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The Cyst-Dividing Bacterium *Ramlibacter tataouinensis* TTB310 Genome Reveals a Well-Stocked Toolbox for Adaptation to a Desert Environment

Gilles De Luca¹,²,³,⁴, Mohamed Barakat¹,²,³, Philippe Ortet¹,²,³, Sylvain Fochesato¹,²,³, Cécile Jourlin-Castelli⁴, Mireille Ansaldi⁴, Béatrice Py⁴, Gwenaelle Fichant⁵,⁶, Pedro M. Coutinho⁷, Romé Voulhoux⁸, Olivier Bastien⁹, Eric Maréchal⁹, Bernard Henriassat⁷, Yves Quentin⁵,⁶, Philippe Noirot¹⁰, Alain Filloux¹¹, Vincent Méjean⁶, Michael S. Dubow¹¹, Frédéric Barras⁶, Valérie Barbe¹², Jean Weissenbach¹², Irina Mihalcescu¹³, André Verméglio¹,²,³, Wafa Achouak¹,²,³, Thierry Heulin¹,²,³

¹ CEA, Lab EcoL MicrobiennE Rhizosphere & Environm Extre, IBEB, DSV, Saint-Paul-lez-Durance, France, ² CNRS, Unité Mixte Rech Biol Vegetale & Microbiol Enviro, UMR 6191, Saint-Paul-lez-Durance, France, ³ Université Aix Marseille, Saint-Paul-lez-Durance, France, ⁴ Laboratoire de Chimie Bactérienne, UPR-CNRS 9043, Institut de Microbiologie de la Méditerranée, Aix-Marseille Université, Marseille, France, ⁵ Laboratoire de Microbiologie et Génétique Moléculaire, Université de Toulouse, UPS, Toulouse, France, ⁶ CNRS, LMG, Toulouse, France, ⁷ Architecture et Fonction des Macromolécules Biologiques, UMR 6098, CNRS, Université de la Méditerranée, Marseille, France, ⁸ Laboratoire d’Ingénierie des Systèmes Macromoléculaires, CNRS-Aix Marseille Université, Institut de Microbiologie de la Méditerranée, Marseille, France, ⁹ Laboratoire de Physiologie Cellulaire Végétale, CNRS/CEA/INRA/Université Joseph Fourier, CEA-Grenoble, Grenoble, France, ¹⁰ INRA, Micaols, Thiverval-Grignon, France, ¹¹ Laboratoire de Génomique et Biodiversité Microbienne des Biofilms, Université Paris-Sud 11, Institut de Génétique et Microbiologie, CNRS UMR 8621, Orsay, France, ¹² CEA, DSV, IG, Genoscope, Evry, France, ¹³ Université Grenoble 1/Centre National de la Recherche Scientifique, Laboratoire Interdisciplinaire de Physique, Unité Mixte de Recherche 5588, Grenoble, France

**Abstract**

*Ramlibacter tataouinensis* TTB310⁷ (strain TTB310), a betaproteobacterium isolated from a semi-arid region of South Tunisia (Tataouine), is characterized by the presence of both spherical and rod-shaped cells in pure culture. Cell division of strain TTB310 occurs by the binary fission of spherical “cyst-like” cells (“cyst-cyst” division). The rod-shaped cells formed at the periphery of a colony (consisting mainly of cysts) are highly motile and colonize a new environment, where they form a new colony by reversion to cyst-like cells. This unique cell cycle of strain TTB310, with desiccation tolerant cyst-like cells capable of division and desiccation sensitive motile rods capable of dissemination, appears to be a novel adaptation for life in a hot and dry desert environment. In order to gain insights into strain TTB310’s underlying genetic repertoire and possible mechanisms responsible for its unusual lifestyle, the genome of strain TTB310 was completely sequenced and subsequently annotated. The complete genome consists of a single circular chromosome of 4,070,194 bp with an average G+C content of 70.0%, the highest among the *Betaproteobacteria* sequenced to date, with total of 3,899 predicted coding sequences covering 92% of the genome. We found that strain TTB310 has developed a highly complex network of two-component systems, which may utilize responses to light and perhaps a rudimentary circadian hourglass to anticipate water availability at the dew time in the middle/end of the desert winter nights and thus direct the growth window to cyclic water availability times. Other interesting features of the strain TTB310 genome that appear to be important for desiccation tolerance, including intermediary metabolism compounds such as trehalose or polyhydroxylalkanoate, and signal transduction pathways, are presented and discussed.


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**Funding:** Work in our laboratories is supported by the Commissariat à l’Energie Atomique et aux Energies Alternatives (CEA), and the Centre National de la Recherche Scientifique (CNRS). Genome sequencing was realized by the Genoscope (Evry, France) with the financial support of the GEOMEX (“Geomicrobiology of Weathering” [1,2], the presence of bacterial rods with an unusually weathering) and secondary calcite crystals resulting from terrestrial weathering [1,2], the presence of bacterial rods with an unusually...
small diameter. The strain TTB310 was isolated among a large diversity of bacterial strains based on its cell diameter as the main criterion for the selection, and secondly on its ability to cause the weathering of orthopyroxene. This strain was characterized by the presence of a pleomorphic form [3] with motile rod-shaped (diameter 240 nm) and spherical cells (diameter 800 nm). It was later identified as a new genus and species, Ramlibacter tataouinensis [4]. TTB310 is the type strain of this species. One of the most unusual characteristics of strain TTB310 is the coexistence of both spherical and rod-shaped cells [4–6]: these features reveal an original cell cycle that likely constitutes the main adaptation of this bacterium to this desert environment, characterized by cycles of air-drying and rehydration events and long-term desiccation.

The strain TTB310 spherical cells present traits similar to Azotobacter cysts, such as the absence of motility, cells embedded within thick extracellular polymeric substances (EPS), the presence of polyhydroxyalkanoate granules in the cytoplasm and a long-term resistance to desiccation [4]. Contrary to cysts of Azotobacter, for which the differentiation into rods is necessary for cell division, cell division of strain TTB310 occurs under its “protected” form (cyst), when water and nutrients are available. We thus proposed that spherical cells should be considered “cysts” due to their desiccation tolerance, even if they are not resting cells [4]. This binary fission of spherical “cyst-like” cells (“cyst-cyst” division) in an embedded EPS is the basic mechanism by which a bacterial colony grows on solid surfaces and probably an important trait related to its adaptation to desiccation [4,5]. The rod-shaped cells formed at the periphery of a colony (consisting mainly of cysts) are highly motile (0.1 μm/min), and colonize a new environment, where they form a new colony by reversion to cyst-like cells (“cyst-rod-cyst” differentiation) [5,6]. The formation of the rod-shaped bacteria requires lysis of the EPS, reshaping of the cyst cell including a condensation of cytoplasmic material, and synthesis of a motility apparatus. Conversely, the “rod-to-cyst” transition requires the reshaping of a rod and the synthesis of a new EPS. This original cell cycle of strain TTB310 with desiccation tolerant cyst-like cells capable of division and desiccation sensitive motile rods capable of dissemination seems to be well suited for life in a hot and dry desert and is summarized in Fig. 1.

In order to gain insights into strain TTB310’s underlying genetic repertoire and possible mechanisms responsible for its unusual lifestyle, we sequenced the genome of strain TTB310. DNA sequence annotation, using both bioinformatics and manual re-examination by experts in various microbiology fields, shows that strain TTB310 has classical and specific mechanisms for adaptation to desert life, combining both enzymatic and mechanical protective schemes. Both for environmental sensing and for cell cycle control, genomic data suggest that strain TTB310 has developed a highly complex network of two-component systems, which seems to implicate light and perhaps a rudimentary circadian hourglass.

**Results and Discussion**

**General features on the genome sequences and structure**

The complete genome consists of a single circular chromosome of 4,070,194 bp with an average G+C content of 70.0%, which is the highest of the Betaproteobacteria sequenced to date (Table 1). A total of 3,899 predicted coding sequences (CDS), covering 92% of the genome, were identified. Among these, 72% are proteins with a function assigned on the basis of their similarity to other known
proteins, 19% are conserved hypothetical proteins and 9% did not display any significant similarity to proteins identified in other organisms. In addition to protein-encoding genes, a single copy of the ribosomal (rRNA) operon, 43 transfer RNAs (tRNA) genes representing all amino acids, and 10 non-coding RNAs were identified. Genome comparisons showed that the strain TTB310 genome was highly similar with those of the Betaproteobacteria such as Polaromonas sp. JS666, Delftia acidovorans SPH-1 and Acidovorax avernans sp. citrulli AAC00-1 sharing with them 66, 60 and 60% of its encoded proteins, respectively (Fig. S1).

Carbohydrate metabolism

As expected, strain TTB310 presents the genetic characteristics of an aerobic, chemo-organotrophic bacterial strain [4] (see Table S1 for details). Considering the oligotrophic character of deserts (organic matter <1 mg/g; [7]), we explored the carbon metabolism of strain TTB310 with particular attention. Acetate is used as a carbon and energy source by strain TTB310 [4]. We found in strain TTB310 genes encoding the enzymes catalyzing the transformation of acetate into acetyl-CoA (acetate-CoA ligase, Rta_13940), and the first enzymes of the autotrophic dicarboxylic/hydroxybutyrate pathway [8] (Table S1). The first steps of this pathway, from acetyl (C2) to oxaloacetate (C4), allow the incorporation of two molecules of CO2.

Propionate and β-hydroxybutyrate are also used as carbon and energy sources by this bacterium [4]; propionate can generate acetyl-CoA with propionyl-CoA as an intermediate (propanoate metabolism), and β-hydroxybutyrate can generate acetoclastic β-hydroxybutyrate dehydrogenase, Rta_17330. These three organic acids (acetate, propionate and β-hydroxybutyrate) are well-known carbon substrates for the biosynthesis of polyhydroxalkanoate (PHA), representing the carbon and energy storage of strain TTB310 [4]. Key enzymes for PHA biosynthesis (PHA polymerase, Rta_18090) and catabolism (PHA depolymerase, Rta_29420) are present. The pentose phosphate pathway is complete, along with that for pyruvate metabolism. The citric acid cycle (TCA cycle) is also complete and associated to the glyoxylate bypass (malate synthase, Rta_02700; isocitrate lyase, Rta_25660). In the glyoxylate cycle, oxaloacetate (C4) can be regenerated from phosphoenolpyruvate (C3) with PEP-carboxylase with the fixation of one CO2 (Rta_29890). All genes necessary for glycolysis or gluconeogenesis (from α-D-glucose and β-D-glucose to pyruvate) are present, but glucose assimilation was not detected in strain TTB310 [4]; this is probably due to the absence of glucose transporter. Among all the transporters, Rta_24150 appears to be the best candidate to import the different carbon sources metabolized by strain TTB310 including acetate, pyruvate, β-hydroxybutyrate, γ-hydroxybutyrate, DL-lactate, and propionate.

Tolerance to oxidative stress and DNA repair mechanisms: enzymatic protections

We examined the strain TTB310 genome for the presence of genes encoding for proteins involved in defense mechanisms against the toxicity of reactive oxygen species (ROS), strain TTB310 possesses basic but apparently sufficient equipment with one cytoplasmic (Rta_11320) and one periplasmic superoxide dismutase (Rta_21800) to cope with the presence of superoxide. Concerning peroxide elimination, all various pathways present in organisms such as Escherichia coli, Xanthomonas campestris and Sarcosynthesmes cressieris are found in strain TTB310, with some enzymes even found in multiple copies. The genes of strain TTB310 potentially involved in peroxide scavenging pathways are summarized in Fig. S2. The reductase enzymes, such as TrxB and AhpF, are also present. Although the genes encoding one glutathione-synthetase (Rta_02450) and five thiorodoxins (Rta_05290, Rta_17070, Rta_23420, Rta_30710, Rta_36760) to complete the pathways are present, genes encoding for a glutathione reductase could not be found. However, four additional genes (Rta_11590, Rta_13470, Rta_22660, Rta_29620) similar to trxR (Rta_31670) and ahpF (Rta_24200) are present, though whether one of them is a glutathione reductase remains to be determined. Strain TTB310 is therefore equipped to adapt to various peroxide and superoxide stresses with a classical set of enzymes. One can however note the presence of genes encoding for enzymes involved in carotenoid biosynthesis (Rta_07600 to Rta_07730) to quench ROS in the presence of light, in accordance with the presence of carotenoid pigments in strain TTB310 [4].

Strain TTB310 encodes a complete set of enzymes known to be required for DNA replication, DNA recombination, and for various DNA repair mechanisms. Relevant to the strain TTB310 life cycle, three proteins are potentially repairing DNA photo-damage: (i) a candidate deoxyribouridylinuridine photolysate (photoreactivating enzyme) PhrR (Rta_34120) highly common in Betaproteobacteria and responsible for the repair of UV-induced DNA damages in a blue light dependent manner; (ii) a candidate deoxyribouridylinuridine photolysate (photase) Rsa_37150 highly similar to the Rhodobacter sphaeroides RSP_3077 protein proposed to act on DNA photorepair [9]; and (iii) a conserved hypothetical protein (CHP) distantly related to the spore photoprotein lyase protein SpbB from Bacillus subtilis (Rta_25110). In conclusion, both for tolerance to oxidative stresses and DNA repair mechanisms, strain TTB310 seems to use a “classical” set of enzymes to cope with the drastic semi-desertic conditions, including enzymes for carotenoid biosynthesis and for DNA photo-damage repair.

Carbohydrate-active enzymes: mechanical protections (exopolysaccharide and trehalose synthesis and degradation)

As explained in the introduction and illustrated by the “classical” set of enzymes used for the tolerance to oxidative stresses and DNA repair mechanisms, we hypothesize that the cyst extracellular polymeric substances (EPS), including exopolysaccharides, constitutes the main physical barrier protecting strain TTB310 from dessiccation/rehydration cycles. A systematic search for genes encoding carbohydrate-active enzymes was thus carried out to corroborate the existence of exopolysaccharide synthesis and degradation proteins in strain TTB310. A total of 25 glycosyl-hydrolases (GHS) and 40 glycosyl-transferases (GTs) could be identified (Table S2), corresponding respectively to 0.65% and

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https://doi.org/10.1371/journal.pone.0023784.t001
1.0% of the CDSs of the genome. These percentages are in the average range for bacterial and eukaryotic genomes, whether for GHs alone or GTs alone [10]. The genome encodes a number of expected features such as peptidoglycan, osmoregulated periplasmic glucans, lipopolysaccharide and exopolysaccharide biosynthesis pathways (Table S2).

Interestingly, in strain TTB310 all but one of the identified GHs belong to families known to degrade equatorial glycosidic bonds of substrates (e.g. β-linked for a D-glucose configuration). The only exception is a gene that encodes a candidate intracellular α,β-trehalase (Rta_36490) that belongs to a distinct subfamily of the large glycosidase family GH15 found in an operon-like gene cluster also containing a gene encoding a candidate trehalose 6-phosphate phosphatase (Rta_36480) and a α,α-trehalose-6-phosphate synthase (Rta_36500). The disaccharide trehalose is widely distributed in nature and can be found in many organisms, including bacteria, fungi, plants, invertebrates and mammals. It has been shown that trehalose can protect proteins and cellular membranes from inactivation or denaturation caused by a variety of stress conditions, including desiccation, dehydration, heat, cold, and oxidation [11]. Trehalase is likely to be an essential component of the metabolism of strain TTB310 since this organism is subjected to all of the above. Many free-living bacteria store carbon in the form of bacterial glycogen. It has been shown that obligate bacterial parasitises and symbionts tend to lose their glycogen metabolism [12]. Strain TTB310 is remarkable in that it has no candidate gene involved in glycogen metabolism despite being a free-living bacterium (in strain TTB310, carbon is stored as PHA). Due to the absence of the glycogen pathway, all the pool of glucose in strain TTB310 can be directed towards the trehalose pathway.

The analysis of the stereochemistry of the glycosidic bonds built by the 40 GHs found in the strain TTB310 genome reveals that a majority are involved in the formation of equatorial (eg β-linked for a D-glucose configuration) glycosidic bonds, but 12 (from families GT4, GT18 and GT20) are likely to be involved in the formation of axial (eg α-linked for a D-glucose configuration) glycosidic bonds. The function of only one of these 13 α,β-bond building GTs can be confidently assigned, namely the α,α-trehalose-6-phosphate synthase, which is accompanied by its hydrolytic counterpart. This leaves a dozen genes encoding GTs involved in the formation of axial (eg α-linked for a D-glucose configuration) glycosidic bonds with no known degrading counterpart. It is conceivable that the glycoconjugate products of some these GTs are a series of glucans, lipopolysaccharide and exopolysaccharide biosynthesis pathways (Table S2).

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In strain TTB310, the only α,β-degrading GH is a likely intracellular α,β-trehalase and all other candidate GHs belong to families known to cleave β-glycosidic bonds. This suggests that the subset of β-glycosidases that are exported (Table S2) could be secreted and involved in the rapid breakdown of the abundant EPS during the “cyst-to-rod” transition and, by inference, that the EPS is made of mainly β-linked carbohydrates. If the α,β-bond building glycosyltransferases discussed earlier were involved in the synthesis of the EPS, then its breakdown would be performed by classes of enzymes yet to be discovered (we note that no polysaccharide lyases have been identified in the strain TTB310 genome).

Membrane glycerolipids: a complex fatty acid biosynthetic system allowing a versatile tuning of membrane fluidity

After the EPS, membranes are the second physical barriers for protecting bacteria from environmental damages. Therefore, the strain TTB310 genome was carefully examined for glycerolipid biosynthesis systems and was completed by a biochemical analysis of inner membrane lipids. Genes for the complete biosynthetic pathway of lipid A derivatives, which characterize the outer membrane of Gram negative bacteria, are present in the strain TTB310 genome, equipping the cell with a robust hydrophobic barrier anchored to the cell wall. For the inner membrane, lipid content analysis reveals that it is characterized by a phospho-glycerolipid profile with little complexity regarding polar heads (Fig. S3). The major phospholipid is phosphatidylethanolamine. No phosphatidylserine could be detected, although two phosphatidylserine synthases were identified in the genome. One fifth of the glycolipids is phosphatidylcholine, a lipid that is absent from the vast majority of bacteria [13], particularly from E. coli or B. subtilis, and whose synthesis in strain TTB310 is attributed to a phospholipids-N-methyl transferase (pmtA, Rta_17000).

Analysis of fatty acid composition by gas chromatography of the acyl methyl esters indicated a striking complexity, with more than 30 molecular species ranging from 14 carbon atoms (C14) to more than 20 carbon atoms (Table S3). The usual straight chain fatty acids (C16 and C18 molecular species) account for half the fatty acids, with a classical profile of saturated (C16:0, C18:0) and unsaturated species (C16:1, C18:1, C18:2, C18:3). The other half comprises even-numbered very-long chain fatty acids (C20, C22, C24), odd-numbered straight chain fatty acids (C15:0, C17:0) and branched chain fatty acids (methyl in iso and anteiso positions). At the genomic level, we detected strain TTB310 genes for fatty acid biosyntheses initiating with a very large set of primers (Fig. S4). In summary, we found that strain TTB310 presents the ability to synthesize even- and odd-numbered, straight and branched chain fatty acids from acetyl-CoA, propionyl-CoA and branched chain amino acid derivatives as starting units. Three key enzymes are involved in the determining steps of these biosyntheses: the branched chain amino acid transaminase (ltaT, Rta_01070), the α-keto acid dehydrogenase (bkd) cluster (bkdA1, Rta_10480; bkdA2, Rta_10490; bkbd, Rta_10500; bkd, Rta_10510) and the β-ketoacyl-ACP synthase III (fabH) (possibly fabH-like1 (Rta_04890) and fabH-like2 (Rta_04120)). This complex fatty acid biosynthesis system therefore provides strain TTB310 with both means by which membranes can adjust their fluidity at the level of acyl-lipids: (i) addition of unsaturations and (ii) addition of methyl-branches. Tuning the derived membrane fluidity is therefore one of the possible determining mechanisms operating in the tolerance to temperature [14] and hygrometry variations, and in the shift between growing, gliding, differentiating, and resisting stages.

Transporters: involvement in osmotic stress tolerance and cell cycle

A detailed study of the strain TTB310 transporters has been carried out. In summary, compared to other betaproteobacterial genomes, the relative transport capability of strain TTB310 and its percentage of importers (~70%) are similar to those of Ralstonia solanacearum and to what is observed in Burkholderia species. Due to possible sudden and drastic fluctuation in osmolality (osmotic stress) encountered in the Saharan environment, special attention has been dedicated to transporters involved in these mechanisms, including: transporters responsible for the fast uptake of potassium (or, less frequently, sodium) to increase the internal osmolality in response to a hyper-osmotic shock (reviewed in [15]), ABC systems of the opu subfamily involved in the uptake of less harmful solutes for the subsequent replacement of K+, mechanosensitive (MS) channels implicated in response to hypo-osmotic stress and major intrinsic proteins (MIP) channels involved in passive transport of water and small solutes such as glycerol and urea [16].
The strain TTB310 genome encodes genes similar (Rta_02420, Rta_26850 and Rta_05740) to E. coli low (Kup or TrkD) and high (TrkH) efficiency K⁺ transporters. The presence of several K⁺ uptake systems might be due to different pH requirements, since TrkA mainly functions at an alkaline pH and Kup at a low pH in E. coli [17]. However, analysis of the strain TTB310 genome did not reveal ABC systems of the opu subfamily involved in histidine, proline, proline betaine, glycine betaine and choline uptake nor homologs of the betaine/carnitine/choline transporter (BCCT) family of betaine transporters. This class of compatible solutes, very common in rich soil, may be absent in the cell environment of strain TTB310. In such a case, bacteria can respond to the osmotic up shift by synthesizing glutamine, proline and trehalose. The trehalose-centered metabolism of strain TTB310 reported above suggests that this sugar may be used as a compatible solute.

We identified two candidates (Rta_25200 and Rta_26800) and one putative (Rta_15000) mechanosensitive-encoding gene, but all of them belong to the small mechanosensitive ion channels (MscS) family.

Finally, a member of the major intrinsic proteins (MIP) family has been predicted (Rta_23560). The best-characterized MIP in bacteria (AqpZ from E. coli) is involved in short and long-term osmoregulation, exponential growth and bacterial virulence [18]. It mediates the rapid entry or release of water from the cell in response to sudden shifts in extracellular osmolarity. Rta_23560 likely plays a similar role in strain TTB310 and might be involved in the “water” loss of two-thirds of the cell volume during cyst-to-rod differentiation.

Protein export and secretion systems: involvement in EPS hydrolysis and cell motility

Genes encoding the general inner membrane export system (Sec; [19]), the outer membrane protein insertion system (Bam/Omp85; [20]), the lipoprotein transport system (Lol; [21]) and the non-essential Twin Arginine Translocation (Tat; [22]) system, involved in the transport of folded proteins across the inner membrane, are present in strain TTB310 (Fig. 2, see Table S4 for details including predicted Tat substrates and lipoproteins). Moreover, at least one type II secretion system (T2SS) [23,24] was found in strain TTB310 (Fig. 2, Table S4), which may be involved in the release of hydrolases required for the breakdown of the exopoly saccharide during the transition from cyst to rod-shaped cells. Indeed, a subset of predicted β-glycosidases displays typical N-terminal signal peptide (Table S2). This is a hallmark for T2SS substrates, which are first translocated in a Sec- or Tat-dependent manner across the inner membrane [25]. Once the EPS is degraded, the rod-shaped cells can move in the environment. The strain TTB310 genome analysis indicates that the motility of

Figure 2. Schematic representation of envelope transport systems in Ramlibacter tataouinensis TTB310. In addition to general export pathway (Sec and Tat systems), the strain TTB310 genome encodes one type I secretion system potentially involved in secretion of a large protein, which is a putative adhesin (Rta_27720) as found in Pseudomonas fluorescens [76], and two type II secretion systems (T2SS) potentially involved in secretion of putative hydrolase implicated in EPS remodelling. The T2SSs clusters (gspFGHIJKLMCDE or gspDEFGH), each encodes an ATPase (GspE), a secretin (GspD) and a major pseudopilin (GspG), though they contain only one copy of the gspA8 genes. One type IV pilus machinery with different pilins and three PilB paralogs is present in strain TTB310 and is involved in gliding motility. There is only one gene (pilD/gspO) encoding a prepilin peptidase involved in the maturation of both type II secretion system and type IV pilus machinery. The strain TTB310 type III secretion system (T3SS) may be an additional example of the presence of T3SS genes in a nonpathogenic bacterium [29]. It could be involved in the secretion of chitinases through the thick extracellular polymeric substances (EPS) of cyst-cells. doi:10.1371/journal.pone.0023784.g002
rod-shaped cells is not supported by flagellar genes (absent in strain TTB310), but probably requires at least type IV pili, since all genes required for assembly of these appendages were found (Fig. 2, Table S4). These data corroborate previous analyses indicating that gliding, which may require type IV pili, is the preferred motility style observed in strain TTB310 [4–6]. Furthermore, two genes encoding histidine kinases (Rta_19330 and Rta_34130), similar to CheA and related to genes encoding the FrzE and ChinA proteins involved in gliding and twitching motility in Myxococcus xanthus and Pseudomonas aeruginosa, respectively, are present in strain TTB310. We thus propose that the chemotaxis systems in this bacterium may be dedicated to gliding motility [5,26].

Surprisingly, strain TTB310 possesses one additional gene cluster localized between Rta_29650 and Rta_29970. This cluster encodes proteins highly similar to the plant-pathogen type III secretion system (T3SS) of Acidovorax avenae subsp. citrulli AAC001 (T3SS, Hrp2 family: Fig. 2, Table S4), which is involved in pathogenicity in cucurbits [27]. It should be noted that the strain TTB310 genome encodes two enzymes distantly related to chitinases (Rta_26180, Rta_33120) and that one of the gene encoding a candidate chitinase (Rta_29730) is localized in the middle of the T3SS cluster. Within the vicinity of this cluster, additional genes (Rta_29974 to Rta_30025, Table S4) encode proteins similar to those involved in the last steps of chitinolysis, and in the transport of chitodextrin across the inner membrane in Collimonas fungivorans Ter331 [28]. All these genes could confer to strain TTB310 the ability to metabolize extracellular poly-N-acetylglocosamine that could result from a direct biosynthesis by strain TTB310 (Rta_32250; related to poly-β-1,6-N-acetylgluco- samine synthase) or from other β-N-acetylgulcosamine-containing saccharides present in the soil. T3SS is often described as specific to pathogenic bacteria, but has been also found in nonpathogenic bacteria [29]. In strain TTB310, we hypothesize that this T3SS may be used to secrete proteins (for instance chitinases) across the thick EPS of cysts.

Cell division and cell shape differentiation

According to the bacterial cell morphologies reviewed by Margolin [30], strain TTB310 is an original case due to its transformation from cyst to rod and vice versa (Fig. 1). To perform these shape differentiations, the strain TTB310 genome displays highly conserved gene sets required for the cell division and cell shape determination of rod-shaped Proteobacteria, including mreBCD (Rta_03840, Rta_03830, Rta_03820), rodA (Rta_09910), rodC (Rta_18930), two genes encoding Bola-related proteins (Rta_08200, Rta_20200) and several penicillin-binding proteins, including the sidewall elongation penicillin-binding protein 2 (mrkD; Rta_03810). These genetic data and our observations (Fig. 1, Video S1 and Text S1 for details) predict that cylindrical strain TTB310 rod cells grow mainly by extending the length of the cylinder (MreB-dependent sidewall elongation), and that new cell poles are synthesized at cell division (FisZ-dependent septum formation plus constriction) as observed in E. coli [31]. In contrast, strain TTB310 cysts grow via their division septa (FisZ-dependent septum formation) in a manner similar to Streptococcus pneumoniae ovococcii, as some length extension might still occur [4]. The other shape transitions do not correspond to known models. However, we observed that “cyst-to-rod” differentiation begins by an “ovococcal” division (FisZ-dependent), followed by the EPS lysis (Fig. 1). After this step, the morphological transition occurs by reshaping of cells (conservation of membrane surface), associated with loss of two-thirds of the cell volume [6] and leads to a rearrangement of the peptidoglycan from a spherical to a rod form, as seen in Video S1. For the “rod-to-cyst” differentiation, a reverse mechanism could be possible with a rearrangement of the peptidoglycan from a rod to a spherical form, associated with the synthesis of a new EPS. It seems that the ability of strain TTB310 to transform its shape from cyst to rod and vice versa uses a “classical” set and organization of cell division genes. However, the regulation of the strain TTB310 cell cycle must be tightly controlled, possibly at the transcriptional (sigma factors, transcription regulators of one or two component systems) and post-transcriptional (some His-Asp phosphorelay systems) levels.

A sophisticated system of signal transduction and light perception: a key for adaptation to extreme environment?

DNA-binding proteins. To adjust its adaptive response to environmental changes, the strain TTB310 genome encodes 226 DNA-binding proteins which are, for the most part, Helix-Turn-Helix (HTH) domain-containing proteins: 12 sigma factors, 187 one-component system proteins with HTH (181) or other (6) domains (classical transcriptional regulators: 4.8% of the genes), and 27 two-component system proteins with HTH domains (transcriptional) response regulators) (http://www.p2fd.org/page.php?base = RamtaDB, Fig. S3). The global number of HTH domain-containing proteins in strain TTB310 is relatively high (220; 12+101*27), and reflects the situation found in a wide diversity of genomes of free-living bacteria in which the one-component systems (here 181) are the main contributors to the total number of the HTH domain-containing proteins [31,32]. As found in a number of phylogenetically distant free-living bacteria, strain TTB310 exhibits an expansion of the LysR family (27% of the one-component transcription factors) known to be involved in the sensing of a wide range of small molecule ligands [33].

Signal transduction: His-Asp phosphorelays. In addition, strain TTB310 exhibits sophisticated systems involved in adaptive responses to changes in environmental conditions [34]. Indeed, a systematic search for two-component system (TCS) proteins using P2CS (http://www.p2cs.org/page.php?base = RamtaDB) [35,36] and a manual search, allowed us to identify 131 CDSs potentially involved in TCS or His-Asp phosphorelay signalling in strain TTB310. These systems were classically described as the association of two proteins that communicate through a His-Asp phosphorelay, a histidine kinase sensor protein capable of autophosphorylation on a conserved His residue that can transfer the phosphoryl group to the receiver (REC) domain of a response regulator on a conserved Asp residue (Fig. 3) [37]. TCSs account for about 5.5% of the coding region of the strain TTB310 genome, and represent 3.4% of total protein. This proportion is remarkably elevated, reflecting an important role of TCSs in this bacterium, whereas other signal transduction families [34] were almost missing (Table S5). In strain TTB310, among the 131 CDSs predicted to encode TCS proteins, 82 of them encode histidine kinase sensors (HKs) and 49 encode response regulators (RRs), corresponding to about two sensors per regulator. This unusual ratio between HKs versus RRs suggests a convergent signalling network in this strain, in addition to “classical” two component systems (a HK and its cognate RR) also present.

Interestingly, more than half of the HK predicted proteins are hybrid, since they contain at least a REC domain in addition to the classical HisKA kinase domain (Fig. 3). This is also an unusual situation that probably reflects a particular mode of signal transduction in this organism.

We noted a relative low number of transcriptional regulators (27) in the strain TTB310 genome, which represent only 55% of the 49 predicted RRs, against 80 to 90% usually found (Fig. 3).
The fact that about half of the predicted RRs are not transcriptional regulators suggests that TCS outputs could involve protein-protein interactions. These interactions might directly modulate the activity of the RR interacting proteins, and therefore allow a rapid adaptation to environmental changes.

Another particularity of TCSs in strain TTB310 concerns signal detection by HKs. Indeed, more than half of the predicted HKs (42) contain no transmembrane segment (TM), and are therefore predicted to be unable to detect any extracellular signal directly. This observation can be correlated with the elevated number of PAS (59) and PAC (50) domains, described as metabolism related intracellular sensors [38] that are found in 27 soluble HKs and 13 membrane-bound HKs. Among the soluble HKs devoid of PAS/PAC domains, 12 contain a GAF domain, and 2 are associated to a bacteriophytochrome domain. These observations indicate that signal detection in strain TTB310 may occur mostly inside of the cell through PAS and PAC domains.

Regarding TCS signal transduction in strain TTB310, our observations suggest: (i) a convergent signalling network due to the higher proportion of histidines kinases (HKs) (82) versus response regulators (RRs) (49); (ii) an intracellular network of signal transduction since half of the HKs (42) are soluble and appear to detect intracellular signals, (iii) the involvement of many two-component system (TCS) (20 CheY-like RRs) in post-transcriptional regulation that likely allow a more rapid adaptation compared to transcriptional regulation (light green dotted arrows indicate possible phosphorylations), and (iv) two chemotaxis systems dedicated to a form of gliding motility.

Light sensing: two red/infrared and four blue-light potential photoreceptors. Strain TTB310 presents one of the higher proportions of light sensing proteins exhibited by a chemotrophic non-phototrophic bacterium [41]. Indeed, six genes encoding potential light sensors that contain all the hallmarks of a bacteriophytochrome [42], a phototropin [43] or a blue-light using flavin adenine dinucleotide (BLUF) protein [44] have been identified in strain TTB310: two red/infrared light sensing histidines kinases or bacteriophytochrome photoreceptors (Rta_25470 and Rta_28950), a blue-light sensing histidine kinase or phototropin (Rta_12790), and three sensors of blue-light corresponding to BLUF proteins (Rtu_25470 and Rtu_28950), a blue-light sensing histidine kinase or phototropin (Rtu_12790), and three sensors of blue-light corresponding to BLUF proteins (Rtu_31060, Rtu_20590, Rtu_26080). These proteins may allow strain TTB310 to sense red/infrared (650–750 nm) and blue-light (350–450 nm), which could be an essential feature for adaptation to desert conditions. Indeed, due to the strong correlation existing between light, heat and desiccation in a desert environment, light should be
one of the more important external cues allowing strain TTB310 to anticipate desiccation events by induction of protective mechanisms such as rod encystment. In agreement with this hypothesis, preliminary experiments using day/night cycles with continuous light provided by a cool white fluorescent lamp (SYLVANIA GRO-LUX®, 140 μE m⁻² s⁻¹) shows that strain TTB310 growth is greatly reduced during the light period. This phenomenon is associated with a morphological change of rod-shaped cells, which seem to be transformed into the more resistant cyst-like cells that quickly become dominant after light exposure. Due to the emission properties of this fluorescent lamp, which contains little red or far-red light, this suggests that some of the blue-light receptors described above could be involved in rod-shaped cell to cyst-like cell differentiation. Finally, the two bacteriochromes (Rta_25470, Rta_28950) could be involved in the synthesis of the strain TTB310 carotenoids [4], as demonstrated in D. radiodurans [45].

The Rta_04330 (KaiC ATPase)/Rta_04340 (Histidine Kinase) signalling pathway: an ancestral simple hourglass timing mechanism dedicated to anticipate night/day cycle?

Two genes (Rta_04330 and Rta_35460) encoding proteins similar to Synchococcus elongatus PCC7942 KaiC protein (SYNPCC7942_1216; SynKaiC) were found in the strain TTB310 genome (RtaKaiC). SynKaiC is the core component of a circadian clock that controls the cyclic expression of almost 30 to 64% of Synchococcus genes [46]; see [47–52] for recent reviews). Two other proteins, KaiA and KaiB, are important in the robustness of the Synchococcus clock. Indeed, oscillations in the phosphorylation state and more recently in the ATPase activity of KaiC have been proposed as the pacemaker of the circadian clock. These oscillations require the action of KaiA and KaiB, which enhance autokinase and autophosphatase activities of KaiC, respectively. A simplified timing system acting only as a 24 h timer, more like an hourglass than a clock, has been recently demonstrated in Prochlorococcus in the absence of KaiA protein [53]. Contrary to SynKaiC, ProKaiC is constitutively phosphorylated when incubated alone, and this activity is not modified by the addition of SynKaiA or KaiB from either species [54,55]. Although two copies of gene encoding core component of a circadian clock are present, surprisingly, neither kaiA nor kaiB homologs could be found in strain TTB310. However, based on the biochemical properties of the hourglass mechanism found in Prochlorococcus, we hypothesized a possible timing role of RtaKaiC, in the absence of both KaiA and KaiB partners.

To evaluate this hypothesis, we compared the gene context of kaiC in various prokaryotes (Fig. 4). Three kaiC-contexts were defined from the phylogenetic tree (Fig. 4 and Fig. S6). In the first kaiC-context («orange group»), kaiC-kaiB genes are clustered. Except for cyanobacteria, almost all show the presence of a histidine kinase or a GGDEF/EAL domains containing protein immediately downstream of a kaiC or kaiB gene (Fig. 4). A second kaiC-context («dark-blue groups») shows a simpler and highly conserved organization with kaiC followed systematically by a specific histidine kinase (HK) gene and the absence of kaiB gene elsewhere in the genome (Fig. 4). A more diverse kaiC-context («black group») exhibits a less conserved gene arrangement. The kaiC gene is frequently followed by a gene encoding a receiver protein or localized near a signaling protein (HK, GGDEF/EAL domains containing protein) (Fig. 4). These three kaiC-contexts are consistent with the phylogenetic tree of KaiC (Fig. S6). The phosphorylation capacity of KaiC also presents a similar pattern. Indeed, almost all the KaiC proteins of the first and second families exhibit phosphorylatable residues at the key positions necessary for their oscillatory activity (Fig. S7). In the third KaiC family («black groups»), only one (or none) phosphorylation site conservation is present with the exception of PSEEN2290 (SS profile) or NOC_1320, Caur_0239 and rrnAC0131 (SY profile) (Fig. S6 and S7).

It appears that almost all kaiC bacterial genes, with the exception of the cyanobacterial ones, occur near signaling proteins, more frequently upstream of histidine kinase encoding gene. The KaiC homologs unable to phosphorylate two residues, like Rta_35460, probably fail to sustain a cyclic timing mechanism. On the other hand, it is debatable whether KaiC homologs containing two phosphorylation sites, like Rta_04330, could potentially represent an hourglass timing mechanism, even in the absence of KaiB («dark-blue group»). In this family, the kaiC gene is systematically followed by histidine kinase (HK) encoding gene (Fig. 4). In the case of strain TTB310, RT-PCR experiments indicate that Rta_04330 and Rta_04340 are cotranscribed as part of a single operon (see materials and methods for details), suggesting that they are partners in the same regulatory pathway.

From the high sequence similarity of the N-terminal sensor domain (denoted RtnNt) of these histidine kinases, we defined a specific consensus sequence. RtnNt exhibits 19% identity (33% similarity, E-value 5e^-05) with the N-terminal receiver domain of a Thermosynechococcus elongatus BP-1 putative two-component response regulator. Moreover, chlstral alignment shows that RtnNt exhibits 16% identity (44% similarity) and 10% identity (40% similarity) with the cyanobacterial N-terminal sensor domain of the KaiC-Interacting sensory histidine kinase SasA and KaiB proteins, respectively. These two proteins are known to interact with SynKaiC, with SasA being the key player in the output pathway of the clock «signal». All these observations suggest that these HKs define a highly conserved KaiC-interacting specific sensory HK family, as does SasA protein in cyanobacteria, via the protein-protein interaction module RtnNt.

It is now necessary to demonstrate whether these KaiC «homologs» have a timing function and to search for the cellular processes controlled by this potential rudimentary hourglass, as recently suggested in the heterotrophic bacterium Pseudomonas putida [56], and in Legionella pneumophila [51]. In the case of strain TTB310, this predicted rudimentary hourglass could be used, in addition to light signals (see above), to anticipate water availability at the dew time in the middle/end of desert nights (winter) and thus direct the growth window to cyclic water availability times.

Conclusion

The resistance to desiccation of strain TTB310, a bacterium capable of cyst-division, represents a novel adaptation to drastically changing conditions in the desert environment. Strain TTB310 possesses a single circular chromosome of 4,070,194 bp, with the highest G+C content ever observed (70%) for a betaproteobacterial genome, encoding 3,899 predicted proteins (Table 1). DNA sequence annotation, using both bioinformatics and manual re-examination by experts in various molecular microbiology fields, shows that strain TTB310 uses both classical and special toolboxes for adaptation to desert life. Strain TTB310 is only equipped with a classical set of enzymes to adapt to various peroxide and superoxide stresses. However, we note the presence of genes encoding enzymes involved in carotenoid biosynthesis to quench ROS in the presence of light, as expected [4]. In the same way, the strain TTB310 genome encodes a complete set of classical enzymes known to be required for DNA replication, recombination, and for various DNA repair mechanisms, including photo-damage. Besides these «classical» enzymatic
Figure 4. Schematic representation of predicted KaiC genetic organization compared to cyanobacterial KaiABC-SasA «clock system». (SasA is found isolated in Cyanobacteria genomes). This representation is based on the phylogeny of predicted KaiC according to TULIP tree (Fig. S6). The first clustering corresponds to colour and KaiC-context group name (1st, 2nd, 3rd) according to the text and exhibits nature of the phosphorylation sites (ST, SS, SY, TY etc…). KaiC proteins (red colour) have been named according to their encoding gene position in database. KaiC neighbouring proteins were represented according to their proteic domain contents: HK, histidine kinase domain constituted of a HisKA and an HATPase_c domains; Rec, single domain receiver protein; PAS, PAS domain; PAC, PAC domain; GAF, GAF domain; GGDEF/EAL, GGDEF and EAL domains. For HK, the N-terminal, PAS, PAC or GAF domains have been replaced by blue-light colour (for details see Fig. S6). Nt_HK: HK with a N-terminal «orange» domain exhibiting similarities with cyanobacterial KaiB protein and kaiB-like N-terminal KaiC-interacting sensory HK SasA. Genes are not drawn on scale.

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Genomics of a Bacterium Adapted to Desert Life

Materials and Methods

Cultivation of cells and preparation of genomic DNA

*Rambhacter tataouinensis* TT3B310\(^T\) (strain TTB310) (described in [4] and available in public strain collection as strain DSM 14655\(^T\), ATCC BBA-407\(^T\) or LMG 21543\(^T\)) was cultured in tenfold diluted tryptic soy broth (TSB 1/10, Difco Laboratories). After incubation at 30°C for 72 h with shaking, the cells were harvested for 20 min at 15,000 g and subsequently washed in sterile distilled water. DNA from strain TT3B310 was prepared from 200 ml of cultures according to standard procedures [57]. The supernatant fluid was then subjected to a phenol/chloroform extraction and the DNA was recovered after ethanol precipitation.

Genome Sequencing

The sequencing of the strain TT3B310 genome was entirely executed by the Genoscope (Evry, France), using a conventional whole genome shotgun strategy [59]. Four libraries were constructed using different vectors and insert sizes. Three of them were prepared after genomic DNA fragmentation by mechanical shearing. The 3 kb (A, B) and 10 kb (C) fragments were cloned onto pcdna2.1 (A) (INVITROGEN) or pCNS (pSU18 derived) (B, C) vectors. A forth library were obtained using a BamHI partial digest of the genomic DNA and 20 kb inserts were introduced onto pBeloBac11 (D). Vector DNAs were purified and end-sequenced (31202 (A), 21867 (B), 18139 (C) and 6146 (D)) using dye-terminator chemistry on ABI3730 sequencers. A pre-assembly was made without repeat sequences as described by Vallenet et al. [59] using Phred/Phrap/Consed software package (www.phrap.org). The finishing step was achieved by primer walking, PCR and in vitro transposition technology (Template Generation System II Kit; Finnzyme, Espoo, Finland), corresponding to 1525, 219 and 228 additional reads, respectively. The strain TT3B310 nucleotide sequence and annotation data have been deposited at GenBank under accession number CP000245 (taxon ID 365046; project ID 35861).

Gene prediction and annotation

Protein-coding regions in the assembled genome sequence were identified using the gene prediction software FrameD [60] and AmiGene [61]. The results were combined and a search for common genes between the gene identification tools made it possible to eliminate redundancy. All predicted proteins larger than 20 amino acids were analysed for sequence similarity against protein databases (SWISSPROT, TREMBL and PIR). Similarity searches were carried out using BLASTP [62].

Annotation of the complete genome was performed using a bioinformatic tool allowing data management, developed in-house (P. Ortet and M. Barakat, unpublished data). Our tool allows an expert annotation by manual verification and curation of functional protein categories after automatic assignment.

Regions of the genome without CDSs, and CDSs without a database match are re-evaluated by using BLASTX as the initial search, and CDSs are extrapolated from regions of alignment.

Protein functional annotation was based on similarity searches against public databases and domain analysis with HMMER (Scan Eddy http://hmmer.wustl.edu/ 2001).

Functional classification was based on homology searches against the Clusters of Orthologous Groups of proteins (COGs, [63]); rRNA and tRNA genes were identified with BLASTN and tRNA-Scan.

Paralogous families were built as described in Bastien et al. [64]. Briefly, a random proteome database of strain TT3B310 was built. The longest sequences (>5 kb, 7 sequences) were removed to build up non-redundant proteomes. Each apparent protein of the non-redundant proteome of strain TT3B310 was compared to all the sequences of the corresponding random database, using the BLASTP algorithm [62] and the best alignment P-values were collected. From the distribution of the self-random P-values, a
0.99-percentile was set to define a cutoff. A Z-value was deduced and used as a cutoff value according to the TULIP theorem [65]. Then, the calculated cutoff was used as a criterion to partition the proteome owing to the single-linkage clustering method, using the SW algorithm [66]. We define paralogs as proteins sequences satisfying a Z-value cutoff of 18 and having at lest 30% sequence identity over more than 60% of their lengths.

Glycerolipids analysis
Glycerolipids have been extracted using organic solvents, and analysed by two-dimensional thin-layer chromatography coupled with methanolysis and gas chromatography, as previously described [67].

Analysis of the Carbohydrate-Active Enzyme encoding genes
All CDSs were compared, using gapped-BLAST [62] against a library of catalytic and ancillary modules covered by the sequence-based family classification Carbohydrate-Active Enzymes (CAZy) at URL: http://www.cazy.org [68,69]. The assignment to the various families of glycosidases and transglycosidases (hereafter referred to as glycoside hydrolase or GHs), glycosyltransferases (GTs), polysaccharide lyases (PLs), and ancillary carbohydrate-binding modules (CBMs), provides the foundation to the sequence and mechanism-based annotation of the carbohydrate-active enzyme-encoding genes [70]. This analysis, which integrates the frequent modular structure of this class of enzymes and the polyspecificity of many families, provides an insight into the metabolism of oligo- and polysaccharides by strain TTB310. The list of CDSs assigned to GHs and GTs families is provided in Table S2.

Analysis of transporter candidates
The annotation of transporter candidates was achieved with the bioinformatic strategy developed for the annotation of ABC transporters [71]. The method has been extended to other transport systems with the annotated transporters retrieved from TransportDB (http://www.membranetransport.org/) [72] and functional annotation was completed with the help of TGDB (http://www.tgdb.org/).

Cultivation of cells in light/dark cycles
Strain TTB310 was cultured in tenfold diluted tryptic soy broth (TSB 1/10, Difco Laboratories). After incubation at 30°C for 72 h with shaking in the dark, bacteria were spread on TSB 1/10 agar plates (1.5 g 1⁻¹) and cultured at 30°C in the dark or in light/dark conditions (12 h/12 h) in an incubator equipped with fluorescent lamp (Infors multilon 2). Continuous light was provided by cool white fluorescent lamps (SYLVANIA GRO-LUX®, 140 μE m⁻² s⁻¹). Every hour, a small piece of agar supporting one colony was cut to observe bacteria with a BX50 Olympus microscope equipped with a differential interference contrast (DIC) device and a 100× oil immersion objective (UPlanApo, Olympus) according to [6].

RNA isolation and RT-PCR
For analysis of Rta_04330 (1.488 kb) and Rta_35460 (1.515 kb) gene expression, cells were treated with RNAProtect Bacteria Reagent (Qiagen) prior to RNA isolation using the RNeasy Mini Kit (Qiagen) according to the manufacturer’s instructions. RNA samples were treated twice with DNase. For RT-PCR, cDNA was synthesized in 20 μL reactions using 1 μg of RNA and the Transcriptor First Strand cDNA Synthesis Kit (Roche). DNA fragments of 2.5 kb were then amplified in 25 μL reactions using 1 μL of cDNA from the first step, Taq polymerase (Sigma) and two primers designed in kaiC gene (Rta_04330: Rta_04330_Forward GCACTGTGCTGATTGCTG and at the end of the adjacent gene encoding an HK (Rta_04340: Rta_04340_Reverse GAG-GAAGTGGAAGTGCAAAGC), respectively. These amplifications were carried out by incubating reactions at 95°C for 5 min prior to 35 cycles of 30 s at 95°C, 30 s at 56°C and 2 min at 72°C, followed by a final step at 72°C for 2 min. Controls for DNA contamination were performed with reactions lacking reverse transcriptase. The amplification of a fragment of 2.5 kb corresponding to 1 kb of Rta_04330 and to the entire 1.5 kb length of Rta_04340, demonstrates that the two genes are co-expressed.

KaiC phylogenetic analysis
Rta_04330 and Rta_35460 were first aligned with SYNPCC7942_1216 (SynKaiC) with the Basic Local Alignment Search Tool software (BLAST: Align two or more sequences). Other KaiC sequences were retrieved from the non-redundant protein sequences database (nr: NCBI) with Rta_04330 as query and then aligned with the Multiple Sequence Alignment software CLUSTALW (Fig. S7). Cyanobacteria and Proteobacteria represents the most abundant KaiC containing phylogenetic groups. Therefore, we voluntarily excluded redundant sequences, mostly from Cyanobacteria and Proteobacteria, for a greater clarity of the representation. Classification of protein sequences was performed with the TULIP 1.1 server (http://malport.bi.xp.ac.za/TULIP/index.php) [65], and was based on pairwise alignments and following evolutionary assumptions, according to the TULIP theorem (Theorem of the Upper Limit of a score Probability). Input sequences were compared with the Smith-Waterman method using the following substitution matrix: blossum62.bl. Z-values were estimated after 1000 sequence randomizations. Proteins were classified using a distance matrix derived from Z-value probabilities. The resulting unrooted Tulp tree was drawn with the TreeDyn online software (http://www.phylogeny.fr) [73,74]. In this case, TULIP tree was consistent with phylogenies described by Dvornyk et al. [75] and Loza-Correa et al. [51]. The nature of the phosphorylable residues and of the neighbouring genes was added manually on the Fig. S6.

Supporting Information
Figure S1 Comparison of the Ramlibacter tataouinensis TTB310 genome against the closest proteobacterial genomes. Similarity searches were carried out between strain TTB310 and all the complete proteomes present in NCBI database, using BLASTP. The figure was generated with the results of the thirteen most similar genomes (12 betaproteobacteria, 1 alphaproteobacterium). Genomes are represented by successive circles made of coloured sticks representing individual genes. Color code of sticks: orange, strain TTB310 CDS forward; yellow: strain TTB310 CDS reverse; green: similar genes present and found in the same genomic environment in the other genomes (synteny); red: similar genes present in the other genomes. White holes represent an absence of similar genes in the other genomes. Names of the thirteen strains used for genome comparison classified from the inner (most similar) to the outside of the circle: Polarononas sp. JS666, Delftia acidovorans SPH-1, Acidovorax avenae subsp. citrulli AACC00-1, Polarononas napthalentivorans CJ2, Acidovorax sp. JS42, Leptothrix cholodnii SP-6, Methylbacterium petroleiphilum PM1, Rhodobacter furvusreducens T118, Azorarcus sp. BH72, Rhodinilus eutrophpha H16 chromosome 1, Bordetella petrii DSM 12804, Burkholderia xenovorans LB400 chromosome 1, Baudyshizobium sp. ORS278. (TIFF)
Figure S2  Genes of Ramlibacter tataouinensis TTB310 potentially involved in peroxide scavenging pathways. (TIFF)

Figure S3  Glycolipid composition of Ramlibacter tataouinensis TTB310 membranes. PE, phosphatidylethanolamine, PC, phosphatidylcholine, PG, phosphatidylglycerol, DPG, diphosphatidylglycerol, PI, phosphoinositides. Glycolipids (100 µg) were resolved by two-dimensional thin layer chromatography (first dimension, chloroform/methanol/water 65:25:4; second dimension, chloroform/aceton/water 40:40:20:10) and visualized after 8-anilino-1-naphthalenesulfonic acid spray. (TIFF)

Figure S4  Biosynthesis of even- and odd-numbered, straight and branched chain fatty acids from acetyl-CoA, propionyl-CoA and branched chain amino acids derivatives as starting units in Ramlibacter tataouinensis TTB310. Determining steps for the distribution of fatty acid molecular species in the final profile include the branched chain amino acid transaminase (bbt) cluster and the β-ketoacyl-ACP synthase III (fabH). (TIFF)

Figure S5  DNA-binding proteins in Ramlibacter tataouinensis TTB310. This figure represents the distribution of the transcription factors found in R. tataouinensis. (TIFF)

Figure S6  Representation of prokaryotic predicted KaiC proteins according to (1) their TULIP tree position, (2) nature of their phosphorylable sites and (3) their genetic organization. Proteins were classified using a distance matrix derived from Z-value probabilities (see Materials and Methods). We have integrated the RecA protein [Rta_37450, 351 residues] as an outgroup and two archaeal KaiC single domain proteins (SSO1861, 280 residues; SSO2452, 262 residues) recently classified as archaerial RadC and thought to be implicated in DNA repair [77]. (ST) represents the nature of the conserved KaiC phosphorylation sites residues (S, serine; T, threonine; Y, tyrosine; F, phenylalanine; A, alanine; L, leucine; H, histidine; D, aspartic acid). KaiC neighbouring proteins were represented according to their protein domain contents: REC, single domain receiver protein; Ni_PAS-PAC_GAF_HK_REC, hybrid histidine kinase with N-terminal domain composed of a N-terminal region, one PAS, one GAF and one GAF domains; PAS_2PAC_GGDEF_EAL, protein containing one PAS, two GAC and one GAF domains. HP, Hypothetical Protein. Ni_HK: HK with an «orange» N-terminal domain exhibiting similarities with cyano bacterial KaiB protein and kaiB-like N-terminal KaiC-interacting sensory HK SasA (see text). Orange branches represent kaiC genes (ST or SS) localized in the vicinity of a kaiB gene. Deep-Blue branches represent kaiC genes (SY, TY, SF) localized upstream a conserved specific histidine kinase designated Ni_HK (see above and text). Light-blue branches represent kaiC genes (SY, NV, SP, SH) branched with deep-blue family, but included in the «third black family» (see text). Black branches represent kaiC genes with poorly conserved phosphorylation sites (SS, SA, SF, AF, DY, SL ...) and more heterogeneous organization. α, β, γ, δ, ε represent α, β, γ, δ, and ε-Proteobacteria. KaiCα1, KaiCα2, KaiCα3 indicate that the strain «α» contains 3 different KaiC copies called 1a, 2a and 3a. (TIFF)

Figure S7  Sequence alignment of KaiC proteins centered on SynKaiC phosphorylable residues (T426, S431 and T432). Conserved T, ST are red coloured, S replacing T are green coloured, Y replacing T are blue coloured, T replacing S are pink coloured and other replacement with a non phosphorylatable residue are italicized. KaiC proteins exhibiting one or several replacements with a non phosphorylatable residue are in bold. RukKaiC are underlined. Cyanobacteria; α, β, γ, δ, ε represent α, β, γ, δ, and ε-Proteobacteria. (TIFF)

Table S1  Genes involved in autotrophic dicarboxylate/hydroxybutyrate cycle (carbohydrate metabolism), energetic metabolism, dissipative nitrate reduction and cofactors and vitamins synthesis in Ramlibacter tataouinensis TTB310. Note that: i) ATP is generated by classical and complete oxidative phosphorylation including the five complexes [complex I (NADH ubiquinone oxidoreductase), complex II (fumarate reductase/succinate dehydrogenase), complex III (cytochrome b6f), complex IV (cytochrome oxidase), and complex V], plus two additional oxidases [one additional cytochrome oxidase, and one cytochrome d (bd-I) ubiquinone oxidase, known to function at low oxygen concentration in Escherichia coli], ii) enzymes for complete denitrification and dinitrogen reduction are absent, and iii) key enzymes for the biosynthesis of thiamine, pantothenate and biotin are missing, confirming the growth factor requirement of this bacterium [4]. (XLS)

Table S2  Carbohydrate-active enzymes (CAZymes) found in Ramlibacter tataouinensis TTB310. Note that this table contains: i) a list of CAZymes found in strain TTB310, ii) a comparison of CAZymes from strain TTB310 against seven betaproteobacterial genomes, and iii) a list of exported and potentially secreted glycosyl hydrolases. (XLS)

Table S3  Fatty acid composition of each membrane glycolipid class extracted from Ramlibacter tataouinensis TTB310 cells. PE, phosphatidylethanolamine, PC, phosphatidylcholine, PG, phosphatidylglycerol, DPG, diphosphatidylglycerol, PI, phosphoinositol, FA, fatty acid. (DOC)

Table S4  Characteristics of cell envelope transport systems in Ramlibacter tataouinensis TTB310. This table contains genes involved in: general export pathway (Sec translocation, SRP insertion and Tat translocation pathways, including predicted Tat substrates), Outer Membrane Protein (OMP) insertion machinery, Outer Membrane (OM) lipoproteins synthesis (including Predicted lipoproteins), type I, type II and type III secretion systems, and type IV pilus machinery. (XLS)

Table S5  Additional signal transduction, regulator and bifunctional proteins in Ramlibacter tataouinensis TTB310. (DOC)

Text S1  Experimental conditions for live optical imaging of Ramlibacter tataouinensis TTB310 (video S1). (DOC)

Video S1  Live optical imaging of Ramlibacter tataouinensis TTB310 exhibiting both “cyst-to-rod” division step (in the middle of the screen) and “rod-to-rod” division (last images) (See Text S1 for details). (AVI)

Author Contributions
Conceived and designed the experiments: GDL MB IM EM JW TH. Performed the experiments: GDL MB SF IM VB. Analyzed the data:
GDL MB PO SO CJ MA BP GF PMC RV OB EM BH YQ PN AF VM
MSD FB IM AV WA TH. Contributed reagents/materials/analysis tools: PO MB PMC BH GF YQ. Wrote the paper: GDL MB AV TH.

References


