Comparative Analysis of Acinetobacters: Three Genomes for Three Lifestyles

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Abstract

Acinetobacter baumannii is the source of numerous nosocomial infections in humans and therefore deserves close attention as multidrug or even pandrug resistant strains are increasingly being identified worldwide. Here we report the comparison of two newly sequenced genomes of A. baumannii. The human isolate A. baumannii AYE is multidrug resistant whereas strain SDF, which was isolated from body lice, is antibiotic susceptible. As reference for comparison in this analysis, the genome of the soil-living bacterium A. baylyi strain ADP1 was used. The most interesting dissimilarities we observed were that i) whereas strain AYE and A. baylyi genomes harbored very few Insertion Sequence elements which could promote expression of downstream genes, strain SDF sequence contains several hundred of them that have played a crucial role in its genome reduction (gene disruptions and simple DNA loss); ii) strain SDF has low catabolic capacities compared to strain AYE. Interestingly, the latter has even higher catabolic capacities than A. baylyi which has already been reported as a very nutritionally versatile organism. This metabolic performance could explain the persistence of A. baumannii nosocomial strains in environments where nutrients are scarce; iii) several processes known to play a key role during host infection (biofilm formation, iron uptake, quorum sensing, virulence factors) were either different or absent, the best example of which is iron uptake. Indeed, strain AYE and A. baylyi use siderophore-based systems to scavenge iron from the environment whereas strain SDF uses an alternate system similar to the Haem Acquisition System (HAS). Taken together, all these observations suggest that the genome contents of the 3 Acinetobacters compared are partly shaped by life in distinct ecological niches: human (and more largely hospital environment), louse, soil.

Introduction

Although low-grade pathogens in humans, human-adapted Acinetobacter species mainly belong to the A. baumannii-A. calcoaceticus complex are of growing interest due to increased incidence of multidrug resistance (MDR) [1]. A. baumannii strains are isolated in up to 1% of nosocomial infections mostly from immunocompromised patients hospitalized in intensive care units. Although A. baumannii isolates are commonly found in clinical environment, Acinetobacters are mostly free-living saprophytes ubiquitously found in nature (soil, water, sewage). Acinetobacter species have been also identified in small-size living organisms (body lice, fleas and ticks) that are potential vectors for infection transmission [2].

The genus Acinetobacter consists of strictly aerobic, Gram-negative coccobacillary rods, non-motile, catalase positive, oxidase negative and growing at 20°C–30°C on usual laboratory culture media. g-proteobacteria classified as members of the genus Acinetobacter have a long history of taxonomic changes moving from the family Neisseriaceae to the family Moraxellaceae. Various methods (DNA-DNA hybridization [3], biotyping [4], Amplified Ribosomal DNA Restriction Analysis [5], AFLP [6]) now make it possible to distinguish 32 different species within the genus Acinetobacter, 17 of which have officially been given names. Nevertheless, unambiguous species identification may be difficult in particular for some genetically closely related species. Standard tests indeed fail to distinguish A. baumannii, A. calcoaceticus and the unnamed genomic species 3 and 13TU (the A. calcoaceticus-A. baumannii complex [7]).

Natural competence as well high metabolic capacities have been reported in several Acinetobacter species making those species very attractive for environmental and biotechnological use [8]. For example, Acinetobacter baylyi ADP1 is highly competent and may grow on a large variety of compounds [9].

Two Acinetobacter baumannii strains (AYE and SDF) were initially sequenced in a clinical/medical context. Since the primary goal of the project was to identify the complete repertoire of genes involved in resistance to various antibiotics [10], much of our effort was concentrated on a resistance island of ca. 86-kb long which has been uncovered in the genome of the multi-drug resistant human clinical isolate strain AYE responsible for a
nationwide outbreak in France in 2001. In contrast, this resistance island was not present in *A. baumannii* strain SDF associated with human body louse, partly explaining its susceptibility to antibiotics.

A few years ago, we published the complete genome of another Acinetobacter (*A. baileyi* ADP1 [9]) for which human experts have performed the annotation process. This complete annotation set therefore appeared to be a strong basis for fast and accurate annotation of the two *A. baumannii* strains.

The availability of three complete genome sequences from members of the same genus (i.e., AYE, SDF and *A. baileyi* ADP1 hereafter referred as *A. baileyi*prompted us to compare them in a more general context. Here we provide a detailed comparison of the three genomes that highlights differences that might reflect adaptation to a specific environment. The in-depth analysis of gene contents reveals that though the three organisms share a large fraction of genes, large differences exist. For instance, we show that strain AYE has high catabolic and drug/metal resistance capacities whereas strain SDF is riddled with numerous prophage regions and Insertion Sequences (ISs). Moreover, the example of iron uptake illustrates the diverse strategies used by *Acinetobacter* to thrive in various environmental conditions. These features emphasize the diversity of the *Acinetobacter* genus. We conclude this report with an analysis of potential virulence factors.

**Results and Discussion**

**Three Acinetobacter genomes: general features and taxonomic considerations**

The genome of the *A. baumannii* isolates is made of a single chromosome and several plasmids (4 and 3 for AYE and SDF, respectively). In *A. baileyi*, no plasmid was detected [9]. Strain AYE has the largest chromosome (ca. 3.9 Mb versus 3.4 Mb for strain SDF and 3.6 Mb for *A. baileyi*, Table 1). The GC-content of the three sequences is around 40%, a value corresponding to that reported for other members of the *Acinetobacter* genus.

Although tRNAs for each of the 20 amino acids were found in both *A. baumannii* strains AYE and SDF, the latter has a lower copy number of tRNAs for eight amino acids namely Ala, Arg, Asp, Glu, Ile, Ser, Tyr and Val. The largest differences were found for tRNA-Asp (a single copy instead of three) and for tRNA-Glu (2 copies instead of 4 in AYE and 5 in *A. baileyi*). Dolzani and colleagues [11] showed that the number of rRNA operons may vary between 5 and 7 for the *Acinetobacter* species. Confirming these data, strain AYE possessed 6 rRNA clusters whereas strain SDF contained only 5. Like in the case of tRNAs, the missing rRNA cluster may have been lost during one of the numerous recombination events probably mediated by Insertion Sequences (ISs; see below). As reported in the literature, the 16S–23S Intergenic Spacer Region (16S–23S ISR) of *A. baileyi* strain ADP1 rRNA clusters is of variable length and probably resulted from recombination between rRNA operons [12]. This does not seem to be a feature shared by species belonging to the *Acinetobacter* genus since rRNA clusters 16S–23S ISRs in both *A. baumannii* strains are of constant length (663 bp). Strain SDF’s species status was uncertain because this strain has no β-lactamase activity and is resistant to AmpC. Strain SDF’s species status therefore appeared to be a strong basis for fast and accurate annotation of the two *A. baumannii* strains.

For the three species under study, genes were assigned to three or that do not have any significant homolog in any of the two other species (Figure 1). The candidate core genome contains 2,327 genes corresponding to 57.2%, 70.7% and 62.6% of the DNA sequences of *A. baumannii* strain AYE, strain SDF and *A. baileyi*, respectively. The sizes of the flexible gene pools may be correlated with different life styles in distinct ecological niches. Even though 361 genes are shared only by AYE and *A. baileyi*, each species possesses almost 800 specific genes. These figures may reveal a high capacity of adaptation in fluctuating environmental conditions. Consistent with life in a less variable environment (hematophage gut), the amount of specific genes in SDF is significantly lower (*n* = 398; see Figure 1).

For the three species under study, genes were assigned to various functional categories (Figure 2). At first sight, some of the categories display peculiar patterns. Considering *A. baumannii* AYE, 42% of the genes dedicated to catabolic functions and two third of genes involved in drug/metal resistance are specific. In turn in strain SDF, 80% of prophagic genes and all ISs are specific to this organism. The specificity of strain SDF mainly resides in its extrachromosomal elements content whereas strain AYE has pronounced capacities in catabolism and drug/metal resistance.
which may explain its successful adaptation to the hospital environment (see below).

IS elements in the three strains were strikingly different (Table 1). Strain SDF has by far the largest number of IS elements made of two novel elements (IS\textsubscript{Aba6} and IS\textsubscript{Aba7}) in about equal proportions and evenly distributed along the chromosome (Figure 3). Those elements belong to IS\textsubscript{992} and IS\textsubscript{3} families, respectively. It is very likely that these IS elements have significantly contributed to the genome size reduction, especially via recombination events and gene disruptions. Twenty-one copies of IS\textsubscript{Ab1} (IS\textsubscript{4} family) were detected in the genome of the human strain \textit{A. baumannii} AYE. The IS element IS\textsubscript{Ab1} has been recently identified from human isolates of \textit{A. baumannii} [13]. Although its role is unclear, it has been demonstrated to contribute at least to overexpression of the naturally-occurring \textit{\beta}-lactamase \textit{ampC} gene leading to high-level resistance to \textit{\beta}-lactams and to overexpression of acquired \textit{\beta}-lactamases genes [13]. Whereas no IS\textsubscript{Ab1} copy was identified on any of the plasmids of isolate AYE, chromosomal copies showed no site integration preference (Figure 3). It is important to note that although IS\textsubscript{Ab1} is supposed to be “customized” for \textit{A. baumannii} [14], this element is not present in strain SDF genome.

DNA acquisition/exchanges in bacteria can occur between organisms of the same or different species via one of three mechanisms: conjugal transfer, phage transduction, or natural transformation. The last mechanism relies on the ability of cells to take up and stably maintain large pieces of “alien” DNA. This phenomenon called “natural competence” has been extensively studied in two Gram-negative soil living bacteria, namely \textit{A. baylyi} and \textit{Pseudomonas stutzeri} [see for instance 15]. Besides their involvement in biofilm formation (see below), some components related to type IV pili biogenesis play an important role in natural transformation process [16]. This is consistent with the fact that free extracellular DNA itself may trigger biofilm formation [17]. Almost all genes previously identified in the two models (\textit{com} and \textit{pil} genes) have been found in \textit{A. baumannii} strain AYE whereas their counterparts are either absent or disrupted in strain SDF, suggesting that the latter strain is not competent for natural transformation (Table 2). Several putative prophage regions were roughly delimited in both \textit{A. baumannii} genomes (six for AYE and eight for SDF; Table 2). Though not exceptional, these regions constitute a sizable part of both genomes accounting for 5.1% and 6.7% of whole chromosomes of strain AYE and SDF, respectively. Notably, all prophage regions detected were not similar (within and between genomes; Table 2) as suggested by very low similarities between well-known phage markers and by the obvious absence of synteny between the three genomes. Even though plasmids can be gained via natural transformation, a more specific process of plasmid acquisition is conjugative transfer. In contrast to \textit{A. baylyi}, strains AYE and SDF possess several plasmids (4 and 3 respectively) on which no gene involved in resistance and/or virulence has been characterized. Nevertheless, putative mobilization systems Mob\textsubscript{S}/Mob\textsubscript{L} for DNA exchange and putative toxin/antitoxin systems for plasmid maintenance are present.

Cell-cell signaling and related processes: biofilm formation and quorum sensing

In a hospital environment, \textit{Acinetobacter} strains may survive several days under severely dry conditions [18]. Vidal and colleagues [19] reported the ability of the nosocomial pathogen \textit{A. baumannii} biotype 9 ACAB715 to form a biofilm on a glass surface, suggesting that this phenomenon plays a key role for the survival of this bacterium under unfavorable environmental conditions. Since biofilm formation may be associated with resistance to immune host response, many clinically significant bacterial species have been studied for their capacity to form biofilm [20]. The different appendages that have been proved to be involved in biofilm formation are type IV pili, flagella, curli and fimbrins. In \textit{A. baumannii} strain AYE, four putative chaperone usher secretion (\textit{csu}) systems have been identified (Table 2). The first system (ABAYE1319-24) has an organization similar to the locus described by Tomaras and colleagues [21] in \textit{A. baumannii}.
strain ATCC19606 including the Fur box also detected upstream the gene cluster. Furthermore, three putative surface adhesion protein regions have been detected only in strain AYE (Table 2). Apart from the two csu systems previously identified in *A. baylyi* [22], the present comparative genomic analysis led to the conclusion that the cluster ACIAD3332-37 might be a third system. Diverse regulation networks such as Crc (Catabolite repression pathway) [23] or two-component systems [24] regulate biofilm formation. Further experiments are therefore required to unravel the respective roles of ABAYE0143 (Crc), ABAYE0258-0259 (EnvZ/OmpR) and the regions ABAYE0667-0671/ABAYE3534-3535 (type IV pili biogenesis regulators/twitching motility) in biofilm production by *A. baumannii* strain AYE.

In many Gram-negative bacteria, quorum sensing (QS) relies on small diffusible molecules, the N-acylhomoserine lactones (AHL). In response to population density, AHL-mediated QS systems modulate expression of genes involved in various biological functions including biofilm formation [25], antibiotics production [26] or Ti plasmid conjugal transfer [27]. AHLs are also known to alter gene expression in host cells [28]. A genomic region (ABAYE3750-ABAYE3761) of strain AYE contains an AHL synthase (ABAYE3761) neighboring a LuxR family transcriptional regulator autoinducer (ABAYE3758). Interestingly, this region has been disrupted by an IS*Aba7 copy in strain SDF and completely lacks in *A. baylyi*. Although strain AYE certainly uses QS modulation, further experiments are required to determine in which broader biological process this system takes part. Nevertheless, additional genes found in the QS genomic region provide some clues. They correspond to genes encoding a Non Ribosomal Peptide Synthase (NRPS) coupled with an efflux pump. NRPS systems are known to produce a large family of natural products like toxins, siderophores, antibiotics or pigments.

Degradation of AHLs may be of medical relevance since AHL-mediated QS systems *i*) are widespread and highly conserved in many pathogenic bacteria and *ii*) control the expression of genes involved in pathogenicity *sensu lato*. For instance, Whitehead and colleagues [29] hypothesized that the disruption of AHL-mediated QS systems could possibly help to control diseases. Although the ultimate goal is not clear (competition with other species, neutralization of antibiotics produced by other species...), some bacterial species are able to disrupt a QS signal by the mean of a natural AHL lactonase (see for example [30]). Since other
| Label | Acinetobacter baylyi ADP1 | Acinetobacter baumannii AYE | Acinetobacter baumannii SDF |
|-------|--------------------------|-----------------------------|-----------------------------|
| ACU   | ACIAD0387-ACIAD0390, 4.95 kb - | - | - |
| CSU   | - | ABAYE1319-ABAYE1324, 6.03 kb - | - |
| CSU1-A | ACIAD0119-ACIAD0124, 7.26 kb - | - | - |
| CSU1-R | - | ABAYE1470-ABAYE1473, 4.79 kb - | - |
| CSU2-A | ACIAD3332-ACIAD3337, 7.03 kb - | - | - |
| CSU2-R | - | ABAYE1856-ABAYE1860, 6.07 kb - | - |
| CSU3' | - | ABAYE2132-ABAYE2138, 6.24 kb, pseudo | - |
| PS-A | ACIAD0057-ACIAD0105, 47.43 kb - | - | - |
| PS-R | - | ABAYE3795-ABAYE3824, 34.31 kb - | - |
| PS-S | - | - | ABSDF0059-ABSDF0083, 29.28 kb |
| SAH1-R | - | ABAYE0792-ABAYE0794, 28.13 kb - | - |
| SAH2-R | - | ABAYE0821-ABAYE0821, 10.11 kb - | - |
| SAH3-R | - | ABAYE1394-ABAYE1397, 5.98 kb - | - |
| COB | - | ABAYE1990-ABAYE1995, 5.35 kb | ABSDF1877-ABSDF1884, 4.71 kb, pseudo |
| CYA | ACIAD1276-ACIAD1282, 9.08 kb - | - | - |
| LIP | ACIAD0566-ACIAD0586, 17.72 kb - | - | - |
| ACO | ACIAD1014-ACIAD1022, 9.62 kb | ABAYE1943-ABAYE1950, 9.49 kb | ABSDF1932-ABSDF1934, 2.48 kb, pseudo |
| ALN | ACIAD1614-ACIAD1622, 76.66 kb - | - | - |
| MSU | ACIAD3470-ACIAD3472, 2.37 kb | ABAYE0181-ABAYE0183, 2.40 kb | ABSDF3432-ABSDF3435, 3.27 kb |
| SSU | ACIAD0034-ACIAD0038, 4.88 kb | ABAYE3840-ABAYE3844, 4.83 kb | ABSDF0033-ABSDF0038, 5.84 kb |
| ANT | ACIAD2669-ACIAD2672, 4.58 kb | ABAYE1896-ABAYE1900, 4.46 kb | ABSDF1968-ABSDF1971, 3.85 kb, pseudo |
| ARE | ACIAD1428-ACIAD1431, 5.71 kb - | - | - |
| BEN | ACIAD1433-ACIAD1440, 8.96 kb | ABAYE2553-ABAYE2561, 9.40 kb | ABSDF1496-ABSDF1498, 2.90 kb, pseudo |
| BET | ACIAD1008-ACIAD1012, 7.90 kb | ABAYE2864-ABAYE2868, 7.92 kb | ABSDF2436-ABSDF2440, 7.91 kb |
| CAT | ACIAD1442-ACIAD1451, 9.76 kb | ABAYE1714-ABAYE1721, 7.50 kb | ABSDF1993-ABSDF2000, 7.02 kb |
| HCA | ACIAD1720-ACIAD1728, 11.06 kb | ABAYE2626-ABAYE2635, 11.66 kb | ABSDF1411-ABSDF1412, 2.02 kb, pseudo |
| CBE | - | ABAYE1061-ABAYE1069, 12.07 kb - | - |
| DSZ | ACIAD1503-ACIAD1512, 11.11 kb - | - | - |
| DCA | ACIAD1684-ACIAD1697, 14.71 kb | ABAYE2299-ABAYE2315, 17.94 kb | - |
| EUT | - | ABAYE1457-ABAYE1456, 5.40 kb | - |
| MDC | ACIAD1753-ACIAD1762, 8.26 kb | ABAYE2224-ABAYE2233, 8.31 kb | - |
| NAS | ACIAD1908-ACIAD1914, 10.47 kb | ABAYE1541-ABAYE1546, 9.32 kb | ABSDF1522-ABSDF1524, 5.89 kb, pseudo |
| NAL | ACIAD1565-ACIAD1581, 16.81 kb - | - | - |
| POB | ACIAD1717-ACIAD1719, 3.51 kb | ABAYE2324-ABAYE2325, 2.17 kb | - |
| PEN | - | ABAYE1696-ABAYE1713, 20.60 kb | - |
| PSG | - | ABAYE1722-ABAYE1786, 63.24 kb | - |
| PAA | - | ABAYE2363-ABAYE2376, 13.74 kb | - |
| PHN | - | ABAYE2317-ABAYE2323, 8.09 kb | - |
| PCA | ACIAD1702-ACIAD1712, 9.06 kb | ABAYE1673-ABAYE1690, 18.01 kb | ABSDF2016-ABSDF2024, 7.92 kb |
| QUI | ACIAD1713-ACIAD1716, 6.30 kb | ABAYE1682-ABAYE1685, 6.20 kb | ABSDF2011-ABSDF2014, 5.81 kb, pseudo |
| SAL | ACIAD1424-ACIAD1427, 4.24 kb | - | - |
| SOX | ACIAD2549-ACIAD2552, 5.17 kb | - | - |
| SEU | - | ABAYE2377-ABAYE2390, 16.05 kb | - |
| ATS | ACIAD1586-ACIAD1601, 20.04 kb | - | - |
| TAU | - | ABAYE2209-ABAYE2212, 3.60 kb | - |
| C41T-R | - | ABAYE2267-ABAYE2295, 30.43 kb | - |
| CA2-R | - | ABAYE2418-ABAYE2437, 19.77 kb | - |
| URE | ACIAD1088-ACIAD1096, 6.34 kb | ABAYE2772-ABAYE2779, 5.76 kb | ABSDF2369-ABSDF2378, 7.20 kb |
| VAN | ACIAD0978-ACIAD0988, 10.52 kb | ABAYE2621-ABAYE2625, 5.91 kb | - |
| ComA | ACIAD2639-ACIAD2639, 2.38 kb | ABAYE0884-ABAYE0884, 2.43 kb | ABSDF0886-ABSDF0887, 1.89 kb, pseudo |
Acinetobacter strains produce AHLase [31], genes coding for similar proteins were searched for. This analysis was difficult since i) the similarity between known AHLases is low (ca. 25% identity); ii) a part of the motif that characterizes AHLase (HXHXDH) is shared by several unrelated families of proteins (metallo-b-lactamase, glyoxalase II and arylsulfatase). Nevertheless, we were able to find a candidate in those three species (ABAYE0825, ABSDF0820 and ACIAD0766; Figure S2).

Metabolism: different gene content for different lifestyles

Extensive metabolic pathway reconstruction was undertaken for the three Acinetobacter strains. As reported in A. baylyi str. ADP1 [9], the central metabolism study of both A. baumannii strains confirms the lack of several key enzymes: a glucokinase, proteins of a phosphotransferase transport system, a 6-phosphofructokinase and a pyruvate kinase. The latter activity which exists in Pseudomonas spp. seems to be a good marker to clearly delineate both genera. Few Acinetobacter isolates are able to grow on glucose as sole carbon source and this property was early used as a main criterion to classify Acinetobacter species [32]. The Embden–Meyerhof–Parnas glycolysis can certainly not be performed in Acinetobacter spp. given the lack of the previously mentioned enzymes. An alternative glycolytic route passing through the Entner–Doudoroff pathway was elucidated several decades ago [33]. It starts with glucose periplasmic oxidation and leads to pyruvate formation. All the genes required for this pathway were identified in the three Acinetobacter genomes. Interestingly, A. baylyi and A. baumannii strain SDF only possess the gcd gene which encodes a membrane-bound quinoprotein glucose dehydrogenase [34] whereas strain AYE has two additional genes (ABAYE1605, ABAYE1751) which encode soluble forms of quinoprotein dehydrogenases (s-GDH) [35] thus possibly allowing the utilization of alternative substrates by the cells.

The three studied strains are prototrophic and are able to grow using succinate as sole carbon source.
that soil is also the primary niche of AYE, all these genes are also present supporting the hypothesis of polymer which is produced by plants in response to stress. In strain dicarboxylic acids and aromatic compounds [39]. Interestingly, van genes are gathered and may improve ferulic acid activity is detected, leading to the production of histamine.

Likewise, A. baylyi str. AYE may chelate iron using a siderophore A. baumannii str. AYE harbors nine new gene clusters that are absent in A. baylyi (Table 2). Three of them, called CAI1-R, SEU and CAI2-R, form large-size genomic islands of 30.4-kb, 16-kb and 19.8-kb respectively. These regions contain a high proportion of genes encoding enzymes like oxygenases and need to be deeply investigated in order to determine their exact catabolic role. Other AYE specific regions have been assigned a more precise function.

The TAU cluster of strain AYE contains genes encoding a taurine transporter and the dioxygenase TauD. Like Escherichia coli K12 [43], strain AYE could utilize taurine as a sulfur source when facing sulfite starvation conditions. Taurine plays several important roles in mammals: neuromodulation, bile acid conjugation, detoxification, osmoregulation, membrane stabilization, and regulation of intracellular Ca²⁺ homeostasis [44]. Competition for taurine use might take place during A. baumannii infection process.

Finally, the PEN genomic region of strain AYE chromosome contains fifteen genes which are likely to be involved in penicillin catabolism providing carbon and nitrogen to the bacteria. One of them (ABAYE1713) encodes a putative penicillin acylase (Pac). The substrate specificity of this acylase is still unknown in strain AYE. As reported in E. coli str. W [45], the pac gene is positively regulated by the PaaX repressor of phenylacetate catabolism. Pac could be a scavenger enzyme for natural compounds containing a phenylacetate residue or derivative [46].

Iron uptake systems: toward a high degree of specialization

One possible defense mechanism of human host against bacterial infection is the reduction of free extracellular iron concentration via iron-binding proteins (lactoferrin, transferrin). Indeed, normal concentration of free iron in the body oscillates around 10⁻¹⁰ M, whereas the minimal concentration required for the bacterial survival is ca. 10⁻⁶ M [47]. Iron/heme acquisition can be achieved thanks to direct contact between the bacterium and the exogenous iron/heme sources. Bacteria may also take out iron from their environment using high affinity iron molecules called siderophores/hemophores that are released outside cells.

A. baumannii strain AYE may chelate iron using a siderophore (ABAYE1085-ABAYE1104) that can compete with host iron-binding proteins to overcome the iron starvation imposed by the host. The same siderophore (acinetobactin) has been described in A. baumannii strain ATCC19606; [48], which was structurally related to the anguibactin of the fish pathogen Vibrio anguillarum [49]. One of the key compounds of these siderophores is the histamine which results from histidine decarboxylation. Tolmacky and colleagues [50] showed that when V. anguillarum cells are cultured on 1% histidine, a histidine decarboxylase activity is detected, leading to the production of histamine. Likewise, A. baumannii strain ATCC19606 produces histamine when grown with histidine [51]. As expected, we found a histidine decarboxylase gene (hdc) located within the iron uptake region in strain AYE (ABAYE1096). Interestingly, A. baylyi genome has a
siderophore gene which composition is not based on histamine because this species lacks the hde gene [9].

The transport of the ferri-siderophore (iron-siderophore complex) into the cell is performed by the Iron Regulated Outer Membrane Proteins system (IROMPs). This IROMPs system is typically made of one specific outer-membrane receptor, one periplasmic protein and several inner-membrane-associated proteins acting either as receptors or as energy transducers (i.e., the ExbB/ExbD/TonB complex). The strain AYE potentially possesses two similar uptake systems (ABAYE2046-2051 and ABAYE3318-3320). Once internalised, the ferri-siderophore is reduced to release iron by an enzyme having a ferric reductase activity. We did not identify any structurally related protein. However, Fontecave et al. [52], have reported that several enzymes (nitrite reductase, sulfite reductase...) which are not necessarily tightly linked to iron metabolism could present a ferric reductase activity. Thus, a possible candidate is the gene tandem ABAYE1544-ABAYE1545 which encodes the two subunits (large and small) of the nitrite reductase.

Surprisingly, siderophores were not identified in strain SDF. Since iron is necessarily required for life, strain SDF must use a different strategy to scavenge iron from its environment. Several evidences suggest that A. baumannii strain SDF is able to use haem or haemoglobin as source of iron. A. baumannii SDF is in close contact with the gut of haematophage organisms [53] and therefore is readily in contact with blood cells. In addition, we found in the genome of this strain several haemagglutinin/haemolysin-related genes encoding proteins that can aggregate erythrocytes and destroy their membrane releasing haemoglobin. We located also a gene cluster (ABSDF2280-88) sharing similarities with genes associated with haem acquisition system (HAS) already described in several species (reviewed in [54]). According to the literature the transport system of haem or haemoglobin into the cell could also be ExbB/ExbD/TonB complex dependant but in this case the periplasm intermediary is not required [55]. Several clusters (N=3) of ExbB, ExbD, and TonB genes have been detected on strain SDF genome as well as several associated ABC transporters which are probably involved in the translocation of haem/haemoglobin from the periplasm to the cytosol. Finally, the key enzyme (Haem Oxygense Haemo = ABSDF2291) required for the release of iron has also been found in this strain.

Bacteria generally regulate iron import into the cell according to iron availability. In both AYE and SDF strains, the regulation of this process is likely to be mediated by the ferric regulator uptake protein (Fur: ABAYE2920 and ABSDF2538) which acts as a transcription repressor of genes involved either in the siderophore synthesis, in transport or even in degradation of ferri-siderophore. Furthermore, we identified fur boxes in the upstream region of most of the gene clusters involved in iron capture. Besides the central role of Fur protein, secondary positive regulators may also interfere in the iron uptake process. In Vibrio anguillarum, the assembly of the siderophore anguibactin and the enhancement of iron transport are promoted by products encoded in a transacting factor region of the virulence plasmid pJM1 [56,57].

The present comparison of iron uptake provides a good example of specialization of A. baumannii strains facing different environmental conditions. In the case of A. baumannii strain AYE, the competition against human host for iron using siderophores may explain part of the pathogenicity of this strain. In contrast, strain SDF may not have to compete for iron and hence use an alternate system.

Acinetobacter pathogenicity: insights into virulence factors

Gene products which give a microbe the ability to persist and invade a host of particular species are often referred as virulence factors. These factors generally comprise toxins, cell surface components (adhesins, glycoproteins), and hydrolytic enzymes that may contribute to the pathogenicity of the bacterium. Since no toxin or toxin-like encoding gene has been detected in both A. baumannii strains, their pathogenicity relies essentially on genes which belong to the two last categories.

Outer membrane proteins (OMPs) of Gram-negative bacteria are known to have essential roles in antibiotic resistance as well as in adaptation and pathogenesis in host cells [58]. Several OMPs of the OmpA family were characterized in various Acinetobacter strains and represent one of the major OMP in this genus. The A. baumannii OmpA is a secreted protein having an emulsifying activity [59] whereas other OmpA proteins are associated to virulence properties which induce apoptosis of epithelial cells [60] or stimulate gastrin and interleukin-8 gene expression [61]. The present genome analysis reveals that only one gene in each Acinetobacter strains encodes an OmpA protein (ACIAD0697, ABAYE0640, and ABSDF0605). These proteins share more than 89% of identical amino acids and have the same chromosomal context. These findings suggest that OmpA proteins are ubiquitous in the Acinetobacter genus but also raise questions on their exact role.

Among hydrolytic enzymes, phospholipases have been the subject of extensive investigation, especially the two types of phospholipases C produced by Pseudomonas aeruginosa: PLC-H encoded by the plcS gene is acidic and has a strong hemolytic activity whereas its counterpart PLC-N encoded by the plcN gene is rather basic and does not have any hemolytic activity (for a review see [62]). PLC-H is actually posttranslationnally altered by one of the plcR gene product thus enhancing its hydrolytic capacity [62]. We found in each Acinetobacter baumannii genome two copies of phospholipase C (plc) genes sharing about 50 percent identity (Table S1). This suggests that the proteins arose from an ancient duplication. Interestingly, though each copy has its best BlastP match with PLC-N, each protein has a pI lower than 7 which is rather a feature of PLC-H. We therefore cannot conclude on the hemolytic activity of A. baumannii phospholipases C. Furthermore, no plcR gene homolog has been found in both A. baumannii strains. Whether plcR is required for PLC-H activity is not clear, the hemolytic property of plc genes products will therefore remain an open question.

As other phospholipases (D, A) are thought to be major virulence factors in other species (see for example [63]), we have checked for their presence in the genomes under study. We effectively found one or several copies of the two kinds of phospholipases. The most interesting case is certainly the pld gene copies harbored by the AYE genome. Among the 4 copies, 3 displayed peculiar features. They \( i \) were bordered at both sides by an insertion sequence (ISAbal); \( ii \) were identical indicating that the amplification of the pld copies is rather recent; \( iii \) presented a slippery sequence (GGGGG AAC CUU) resulting in a +1 frameshift analogous to the one found in the pfrB gene of E. coli. Given these evidences, we speculate that the intact copy of pld maintains a basal activity that is necessary for the cell to exploit phosphorous sources whereas the 3 remaining ones are likely to be active but solicited only when facing exceptional environmental conditions (infection process, etc.). Indeed, the strong promoter provided by ISAbal and the programmed frameshift would allow the regulation of the production of fully functional phospholipase D.
While this work was in progress, the sequence of another A. baumannii (strain ATCC17978) was reported [64]. In this human-adapted A. baumannii isolate, the virulence factors previously described in strain SDF and AYE were also present. Moreover, in this study, candidate virulence genes were identified by insertional mutagenesis followed by two screening assays (reduced brood size and inhibition of C. elegans) in which A. baumannii ATCC17978 virulence was primarily induced by 1% ethanol [65]. Among the 35 Ethanol-stimulated virulence (Esv) mutants retained upon analysis, many of the candidate virulence genes were either transcriptional regulators (Table 3). Still according to our work, the presence of true virulence genes in Acinetobacter to various ecological niches.

### Materials and Methods

#### Sequencing

The complete genome sequences of A. baumannii strains AYE and SDF were determined using the whole-genome shotgun method. Two libraries, obtained by chemical shearing of genomic DNA and cloning of generated 2-5 kb and 6-17 kb inserts into the plasmids pNAV (A) and pCNS (B) (pcDNA2.1 and pSU18 derived, respectively), were constructed per genome. DNA Plasmids were purified and end-sequenced (61440 (A) and 20928 (B) for AYE and 62784 (A) and 22272 (B) for SDF) by dye-terminator chemistry on ABI3730 sequencers (Applied Biosystems, Foster City, United States). All reads were first compared to A. baumannii ADP1b rRNA (16S and 23S sequences) and ISfinder database [66], and those sharing at least 80% identity on a length of 100 nt were tagged as rRNA sequences (C) or ISs (D). A first assembly for each genome, using Phred/Phrap/Consed software package (www.phrap.com), was performed without 713 (C) and 2691 (D) reads for AYE and 514 (C) and 18156 (D) reads for SDF. Repeated sequences longer than 600 nt were detected with the RepeatSeek software [67] and subsequently recorded to an internal database. Similarity searches across the newly created database using same criteria as mentioned above, allowed the identification of 1699 and 2434 reads as part of repeated sequences in AYE and SDF, respectively. A new assembly was constructed without rRNA, IS and internal repeated sequences and rRNA. IS and internal repeated reads were then reinserted in the assembly on the clone-links basis. Additional reactions were necessary to complete the genomic sequences of A. baumannii strains AYE and SDF (9640 and 19240, respectively).

#### Annotation and Comparative Genome Analyses

CoDing Sequences were first predicted using the AMIGene (Annotation of Microbial Genomes) software [68]. Each CDS was then submitted to automatic functional annotation. Putative orthologs of the predicted genes were assigned using the Consed software (Foster City, United States), and those sharing at least 80% identity on a length of 100 nt were identified.

### Table 3. Functional annotation proposed for 16 Esv-mutants published by smith and colleagues [64].

| Gene label* | Gene Name | Esv-mutant Name* | Annotation | Putative Ortholog | Essential in A. baylyi ADP1b | Essential in E. coli c |
|-------------|-----------|-----------------|------------|------------------|-----------------------------|----------------------|
| A15_3223    | EsvA      | putative transcriptional regulator | No Homolog | No Homolog       |                             |                      |
| A15_1232    | EsvB      | putative transcriptional regulator | No Homolog | No Homolog       |                             |                      |
| A15_1012    | ureA      | urease gamma subunit | No Homolog | No Homolog       |                             |                      |
| A15_2447    | pstC      | high-affinity phosphate transport protein | No Homolog | No Homolog       |                             |                      |
| A15_2313    | quef      | 7-cyano-7-deazaguanine reductase | No Homolog | No Homolog       |                             |                      |
| A15_2314    | EsvE2     | conserved hypothetical protein | No Homolog | No Homolog       |                             |                      |
| A15_2315    | rodA      | rod shape-determining protein | No Homolog | No Homolog       |                             |                      |
| A15_3218    | czcB      | RND divalent metal cation efflux membrane fusion protein | No Homolog | No Homolog       |                             |                      |
| A15_3290    | EsvF2     | putative transcriptional regulator | No Homolog | No Homolog       |                             |                      |
| A15_0378    | etfD      | electron transfer flavoprotein-ubiquinone oxidoreductase | No Homolog | No Homolog       |                             |                      |
| A15_2262    | rpoH      | sigma H (sigma 32) factor of RNA polymerase | No Homolog | No Homolog       |                             |                      |
| A15_2037    | EsvI      | putative transcriptional regulator | No Homolog | No Homolog       |                             |                      |
| A15_3329    | EsvJ      | conserved hypothetical protein | No Homolog | No Homolog       |                             |                      |
| A15_1586    | EsvK1     | putative phage endonuclease | No Homolog | No Homolog       |                             |                      |
| A15_1587    | EsvK2     | putative phage Terminase | No Homolog | No Homolog       |                             |                      |
| A15_0310    | uvrC      | excinuclease ABC subunit C | No Homolog | No Homolog       |                             |                      |

Automatic functional annotation was first generated using our annotation pipeline [71] subsequently reviewed by human expert.

*Data from E. coli chromosome (PEC) database (http://www.shigen.nig.ac.jp/ecoli/pec/index.jsp).

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orthologous relations between two genomes are defined as gene pairs that satisfy either the Bidirectional Best Hit criterion [69] or an alignment threshold (at least 40% sequence identity on at least 80% of the length of the smallest protein). These relations are subsequently used to search for conserved gene clusters (synteny groups) among several bacterial genomes. The algorithm based on an exact graph-theoretical approach is detailed in [70]. This method allows for i) multiple correspondences between genes and, thus, paralogy relations and/or gene fusions are easily detected; ii) Chromosomal rearrangements (inversion, insertion/deletion). A ‘gap’ parameter, representing the maximum number of consecutive genes which are not involved in a synteny group, was set to five. As a final step, manual validation of automatic annotations was performed using the MaGe web interface [71].

Data Availability

Annotation sets of all A. baumannii replications have been deposited in EMBL database under the following references: Acinetobacter baumannii str. SDF: Chromosome, CU468230; Plasmid 1, CU468231; Plasmid 2, CU468232; Plasmid 3, CU468233. Acinetobacter baumannii str. AYE: Chromosome, CU459141; Plasmid 1, CU459137; Plasmid 2, CU459138; Plasmid 3, CU459140; Plasmid 4, CU459139. These annotations as well as comparisons results are publicly available for consultation at http://www.genoscope.cns.fr/agc<MenuMETATAGS>.

Supporting Information

Figure S1 Phylogenetic tree reconstruction for all ISRs from Acinetobacter spp. available in Genbank (release 160), using as outgroup Escherichia coli. BRCR 15486 ISR. This analysis shows that A. baumannii strain SDF is effectively a baumannii species although it is devoid of ampC gene and is unable to grow at 44°C (two phenotypic traits that characterize species belonging to the A. calcoaceticus-A. baumannii complex). Moreover, it confirms the closeness of the relationship between A. calcoaceticus, A. baumannii and genomic species 3 and 13TU. Sequences were first aligned with MUSCLE [72] and the PhyML software [73] was used to build the tree (substitution model: HKY, 100 bootstrap replicates). Found at: doi:10.1371/journal.pone.0001805.s001 (1.52 MB TIF)

Figure S2 Alignment of presumed AHL lactonases of the 3 Acinetobacters under study together with other known AHL lactonases from Bacillus subtilis, Bacillus thuringiensis, Arthrobacter sp. and Agrobacterium tumefaciens. The red boxes indicate active residues of AHLases. Alignment was performed with MUSCLE [72] embedded in JalView [74]. Found at: doi:10.1371/journal.pone.0001805.s002 (2.43 MB TIF)

Table S1 Labels of genes annotated as (putative) phospholipase in four Acinetobacter genomes. Frameshifted copies are indicated in bold type (part1–part2).

Data from [64]. Found at: doi:10.1371/journal.pone.0001805.s003 (0.02 MB XLS)

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Author Contributions

Performed the experiments: CR VB SM CA BS LP SO JP. Analyzed the data: DV VB CM SC LP AK. Contributed reagents/materials/analysis tools: JW JC CR DR PN LP. Wrote the paper: DV VB SC PN. Other: Provided A. baumannii strain AYE. PN. Did the manual expert annotation of the two strains: VB. Managed informatics resources of the project: CD SG. Designed the initial project: DR PN JC. Provided A. baumannii strain SDF: DR. Contributed to the annotation: DV SC.

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