmission, modifying the infection outcome. Beyond the specific case of X. nematophila, we propose that metabolic mutants are to be found in other bacterial pathogens that stay for many generations inside their host.

KEYWORDS Xenorhabdus nematophila, GASP, transmission, within-host evolution

Bacterial infections, even when they started from a single pathogenic strain, often end up being composed of cells with different phenotypes (1). In cases where groups of cells with distinct phenotypes interact to better exploit their host (2), the molecular mechanisms driving bacterial diversity can be considered adaptations, which ultimately increase pathogen transmission. To demonstrate this theory, it is necessary to understand both what these mechanisms are and how they impact the success of the infection.

Mutation is probably the most obvious mechanism that produces diversity during infection. Its importance is increasingly admitted (1), notably because cases are now
accumulating where it fuels the evolution of pathogens inside the host, in particular in human diseases (3, 4). While mutation generally occurs throughout the whole genome, there are other mechanisms that impact a restricted set of genes. These mechanisms can be epigenetic alterations, where clonal populations of bacteria modify their phenotype by changing their regulatory state (5, 6). These can also be genetic alterations, as in phase variation where a specific high-rate mutation mechanism produces reversible changes in one or a few genes (7, 8). Phase variation is described as the basic mechanism that makes antigenic variation a successful instrument for some pathogens to escape their host immune system (9).

The insect bacterial pathogen *Xenorhabdus* is a promising model to study the adaptive nature of mechanisms that control phenotypic variation inside an infection. This pathogen kills insects and proliferates in their cadavers for 1 or 2 weeks, before it is transmitted by the nematode vector *Steinernema* (10). During this long period, *Xenorhabdus* maintains high densities inside the insect and, therefore, potentially accumulates phenotypic variation. As the complete life cycle of *Xenorhabdus* can be experimentally reproduced (11), it is possible to quantify how this variation impacts each of its different stages.

*Xenorhabdus* isolated from the wild typically are in a form described as primary, but in culture media, they convert to another, secondary form when reaching long-term stationary phase (12). In his seminal paper, Akhurst (13) showed that secondary forms of *Xenorhabdus* also appear during infection and that this occurs at a rate that varies greatly among *Xenorhabdus* strains. Although the phenotypic differences between the two forms can also vary depending on strain and species, only cells of the primary form are able to bind bromothymol blue dye, are motile, agglutinate red blood cells, and produce fimbriae, hemolysins, proteases, antimicrobials, and crystalline inclusion bodies (12, 14–17). Interestingly, genes for which expression differs between primary and secondary forms have also been shown to play a role in the interaction between *Xenorhabdus nematophila*, its nematode vector, and its insect target (18). This strongly suggests that the emergence of secondary forms should impact *X. nematophila* interactions with their invertebrate hosts. This could also explain why nematodes have so far been reported to carry primary forms, although previous experiments suggest that secondary forms of *X. nematophila* are capable of both killing insects (16) and being transmitted by the nematode *Steinernema carpocapsae* (19).

The alternation between primary and secondary forms has so far been interpreted as a case of phase variation (12), and later termed phenotypic variation (17). As the phenotype of secondary forms matches that of *lrp* defective mutants (20–24), it has also been proposed that the Lrp master regulator might be involved in the production of secondary variants in *X. nematophila* (20). However, the mechanism driving phenotypic variation in *X. nematophila* is unknown.

The goals of this study were to better understand (i) the molecular mechanisms that are responsible for the production of phenotypic variants and (ii) the impact of these variants on transmission by the vector. To do so, we investigated a large collection of *X. nematophila* isolates with various phenotypic forms. We found that secondary forms are not phase variants but rather plain *lrp* mutants. We also found that at least a third phenotypic form exists in *X. nematophila* which is not a *lrp* mutant. All these variants have a growth advantage in stationary phase (GASP [25]) which probably explains why they reach higher loads than primary forms during late infection. We then quantified how these variants are transmitted by the nematode vector *S. carpocapsae* and found indications that isolates that reach the highest densities in insects are the least transmitted by nematodes. We therefore propose that *X. nematophila* experiences a trade-off between traits that are favored during late infection and traits that increase transmission.

**RESULTS**

Variant isolates of *X. nematophila* can be classified into three phenotypic groups. Variant isolates of *X. nematophila* are generally classified in two groups.
Compared to group 1, group 2 variants cannot adsorb dye, are not motile, do not secrete antibiotics, and have weak or no hemolytic and lipolytic activities (13). Among our 34 isolates, 14 had such characteristics (Fig. 1A and Table 1). Remarkably, these group 2 variants also had smaller cells than those of group 1 (Fig. 1A), which adds a new characteristic to their set of phenotypes.

The remaining 20 isolates were heterogeneous: they were all motile and had large cells, but 15 of these isolates always formed blue colonies on NBTA medium, while 5 did form both blue and red colonies (Fig. 1A). A clustering analysis restricted to these three quantitative phenotypes (motility, cell size, and proportion of red colonies) confirmed that four isolates formed a third distinct group of variants (isolates G3#9, G3#22, G3#48, and G3#27 [Fig. 1B]). We added isolate G3#47 to this group 3, although it clusters with group 1. Boldface numbers identify isolates that we will use most often as representative of their group.

Compared to group 1, group 2 variants cannot adsorb dye, are not motile, do not secrete antibiotics, and have weak or no hemolytic and lipolytic activities (13). Among our 34 isolates, 14 had such characteristics (Fig. 1A and Table 1). Remarkably, these group 2 variants also had smaller cells than those of group 1 (Fig. 1A), which adds a new characteristic to their set of phenotypes.

The remaining 20 isolates were heterogeneous: they were all motile and had large cells, but 15 of these isolates always formed blue colonies on NBTA medium, while 5 did form both blue and red colonies (Fig. 1A). A clustering analysis restricted to these three quantitative phenotypes (motility, cell size, and proportion of red colonies) confirmed that four isolates formed a third distinct group of variants (isolates G3#9, G3#22, G3#48, and G3#27 [Fig. 1B]). We added isolate G3#47 to this group 3, although it clusters with the first group, because it formed red colonies. Group 3 variants repeatedly combined

**TABLE 1** Average phenotypic characteristics (± standard error) of the three variant groups

<table>
<thead>
<tr>
<th>Phenotypic characteristic</th>
<th>Value for parameter (mean ± SE)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Group 1 (n = 15)</td>
</tr>
<tr>
<td>Dye adsorption</td>
<td>Yes</td>
</tr>
<tr>
<td>Motility (halo [mm])</td>
<td>24.72 ± 0.71</td>
</tr>
<tr>
<td>Cell size (FSC)</td>
<td>4.94 ± 0.02</td>
</tr>
<tr>
<td>Antibiotic activity (halo [mm])</td>
<td>17.89 ± 1.38 A</td>
</tr>
<tr>
<td>Hemolytic activity</td>
<td>1 A</td>
</tr>
<tr>
<td>Lipolytic activity</td>
<td>0.93 A</td>
</tr>
<tr>
<td><em>lrp mutation</em></td>
<td>No</td>
</tr>
</tbody>
</table>

The first three phenotypic characteristics or traits are those used in clustering analysis (Fig. 1B). For other traits, letters indicate significant differences among groups, as determined by a pairwise Wilcoxon test with Holm multiple-test correction. Dye adsorption, hemolytic and lipolytic activities are indicated here as the proportion of variants with high activity, and the significance of differences among groups is then tested by a pairwise comparison of proportions. For each group, we indicate whether or not variants carry a nonsynonymous mutation in *lrp*. G2#31 is one exception to the rule we indicate here, as it clusters with group 2 variants (Fig. 1B) but has no *lrp* mutation.
some characteristics of group 1 variants (large cells, high motility, and high level of lipolytic activity) and other characteristics of group 2 variants (low level of antibiotic activity and, most of all, red color colonies on NBTA [Table 1]).

**Spontaneous mutations in lrp produce the phenotypic difference between group 1 and group 2.** Defective lrp mutants are not motile and have reduced antibiotic and hemolytic activities (20), just like the group 2 isolates of our collection. It is therefore possible that the group 2 variants are lrp mutants. To test this hypothesis, we sequenced lrp and its promoter region for the 34 isolates of our collection. All group 1 and group 3 isolates had an lrp sequence identical to that of the F1 reference genome (26). Conversely, 13 out of the 14 group 2 isolates had one nonsynonymous mutation. Isolate G2#31 (Fig. 1A) was the sole group 2 isolate with no mutation. Interestingly, G2#31 also stands apart as the group 2 isolate with the lowest in vitro growth rate (see Additional file 3 at the above URL).

To validate that these results were not only restricted to our collection, we initiated 24 independent in vitro cultures from the group 1 variant G1#23, which we plated every day on NBTA medium. Beyond being an experimental replicate, this experiment allowed us to monitor the changes of phenotypes over time (at 1, 5, and 7 days). As expected, all clones initially formed blue colonies and were motile (Fig. 2A). After 5 days of incubation, we were able to sample bacteria forming red colonies (Fig. 2A). They did not differ from other isolates in terms of cell size, but they had significantly lower motility and antibiotic activity (by Kruskal-Wallis rank sum test, $P = 1.41 \times 10^{-4}$ and $P = 1.08 \times 10^{-5}$ for motility and antibiotic activity, respectively, using measurements that were first averaged by culture). After 7 days of incubation (Fig. 2A), bacteria forming red colonies were small nonmotile cells, while those forming blue colonies were large motile cells (Kruskal-Wallis rank sum test, $P < 2.2e-16$ for both cell size and motility averaged by culture). Over the 7 days of culture, the frequency of red variants increased from 0% to about 20%.

We then sequenced lrp in clones sampled after 8 days of incubation and found nonsynonymous mutations in 15 out of the 18 sampled red colonies. Red variants sampled at day 5 were also lrp mutants, although in a smaller proportion (8 out of 14 sequenced clones). We then averaged the measurements performed on these clones by culture and found that red variants with and without lrp mutations had similarly low antibiotic activity (Wilcoxon test, $P = 0.26$) but that red variants with no lrp mutation were more motile (Wilcoxon test, $P = 2.66e-3$ and $P = 1.65e-3$ at day 5 and day 8, respectively) and had larger cells than red variants with lrp mutations at day 8 (Wilcoxon test, $P = 1.65e-3$). They therefore match our definition of group 3 (Table 1). Furthermore, their frequency decreased from day 5 to day 8, which suggests that group 3 variants appeared earlier and were replaced by group 2 variants. This is confirmed by another replicate experiment, where we found red colonies appearing early to be significantly more motile than those appearing late (see Additional file 4 at [https://figshare.com/s/4cf02d0aa870dd20d5ab](https://figshare.com/s/4cf02d0aa870dd20d5ab)).

**lrp mutations are diverse and not reversible.** Phenotypic variants in *Xenorhabdus* were considered phase variants (15). If this theory is correct, mutations in lrp should be the product of a specific molecular mechanism (6). Overall, we identified 25 distinct nonsynonymous mutations in lrp (Fig. 2B). Of these 25 mutations, 15 most probably caused profound alterations to the translated protein: five IS5 insertions and three large duplications totally modified the lrp sequence, three indels caused a frameshift, and one indel and three SNPs caused nonsense mutations. The remaining 10 mutations are SNPs that changed a single amino acid in Lrp. The mutations we found in group 2
Group 2 variants are lrp mutants. (A to C) Cell size and motility measured on clones sampled in 24 independent static cultures of variant G1#23. Data are shown after 1, 5, and 7 days of incubation. Filled circles (blue or red) represent clones producing only one colony color, while half-filled circles represent clones producing mixtures of red and blue colonies when streaked on NBTA. (B) Summary of mutations found in the regulatory gene lrp. All the lrp mutations we found in group 2 variants were located in the coding sequence. HTH (helix-turn-helix) is the protein domain that contains the Lrp DNA-binding site, while RAM (Regulation of Amino acid Metabolism) is the coregulator response domain of Lrp. FS stands for frameshift, and asterisks indicate nonsense mutations that cause the truncation of the translated protein. For SNPs that cause a substitution, the change in amino acid is given. Tn1, Tn2, and Tn3 are three transposons. Numbers in parentheses give the number of independent replicate cultures where a mutation has been observed (one if not indicated). The mutations we found are grouped here in four categories: three mutations were tandem duplications of a 26- to 116-bp-long fraction of the lrp sequence; five mutations were insertion sequences (ISs) with Tn1, Tn2, and Tn3 being three different transposons which belong to the group of IS5 insertion sequences, and share the same two insertion points in lrp; four mutations were insertions or deletions of a few bases (indels); 13 mutations were single nucleotide polymorphism (SNPs). (C) Cell size and motility of cells sampled from prolonged culture of eight different group 2 isolates (one sense mutation, one nonsense mutation, and one frameshift in either the HTH domain or RAM coregulator response domain, and two transposon insertions). The colors of the symbols indicate the color of colonies on NBTA medium; gray crosses indicate that the color was neither blue nor red. Eight days after cultures were started, we observed cells that have recovered part of the functions typical of group 1 variants. Many of these reversions, however, are not complete: some revertants have large cells but remain nonmotile; other are motile but have small cells or are still red. (Inset) Number of cultures (out of the 12 we performed for each isolate) where blue or hemolytic colonies were observed. HTH and RAM identify isolates that have a mutation in either of the two main active domains of the Lrp protein. As in Fig. 1C, Tn1 and Tn2 are two distinct insertion sequences, FS stands for frameshift, SNP indicates sense point mutations, and the asterisks indicate nonsense mutations.
variants are therefore highly diverse, which makes them unlikely to result from a single specific mutation mechanism.

If group 2 variants were phase variants, lrp mutations should also be reversible (6). We thus tested the reversibility of group 2 isolates by monitoring prolonged static LB cultures of eight group 2 isolates with distinct lrp mutations. After 8 days of incubation, we observed cells capable of forming blue colonies for most of tested group 2 isolates (Fig. 2C). The sequencing of lrp revealed that none of these phenotypic reversions was associated with a genetic reversion of the initial mutation. Accordingly, most of these phenotypic reversions were only partial, with blue colonies being composed of either small or weakly motile cells (Fig. 2C). This confirms that the lrp mutations in group 2 isolates are not produced by a phase variation mechanism. Interestingly, the probability of phenotypic reversion differed among the isolates tested (Fig. 2C, inset, glm with binomial error, Chi2/df = 31.38, P = 5.28e−05) which suggests that the way phenotypes are restored in lrp mutants depends on the precise nature of the mutation. Finally, we never observed revertants in cultures of the group 3 variants G3#9, G3#22, and G3#48.

**Group 2 and group 3 variants are under positive selection during prolonged in vitro culture.** Variants of *X. nematophila* reach high frequency in prolonged in vitro cultures, which suggests they are under strong positive selection. To test this, we first estimated bacterial survival during stationary phase (Fig. 3A). All three variants tested had the same survival during early stationary phase (Wilcoxon test, P > 0.07), but G1#23 has a 10-fold-lower survival in late stationary phase compared to early stationary phase (Wilcoxon test, P = 5e−4), while G2#25 and G3#9 maintained high survival (Wilcoxon test, P > 0.09). Group 2 and group 3 variants therefore seem to resist better than group 1 variants to the stressful conditions of late stationary phase, explaining why group 2 and group 3 variants reach higher densities than group 1 variants in prolonged culture (see Additional file 2 at https://figshare.com/s/4cf02d0aa870dd20d5ab).
We then investigated competitive ability of the same three isolates (Fig. 3B). For this purpose, we inoculated G1#23, G2#25, and G3#9 in a LB culture of F1V1, a non-GFP-labeled group 1 variant. We then quantified the variation of frequency of green fluorescent protein (GFP)-labeled variants (competitive index [CI]): over 5 days of incubation, G1#23 decreased slightly in frequency (Wilcoxon test, \( P = 0.016 \)), while G2#25 and G3#9 both increased in frequency relative to the nonfluorescent competitor (Wilcoxon test, \( P = 4.88 \times 10^{-4} \) in both cases). G3#9 had an intermediate competitive advantage (Wilcoxon test, \( P = 1 \times 10^{-4} \)) which correlates with the previous observation that group 3 variants had intermediate phenotypes. Altogether, our results suggest that phenotypes of group 2 and group 3 variants have a growth advantage in stationary phase (GASP [25]) and are therefore under positive selection in aged cultures.

**Group 2 and group 3 variants also appear inside insects.** Akhurst, in the first description of *Xenorhabdus* variants (13), mentions that they appear *in vitro* but also in insects during infection. To test this in the case of our particular strain of *X. nematophila*, we monitored the appearance of group 2 and group 3 variants after injecting the group 1 isolate G1#23 in *Galleria mellonella*. As observed *in vitro*, red variants increased in frequency and reached 10% of the CFU on average 10 days after injection (Fig. 4A). Red colonies were initially slightly (although nonsignificantly) more motile than blue colo-
nis, as expected for group 3 variants, but became significantly less motile at both days 3 and 6, as expected for group 2 variants (Fig. 4B). Lack of difference at day 10 comes mostly from a late increase in motility in red variants (e.g., average motility is 9.73 ± 1.74 mm in red variants at day 3 and increases to 13.7 ± 3.15 mm at day 10). Finally, we found that red variants isolated from infected G. mellonella were lrp mutants when they had group 2 phenotypes, but they carried no lrp mutation when they had group 3 phenotypes.

The increase in variant frequency in infections (Fig. 4A) suggests that the conditions that favor group 2 and 3 variants in vitro may also apply inside insects. To test this, we measured bacterial densities of the 34 isolates of our collection 5 days after injection in G. mellonella larvae. We found that the density in vivo positively correlated with the density variants reached in vitro (Fig. 4C; Kendall correlation, \( \tau = 0.40, P = 0.7e−4 \)): the variants that best performed in vitro also reached high densities in insects.

**Group 2 variants are less virulent and least transmitted.** Transmission of Xenorhabdus relies in part on their capacity to kill the insect host. We found that all variants retained this capacity, although group 2 variants took slightly more time than others to kill G. mellonella (Fig. 5A and Table 2). We then calculated a proxy of bacterial transmission \( (R_0) \) for each of the 34 isolates of the collection. This quantity incorporates the parasitic and reproductive success of nematodes, the number of Xenorhabdus bacteria carried per injective juvenile (IJ) and IJ survival during dispersal; it predicts the number of new infections that can be initiated from a single infected insect (11). We found that transmissions were comparable in group 1 and group 3, while group 2 variants had a much lower transmission than the other groups (Fig. 5B, pairwise Wilcoxon test with Holm correction, \( P = 0.14 \) and \( P = 3.1e−07 \), respectively). Reduced transmission in group 2 variants was explained by lower parasitic success, reduced fecundity of nematodes, and an increase in the death rate of nematodes (Kruskal-Wallis test, \( P = 1.11e−5 \), \( P = 3.40e−5 \), and \( P = 2.85e−4 \), respectively). For a complete and detailed analysis of the components of \( R_0 \) transmission, see Additional file 5 at https://figshare.com/s/4cf02d0aa870dd20d5ab. Isolates that reached the highest in vivo (and in vitro) loads were the least transmitted (Fig. 5B, Kendall’s rank correlation, \( \tau = -0.43, P = 1.946e−4 \)), although they did reassociate with nematodes (Fig. 5C, Kendall’s rank correlation, \( \tau = 0.26, P = 0.032 \)). These isolates were not transmitted mostly because they impaired nematode reproduction (Kendall’s rank correlation between \( f \) and in vivo CFU, \( \tau = -0.39, P = 8.55e−4 \)).

As expected, switching occurred during infections: group 1 infections produced some IJs which carry red variants, while the majority of group 2 infections produced some IJs carrying blue variants (Fig. 5D). In contrast to what we observed in vitro, we found that group 3 variants did revert in the insect, with group 3 infections producing IJs that carry bacteria forming blue colonies. Overall, our data indicate that the proportion of group 2 and group 3 infections producing IJs carrying blue revertants is significantly higher than the proportion of IJs emitted from group 1 infections that carry red variants (Wilcoxon test, \( P = 1.34e−3 \)).

**DISCUSSION**

*Xenorhabdus nematophila* secondary variants are characterized by a well-known suite of phenotypic traits (inability to adsorb bromothymol blue, reduced motility, reduced antibiotic, hemolytic, lipolytic, and proteolytic activities [12–14]) to which we added in this work their smaller cell size and the fact that they better survive and reach higher densities than group 1 in prolonged culture. Earlier studies have demonstrated that group 2 variants share many of these traits with *lrp* defective mutants, and it has therefore been proposed that Lrp was controlling phenotypic variation in *X. nematophila* (20). Using a cohort of isolates, we demonstrate here that the switch to secondary forms in *Xenorhabdus* is caused by *lrp* mutations. But in contrast to what is expected in phase variation (5), these mutations were of diverse nature, and we never observed complete phenotypic reversions involving the restoration of a functional *lrp* sequence. Overall, our data therefore demonstrate that secondary variants of *X. nematophila* are
not phase variants, but instead plain \textit{lrp} mutants. The fact that we observed reversion at rates that vary among \textit{lrp} mutants suggests that reversion is achieved through a variety of compensatory mechanisms, probably involving several Lrp regulated genes that are yet to be identified.

Surprisingly, we never observed synonymous mutations in \textit{lrp}. This indicates that \textit{lrp} is not a mutational hot spot: the \textit{lrp} mutants we have found are probably part of the standing genetic diversity present at a low frequency inside the bacterial population, frequently detected in our experiment because they are under positive selection.

\textit{Lrp} belongs to a family of global regulators that are known to respond to nutrient availability and regulate cell metabolism in case of food shortage (27, 28). Previous work (18) and our \textit{in vitro} measurements (Additional file 2 at https://figshare.com/s/4cf02d0aa870dd20d5ab) demonstrate that \textit{Xenorhabdus lrp} mutants grow more slowly in rich culture medium, but we found that they survive better and reach 10-fold-higher loads than nonmutants during prolonged stationary phase. Most importantly, \textit{lrp}
mutants did outcompete group 1 variants in aged cultures, a phenotype described as growth advantage in stationary phase (GASP [25]). This interpretation is further strengthened by the fact that one of the first GASP mutants identified was an \textit{lrp} mutant of \textit{Escherichia coli} K-12 (29, 30). We therefore propose that secondary variants in \textit{X. nematophila} are under selection during late infection because they are GASP mutants.

We also documented here the existence of a third class of phenotypic variants, which do not carry \textit{lrp} mutations and share phenotypic characteristics with both group 2 variants (red colonies, reduced antibiotic activity) and group 1 variants (large and motile cells, lipolytic activity). Interestingly, such a combination of traits has been reported in some variants that Cowles et al. (20) considered secondary forms but that might in fact be similar to our group 3 variants (Table 2 in reference 20). These variants outcompete group 1 variants and thus display a GASP phenotype, although weaker than that we measured in group 2 variants. The genetic or epigenetic mechanism responsible for the emergence of this phenotype is yet to be identified.

\textit{Photorhabdus}, the sister genus of \textit{Xenorhabdus}, provides additional evidence that pathogens can produce a variety of forms during infection. \textit{Photorhabdus} produce both secondary variants and M forms, another type of variant which is the only one capable of reassociating with the nematode vector (31). However, to our knowledge, Lrp is not involved in the production of any kind of variant in \textit{Photorhabdus}. Although the two genera have very similar life cycles, \textit{Photorhabdus} therefore seems to produce variants that differ from those described for \textit{Xenorhabdus}.

We showed that \textit{Xenorhabdus} variants of group 2 and 3 better resist the conditions of \textit{in vitro} late stationary phase compared to group 1 variants. We found indications that the combination of traits that make them more competitive under these conditions is also advantageous in the insect: the variants that reach the highest densities in aged LB cultures also reach the highest loads in late infections. This explains why variants of group 2 and 3 repeatedly appear in insects. This also asks the question of their adaptive value in the natural situation where they interact with their nematode vector. In fact, \textit{lrp} mutants are poorly transmitted, which cannot be explained by a deficiency in reassociation with nematodes, as we found that IJs emitted from group 2 infections carried as many bacteria as those from group 1 infections. This observation contradicts the prediction of Cao et al. (22) but supports previous findings by Sicard et al. (19). Low transmission of group 2 comes instead from a sharp decrease in nematode reproduction, which is in agreement with earlier experimental results (20, 22) and corresponds with the well-established detrimental effect of secondary variants in mass production of \textit{S. carpocapsae} (32). We also found that IJs emitted from group 2 infections have lower survival during dispersal compared to group 1 infections, which is probably yet another indication that infections initiated with \textit{lrp} mutants constitute an unfavorable environment for \textit{S. carpocapsae}, which is consistent with the study of Cao et al. (22). These observations may be compared to those of Morran et al. (33) who have shown that strong positive selection of virulence in \textit{X. nematophila} negatively affects its transmission by \textit{S. carpocapsae}. Finally, we found that a high proportion of IJs produced from group 2 or group 3 infections carry group 1 variants. This might be because reversion occurs in insects at a higher rate than in culture or because dispersing nematodes preferentially associate with blue variants when mixed with red

<table>
<thead>
<tr>
<th>TABLE 2 Analysis of survival data*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Effect</td>
</tr>
<tr>
<td>------------------------------------</td>
</tr>
<tr>
<td>Log CFU injected</td>
</tr>
<tr>
<td>Group</td>
</tr>
<tr>
<td>Interaction</td>
</tr>
</tbody>
</table>

*Time to death has been analyzed using a Cox proportional hazard model. The model includes two random effects that account for variation among replicate experiments and variability among variants within each group. Each simple effect (log CFU injected and group) has been tested, while the other simple effect was kept in the model. Therefore, the significant effect of group cannot be explained by a difference in inoculum size among groups.
Chapuis et al. (11) have demonstrated that death rate of IJs increases with the number of *X. nematophila* cells they carry. As a result, survival of IJs during dispersal trades off against their capacity to initiate a new infection. Here, we show that variants that reach higher loads in late infections are the least transmitted by nematodes (Fig. 4C). This can be understood as yet another trade-off, distinct from that demonstrated by Chapuis et al. (11). Traits favored during infection because they permit high bacterial loads are disfavored during transmission because they decrease nematode reproduction. In *E. coli*, *lrp* mutants are thought to be better adapted to late stationary phase in part because they scavenge some of the amino acids they need, instead of producing them (29, 30). In *X. nematophila*, *lrp* also controls the production of exoenzymes which are known to support nematode reproduction (20–24), and this advantage would come at the cost of a reduction in transmission.

Here, we have investigated the diversity of phenotypic forms that appear in prolonged cultures of *X. nematophila*. We found that these forms can be classified in several distinct groups, which have in common that they have GASP phenotypes and thus increase in frequency both *in vitro* and during late infections, inside the insect host. We finally demonstrate that the variants that reach their highest loads, both *in vitro* and in insects, are those that are the least transmitted, because they negatively impact the reproduction of their nematode vectors (Fig. 6). Similar situations could probably arise in other pathogens that stay for many generations inside their host (34, 35). GASP...
mutants, which can impact transmission, may therefore influence the evolution of pathogens that form long-lasting infections.

MATERIALS AND METHODS

X. nematophila isolates. Xenorhabdus nematophila isolates were obtained from static cultures of the green fluorescent protein (GFP)-labeled strain F1D3 (19). Samples of 10 independent LB cultures of strain F1D3 were streaked onto NBTA plates (13) after 3, 7, and 13 days of incubation at 28°C. Primary forms formed colonies on NBTA, while secondary variants form red colonies (12, 14, 15). Each time a red colony was observed, a blue colony from the same petri dish was also sampled. Overall, we obtained 34 distinct isolates (see Additional file 1 at https://figshare.com/s/4cf02d0a870dd20d5ab) which we stored in 20% glycerol at –80°C.

Irp sequencing. X. nematophila colonies were lysed in sterile Milli-Q water after several freezing-thawing cycles. The Irp gene was amplified using the high-performance GoTaq G2 DNA polymerase (Promega, France) with primers Irp-L (5'-CATATTGGGTTAGG-ATG-3') and Irp-R (5'-GGACTGACATAGCAAGAATAC-3'). PCR products were sequenced by GenoScreen, France, and mutations were determined by comparing aligned Irp sequences to that of the X. nematophila F1 reference genome (26).

Measuring colony phenotypes. For each isolate, we measured four phenotypic traits that differ among Xenorhabdus variants. Swimming motility was measured as the diameter of a halo formed by motile bacteria on 0.35% agar culture medium (14, 15). Antibiotic activity was quantified by measuring the diameter of inhibition halos, using Micrococcus luteus as a target strain (36). Extracellular lipolytic activity was assessed by the presence of precipitated material surrounding the colony cultured on Tween 20 agar (36). Hemolytic activity was quantified by the presence of a clearing surrounding bacteria grown on standard sheep blood agar plates (37).

Measuring cell size. Cell size was first estimated by flow cytometry analysis in three replicate in vitro experiments. In each experiment, exponential-phase cultures of each isolate were fixed with a 0.2% solution (vol/vol) of formaldehyde and analyzed with a FACSCalibur flow cytometer (Becton Dickinson), equipped with an argon air-cooled laser providing 15 mW at 488 nm and the standard filter set-up. Bacterial cells were discriminated from particles by applying a polygonal gate to green (530 ± 15 nm) and red (585 ± 21 nm) log-transformed fluorescence measurements and a rectangular gate on log-transformed side scatter (SSC) and forward scatter (FSC), using tools provided in R Bioconductor (38). We used log-transformed FSC as a proxy for cell size.

In other experiments, when cytometry was not applicable, we sampled colonies, put them on cover slides, and took pictures with an Olympus BX51 microscope with 400× magnification. Images were analyzed using ImageJ (39), and the size of a cell was approximated by the maximum Feret diameter of the cell contour. We measured a minimum of 10 cells per sample and used the average Feret diameter (in microns) as a cell size estimate.

Measuring bacterial density and survival. In vitro bacterial density during stationary phase was measured on agitated LB cultures incubated at 28°C for 91 h. Five replicate experiments were performed, and appropriate dilutions were streaked on NBTA plates with 50 μg kanamycin per ml to estimate density. In vivo bacterial density was estimated by injecting approximately 2000 cells (i.e., 20 μl of cultures diluted to 1:1000) in the last instar larvae of the lepidopteran Galleria mellonella as previously described (19). Insect cadavers were homogenized in 100 μl LB after 5 days of incubation at 28°C, and appropriate dilutions were streaked on NBTA to estimate density.

We estimated bacterial survival on three isolates (G1#23, G2#25, and G3#9) for which we ran 12 independent agitated LB cultures at 28°C. Samples were taken from each culture in late exponential phase, early stationary phase, and late stationary phase. For each sample, we estimated the total number of cells using a Thoma cell counting chamber and the number of cultivable cells by plating appropriate dilutions of samples on NBTA plates and counting the number of CFU. We then used the proportion of cultivable cells as a proxy for the proportion of viable cells and studied how it varied from exponential phase to early or late stationary phase.

Measuring competitive ability. We measured competitive ability of three fluorescent isolates (G1#23, G2#25, and G3#9) by letting them compete in LB cultures with a nonfluorescent primary variant (F1V1). Twelve independent late-stationary-phase cultures of each of the four isolates were used to inoculate these cultures. Before inoculation, cultures of group 2 and 3 variants were 10-fold diluted so that all groups of variants have similar densities. The two competing variants (125 μl each) were then mixed, incubated for 120 h at 28°C, and plated on NBTA. Pictures of these plates were taken using an Olympus Axiozoom (k7) under fluorescent light (535 nm), so that fluorescent and nonfluorescent colonies could be distinguished. The densities of GFP and non-GFP cells were estimated at the onset of the experiment and after 5 days of incubation. From these estimates, we could compute a competitive index (CI) as the rate of increase in frequency of GFP bacteria over 5 days of incubation.

Measuring virulence toward insects. We measured virulence as the time to kill larvae of G. mellonella. This was done for five representative isolates of each group (isolates G1#21, G1#23, G1#42, G1#44, and G1#51 for group 1, isolates G2#25, G2#29, G2#36, G2#39, and G2#40 for group 2, and all members of group 3) and for three injected doses (corresponding to 20 μl of a 1:1,000, 1:100, or 1:10 diluted culture). We conducted two replicate experiments and injected each dose four times. Appropriate dilutions of each injected culture were plated on NBTA to estimate the injected dose. We used the analogous method described by Parmelee et al. (40) to measure time of insect death, and we analyzed data with a Cox proportional hazard model, with variation among replicate experiments and variation among isolates within each group considered a Gaussian random effect. This analysis has been performed using the coxme library (41).
Measuring transmission by *Steinernema carpocapsae*. We associated each of the 34 isolates with the nematode vector *Steinernema carpocapsae* by first infecting G. mellonella with a symbiotic (i.e., deprived of Xenorhabdus) nematodes obtained from *S. carpocapsae* strain SK27 and kept alive for a few months at 8°C in Ringer solution. After 24 h of incubation at 24°C in tubes containing 20 nematodes, insects were injected with the isolates. Insect cadavers were subsequently placed in White traps and incubated at 24°C until new nematode injective juveniles (IJs) dispersed (42). In this experiment, two or three independent cultures of each isolate were performed so that a total of 96 independent inocula were tested against three lots of insects, for a total of 288 tests. Inocula of group 1 isolates were less diluted than others (i.e., 1:100 instead of 1:1,000) so that comparable numbers of bacterial cells were injected for all isolates. We injected 10^{2.45} ± 0.57 cells, as estimated by plating a fraction of the inocula.

For each isolate, we measured the proportion \( \beta \) of infections that yielded new IJs. When all IJs had emerged from insect cadavers, we suspended them in a fixed volume of Ringer solution and counted the number of living IJs in a 20-\( \mu \)l aliquot of each suspension. We then estimated the mortality rate \( r \) of newly emerged IJs by placing four groups of five IJs in Ringer solution, incubating them at 28°C in the dark for 17 weeks, and counting surviving IJs (43). We also quantified the number of bacteria \( r \) carried per IJ by grinding 20 nematodes for each emergence. IJs had previously been cleansed for 10 min in 0.4% bleach and rinsed several times in sterile Ringer solution. They were then placed for 10 min in TissueLyser II (Qiagen) at 30 Hz with three 3-mm glass beads in order to liberate bacterial symbionts. Portions (100 \( \mu \)l) of this suspension were then spread on NBTA plates with kanamycin, and CFU were counted. Finally, following Chapuis et al. (11), we combined these four traits in a single measurement of bacterial transmission, with

\[
R_0 = \beta \left[ 1 - \exp(-r) \right] / \nu
\]

The parasitic success \( \beta \) is measured once for each isolate. Conversely, \( f, \nu, \) and \( r \) are measured for each emergence of a given isolate. In order to obtain an \( R_0 \) estimate for each isolate, we first averaged \( f[1 - \exp(-r)] / \nu \) over the replicate emergences of this isolate and multiplied this average by \( \beta \). We present in the Results section analysis performed with nonparametric rank tests for \( \beta, f, \nu, \) and \( R_0 \). A more-detailed analysis of all components of \( R_0 \) is provided in Additional file 5 at https://figshare.com/s/4cf02d0aa870dd205Sab.

Variant emergence and reversion in *vitro* and *in vivo*. We studied the emergence of variants in 24 independent static in vitro LB cultures of isolate G1#23 incubated at 28°C. Samples from each culture were streaked on NBTA plates on days 1, 5, and 7. Five red colonies (when possible) and an equivalent number of blue colonies were then taken from each sample, and their cell size and motility (see above) were measured. On some of these colonies, we also measured antibiotic and hemolytic activities (see above). Following this procedure, we could detect group 2 and group 3 variants rapidly after they emerged. A similar procedure was followed to study reversion to the primary form, where we looked for isolates forming blue colonies in prolonged static cultures of group 2 and group 3 variants. We also monitored the emergence of variants after injection of G1#23 in G. mellonella. Twenty insects were homogenized after 1, 2, 3, 6, or 10 days of incubation at 28°C. As for in *vitro* emergence, red and blue colonies were sampled from NBTA plates, and their motility was quantified as described above with two replicate measurements for each colony. In all these experiments, measurements performed on red and blue clones were first averaged by culture before being compared using nonparametric tests.

Availability of data and materials. The supplemental files for this article (Additional files 1 to 6) can be found at FigShare (https://figshare.com/s/4cf02d0aa870dd205Sab). The data sets supporting the conclusions of this article are included within Additional file 6.

ACKNOWLEDGMENTS

This work was supported by the French Laboratory of Excellence project “TULIP” (ANR-10-LABX-41 and ANR-11-IDEX-0002-02). We are very much indebted to Frank Gilbert, who helped in running spectrophotometry analyses. We thank Rémi Peyraud for discussions about the evolution of major regulators in pathogens. We also thank David Duneau for his help in clarifying an earlier version of this manuscript and for his insight on our work.

J.-B.F. and A.G. designed the research. S.P. collected the initial collection of variants. N.P. and J.-B.F. performed the experimental evolution experiments. N.P. performed PCR and analyzed sequences. M.C.C. performed virulence and transmission experiments. A.G. and A.L. designed and performed the *lp* complementation experiments. M.C.C. and J.-B.F. performed data analyses. All authors read and approved the final version of the article.

REFERENCES


