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Thank you for your assistance.
The nature of the metabolic network is a fundamental aspect of pathogenic lifestyles. Brucella spp. are the intracellular pathogens responsible for chronic infections of mammals. Here we review new insights on the links between Brucella virulence and metabolism. Understanding of Brucella metabolic abilities will help to decipher its infectious strategies.
Review

Brucella adaptation and survival at the crossroad of metabolism and virulence

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ABSTRACT

“In vivo” bacterial nutrition, i.e. the nature of the metabolic network and substrate(s) used by bacteria within their host, is a fundamental aspect of pathogenic or symbiotic lifestyles. A typical example are the Brucella spp., facultative intracellular pathogens responsible for chronic infections of animals and humans. Their virulence relies on their ability to modulate immune response and the physiology of host cells, but the fine-tuning of their metabolism in the host during infection appears increasingly crucial. Here we review new insights on the links between Brucella virulence and metabolism, pointing out the need to investigate both aspects to decipher Brucella infectious strategies.

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1. Introduction

In order to successfully colonize a host, symbiotic and pathogenic bacteria have to be able to occupy specific metabolic niches within their host. Indeed, it is becoming more and more obvious that the sensing of available carbon source(s) and the related metabolic adaptations are intimately linked to the coordinated expression of other virulence determinants, such as colonization factors. However with the exception of some recent progress on model bacteria, the mechanistic basis for this coordination is still frustratingly poorly understood. Here, we review the current on the links existing between metabolism and virulence of a particular intracellular pathogen: Brucella.

1.1. Brucella, a nasty Mr “Hides”

Brucella spp. are Gram-negative intracellular pathogens phylogenetically related to plant symbionts such as the Rhizobiaceae. Often referred as “nasty bugs” because of their unusual virulence features, or as “Mr Hides”, in reference to their stealthy ability to evade immune detection, they are major zoonotic pathogens, as they are able to induce chronic infections of both animals and humans. In Latin America alone, the annual economic loss in animal production from brucellosis has been estimated to be more than $600.000.000. During the last few decades, efforts to solve the complex jigsaw puzzle of Brucella virulence have focused on “classical” virulence factors, or bacterial factors that interact directly with components of the host. Despite an increasing knowledge of the molecular strategies used by this pathogen to interact with host cells during its infectious cycle, we are still far from understanding it. Moreover, a new piece of this puzzle, long forgotten, has come into view: bacterial metabolism.

2. Brucella virulence and metabolism: two sides of the same coin

The global picture emerging from what is known about Brucella virulence is an extremely efficient adaptation to shield itself from immune recognition and to manipulate key aspects of host cell physiology, for example apoptosis and vacuolar trafficking. It has also become increasingly evident, though still poorly considered, that one of the keys to successful in vivo adaptation of a pathogen is its ability to fine-tune the metabolism to utilize specific nutrients encountered in each niche occupied by Brucella during the infectious cycle.

One aspect of the physiology of the Brucellae that is particularly poorly understood is the architecture and regulation of central metabolic pathways. According to pioneering biochemical investigations, as well as more recent genomic data, hexoses can be catabolized through the pentose–phosphate (PP) pathway and an incomplete Embden–Meyerhof–Parnas glycolytic pathway (EMP), as Brucellae seem to lack a phosphofructokinase. However, in some cases, functions predicted from genomic analysis do not agree with results from biochemical analysis of metabolic function in vivo. For example, while genomic analysis indicated that Brucellae carry two genes predicted to encode enzymes of the Entner–Doudoroff (ED) pathway (gluconate-6-phosphate dehydratase and 2-keto-3-deoxygluconate aldolase), no gluconate-6-phosphate
dehydratase activity could be detected in vitro [19]. This is also true for the two enzymes of the glyoxylate shunt (isocitrate lyase and malate synthase), whose activity has never been demonstrated. Hexoses can be further metabolized through what appears to be a fully active triarboxylic acid cycle (TCA) [19]. Nevertheless, it bears mentioning that hexoses are not the favoured carbon sources for the three best characterized Brucella species: B. abortus, B. melitensis and B. suis. Instead, these bacteria preferentially utilize a four carbon sugar alcohol (erythritol) [20], the catabolism of which yields one triose phosphate [21]. In summary, the actual picture of the central metabolic network of Brucella spp. appears to be: (i) active PP and TCA cycles, (ii) potentially active ED and glyoxylate pathways (iii) an interrupted EMP. It should be kept in mind that the above description reflects what is known about the most thoroughly investigated three main Brucella species. As new genomic sequences become available, species differences in this metabolic network will certainly emerge as illustrated, for example, by the pseudogenization in B. ovis of some genes of the erythritol catabolic and transport operons or of the phosphoenolpyruvate carboxykinase (pckA) gene involved in the first step of gluconeogenesis [22]. While these differences are likely to be of interest to understanding species differences between the Brucellae, due to the limited biochemical characterization of these additional species we will focus our review on three best characterized Brucella species.

The information above outlines the potential “architecture” of the central metabolic network of Brucellae. However, from this “blueprint”, we can glean little about the functional metabolic pathways and nothing about the potential of Brucellae to adapt their metabolism to conditions in the host. However, the first clues on the nature of the in vivo metabolism of Brucella were provided by the identification of attenuated mutant strains.

2.1. Metabolic mutants are frequent among attenuated mutants

Previous studies, aiming to identify virulence factors in B. abortus or B. melitensis by screening for transpositional mutants attenuated in the cellular or the mouse model of infection, revealed a link between persistence of Brucella in its hosts and its metabolism [23,24]. Indeed, several systems for transport and degradation of carbohydrates appear to be essential for Brucella survival. Transporters whose predicted function is uptake of amino acids or peptides also appear to be required during infection. These findings suggest that carbohydrates, but also amino acids and peptides, could be available as energy and/or carbon sources at some points during the infectious process.

It can be expected that some of these carbon sources are likely metabolized through the PP pathway, since among the attenuated metabolic mutants, several are impaired in a gene encoding an enzyme of this pathway (see Fig. 1, boxes n°6). This is consistent with the fact that Brucella seems to lack a phosphofructokinase, for a “classical” glycolysis EMP [18]. The PP pathway is consequently suspected to be crucial for sugar degradation in addition to being essential for the generation of biomass precursors such as ribose required for de novo synthesis of purines and pyrimidines [25–27]. In addition, mutants in global regulators affecting metabolism are attenuated, emphasizing the fact that Brucella has to adapt its metabolic functions (including its central metabolism) for a successful infection. For example, B. melitensis and B. suis rsh mutants with an impaired stringent response are severely attenuated [28]. It has been recently shown in alpha-proteobacteria closely related to Brucella (namely Sinorhizobium meliloti and Rhizobium etli) that the stringent response to nitrogen or carbon limitation not only regulates expression of genes encoding bio-synthetic or catabolic pathways (protein, amino acids, nucleotides, and lipids) but has also an impact on expression of genes encoding the functions of central metabolism (PP and EMP pathways as well as TCA cycle) [29,30]. Furthermore, three mutants in the Brucella Phosphoenolpyruvate-carbohydrate-phosphotransferase system (PTS) are also impaired in their virulence [25] (see below). Similar mutants in S.melloti were affected in their carbon metabolism and in their ability to cope with nutritional stress [31].

2.2. A profound and progressive adaptation of central metabolism occurs as Brucella enters and persists in its intracellular niche

Two recent studies further illustrate the central metabolic adaptation performed by Brucella during intracellular infection. In the first one, the proteome of B. suis was analyzed in [174] macropahges at 48 h post infection (PI) and compared to the proteome of B. suis at the early stationary phase in a rich medium [32]. The majority of the 44 differentially produced proteins are involved in the primary metabolism (metabolism strictly needed for survival) of Brucella, among which nine are related to the central metabolism (see Fig. 1, boxes 1). The results suggest that at 48 h PI Brucella had a restricted glycolytic activity and an increase in gluconeogenesis. Moreover isocitrate lyase (AceA) and malate synthase (AceB), two enzymes belonging to the glyoxylate shunt, were upregulated [32]. The glyoxylate shunt acts as an anaplerotic pathway for the Krebs cycle, providing succinate and malate from acetoyl-CoA and isocitrate. Usually, a functional glyoxylate shunt allows bacteria to grow on fatty acids, which might thus become an important carbon source for B. suis during infection, as has been reported for Mycobacterium tuberculosis [33].

The second study adds a temporal dimension to the physiologic adaptation. Using RAW 264.7 macrophages, Lamontagne et al. performed a proteome analysis on B. abortus at three time points: 3 h PI (when the bacteria are internalized but have not yet reached the replicative niche), 20 h PI (when they have escaped the initial microbicial “burden” and started an active replication) and 44 h PI (when they reached the maximum of their intracellular number) [17]. Ninety proteins were differentially produced in B. abortus and most of them took part in primary metabolism, of which seven are involved in the central metabolism (see Fig. 1 for the 3 h time point boxes 7). The reduced production of enzymes of central carbon metabolism (TCA cycle, pyruvate and PP pathway), and of sugar uptake transport systems suggests that there is a limited sugar supply at the beginning of infection. At this time, amino acid catabolism feeding the TCA could be the privileged alternative to derive the needed precursors. At later time points, once in the ER derived compartment, the PP pathway would be active suggesting a resupplying of sugars [17].

Thus, these in vivo experiments revealing dynamic metabolic adaptations during cellular infection, were particularly valuable, since they unmasked a metabolic flexibility that could not have been predicted using classical in vitro growth conditions.

2.3. Major virulence regulators act as metabolic regulators “and vice versa”

The metabolic adaptations described above allow Brucella to withstand the wide array of environmental conditions existing within a host and its cells. In response to the conditions encountered at each specific stage of the infectious cycle, a tight and coordinated fine-tuning of gene expression is needed while unnecessary (or no longer needed) functions are accordingly switched off. Expression of virulence genes is usually governed by signaling pathways and regulatory mechanisms similar to those that control genes that are not specific to pathogenesis. These signaling pathways are often based on reversible phosphorylation of proteins (two component system or phosphoenolpyruvate dependent sugar
phosphotransfer system) or specialized global regulators acting either at an individual cell or at a population level.

2.3.1. The critical BvrS/R two component system

The BvrS/R two component system (TCS) is a signaling pathway consisting of a membrane-bound histidine kinase (BvrS) and its corresponding response regulator (BvrR). Following the sensing of a (still unknown) specific environmental stimulus, BvrS autophosphorylates on a conserved histidine residue and mediates the transfer of the phosphoryl group to a conserved aspartate of BvrR. The latter coordinates the cellular response, through differential expression of target genes. The BvrS/R TCS is essential for virulence. Transpositional inactivation leads to defects in attachment, invasion, and intracellular replication [34]. A recent transcriptomic analysis revealed a clear impact of the bvrR mutation on the expression of genes related to carbohydrates, amino acids, fatty acids and nitrogen metabolism [35]. Among the genes up-regulated in the bvrR mutant are the phosphoenolpyruvate carboxykinase (pckA) encoding the first enzyme in gluconeogenesis, and four genes involved in TCA cycle and pyruvate metabolism (see Fig. 1, boxes 3).

Fig. 1. Regulations of *Brucella* central metabolism in various conditions (see numbers in boxes). In green (boxes and arrows), up-regulations; in red (boxes and arrows), down-regulations; in grey, attenuated mutants. P: proteomic data, T: transcriptomic data. Pgi, phosphoglucoisomerase; Fbpase, fructose-1,6-biphosphatase; Ald, aldolase; Tpi, triose phosphate isomerase; Gapdh, glyceraldehyde-3-phosphate dehydrogenase; Gpm, phosphoglycerate mutase; Eno, enolase; Pyk, pyruvate kinase; Pck, PEP carboxykinase; Pdc, pyruvate dehydrogenase; AcsA, Acetyl coenzyme A synthetase; Cs, citrate synthase; Acon, aconitase; Idh, isocitrate dehydrogenase; Akgdh, 2-oxoglutarate dehydrogenase; Stk, succinyl-CoA synthetase; Sdh, succinate dehydrogenase; Fum, fumarase; Maldh, malate dehydrogenase; Lac, lactate; Gpm, phosphoglycerate mutase; Pck, PEP carboxykinase; Pdc, pyruvate dehydrogenase; AcsA, Acetyl coenzyme A synthetase; Cs, citrate synthase; Acon, aconitase; Idh, isocitrate dehydrogenase; Akgdh, 2-oxoglutarate dehydrogenase; Stk, succinyl-CoA synthetase; Sdh, succinate dehydrogenase; Fum, fumarase; Maldh, malate dehydrogenase; Lac, lactate.
299 phosphoenolpyruvate (PEP), this system usually consists of two
missing link
2.3.3. The phosphoenolpyruvate phosphotransferase system (PTS) – a
regulatory systems appear to be connected, since BvrR has an acti-
vating effect on central metabolic processes. No growth delay for
the bacteria in minimal medium [35], thus reinforcing the link between this TCS
and S. meliloti metabolism. Whether the effects of bvrR transposi-
tional mutation on the cell envelope (Omp and transporters) is
the consequence or the cause of these growth defects remain to
be investigated by identifying the direct targets of the regulator.
The potential link of this TCS with the metabolism will be
discussed further below in parallel with the Phosphotransferase
System (PTS).

2.3.2. Quorum sensing and starvation sensing
Quorum sensing (QS) is a regulatory system that allows bacteria
to coordinate gene expression at the population level according
to the local bacterial cell density through the individual synthesis and
sensing of diffusible signal molecules. Quorum sensing is also
known to be involved in the regulation of Brucella virulence deter-
minants mostly linked to the cell surface (Type IV secretion sys-
tem, flagellum, outer membrane proteins and exopolysaccharide).
[39–41]. Surprisingly, recent transcriptomic and proteomic analy-
ses have put forward that inactivation of vjbR and babR, two Qs
regulators, has a strong impact on genes involved in metabolism
and particularly on genes encoding enzymes of the TCA cycle and
glycolysis [Fig. 1, boxes 4 and 5 respectively] [42,43]. Interestingly,
VjbR and BabR regulate overlapping sets of target genes in an
opposing manner, suggesting that QS could have a global reorgani-
zation effect on central metabolic processes. No growth delay for
the vjbR and babR mutant strains could be observed though liquid
or solid culture in rich media. However, differences in growth of
these mutants were reported in defined media, depending on the
available carbon source.

Placed into an intracellular context, in the vacuole, sensing a
"Quorum" for Brucella could mean sensing limited diffusion due to
space limitation. That corresponds to "starvation sensing". It can
be suggested that QS is directly or indirectly involved in adjusting
the metabolism of Brucella. Indeed, by slowing down Brucella basic
metabolism, QS (through VjbR) would prevent multiplication until
the ER-derived replicative compartment is reached. Subsequently,
the BabR regulator could play a role in reactivating the basal metab-
olism. A similar proposal was made for the BvsR/TCS [17,35]. Thus,
both the BvsR/R TCS and the QS system could contribute to the adap-
tation of the metabolic network during the nutrient shift faced by
Brucella all along its intracellular trafficking continuum. These two
regulatory systems appear to be connected, since BvrR has an acti-
vating effect on vjbR transcription [35,44]. However, it is not yet
known whether this activation is direct or whether it is mediated
through other global starvation sensing mechanisms like the stringent response [28] and/or the PTS system [45].

2.3.3. The phosphoenolpyruvate phosphotransferase system (PTS) – a
missing link
PTS systems are widespread among bacteria. Activated by
phosphoenolpyruvate (PEP), this system usually consists of two
cytoplasmic energy-coupling proteins (Enzyme I and HPr) as well as
several carbohydrate-specific Enzymes II, which catalyze con-
comitant carbohydrate translocation and phosphorylation [46].
The phosphorylation status of PTS components reflects both the
availability of carbohydrates and the energy conditions of the cell.
In many bacteria, PTS and their associated proteins convert this
information to signals, which are then transduced through differ-
ent mechanisms (allosteric interactions, phosphorylation) and
lead to phenomena including catabolite repression and inducer control
[46,47]. The PTS provides bacteria with an integrated system that
ensures optimal utilization of carbohydrates in complex environ-
ments, a feature that is particularly important in host–bacteria
interaction [1,48,49]. In place of a classical PTS, some bacteria have
evolved parallel systems that serve strictly regulatory functions.
Among such systems are the so-called "Nitrogen PTS", which are
thought to link carbon and nitrogen metabolisms but do not
appear to catalyze substrate transport, as they lack the PTS
permeases [50–53]. Brucella spp., A. tumefaciens, S. meliloti and
other α-proteobacteria possess a Nitrogen PTS system, and their
respective pts mutants were previously shown to be impaired for
interaction with the host [25,54,55].

In all pathogenic or symbiotic α-proteobacteria, three pts genes
(hpr, ptsM and ptsO) are located downstream of the conserved
two-component system genes (bvsR/S, exoA/chvI) essential for
infection or symbiosis [34,38]. This conserved genomic organiza-
tion suggests a functional link between BvrR/PTS and the PTS
[53,56]. Recently two papers substantiated this link by showing [i] that the above mentioned pts genes are co-transcribed with
the bvsR/S genes [45] and (ii) that the hpr gene is downregulated in the bvrR-Tn5 mutant [35]. In addition, a proteomic study with a
B. abortus bvrR mutant [57] revealed that Brucella regulates the 2-oxo-
glutarate dehydrogenase complex that converts 2-oxoglutarate
into succinyl-CoA in the TCA cycle. The subunit SuccA of the same
enzyme was recently shown to interact with the PTS Elia [36].
The type III secretion system proteins encoded by ptsM itself located at the specific conserved locus previously mentioned [45]. Both bvrR and pts mutants have an
unaltered growth in liquid rich media but display a restricted or
abolished growth on minimal medium with defined carbon
source(s) [35,45]. These findings support the hypothesis that the
Brucella PTS senses the metabolic state of the cell (by sensing among others the ratio of PEP/pyruvate and the fructose 1,6-
biphosphate) leading to a coordinated regulation of C and N
metabolisms and as well as some key virulence genes (e.g. the virB
operon [45], flagellar genes . . .). This probably involves cross-talk
with the two-component system BvsR/S. Interestingly, both the
bvrR and one pts mutant (ptsP) seem to share the ability to regulate
the expression of the QS regulator VjbR, which in turn regulates
determinants of virulence and metabolism (see above).

3. What is NOT known about the central metabolism of
Brucella: challenges for the ongoing century
Of course, this paper is not an exhaustive review of all the links
connecting virulence and metabolism of Brucella. Our focus being
mainly the central metabolism, we omitted some known links
(i.e. the recent identification of the virB gene regulator Hutc [58]
or the role of the stringent response in regulating the crucial type
IV secretion system [28]. In the near future other connections
will likely be discovered. A major breakthrough will certainly come
from the newly evolving field of RNA based regulation. Long con-
sidered only as informative macromolecules, small RNAs (sRNAs)
are increasingly recognized as important regulators of gene
expression allowing the rapid adaptation of cell growth in response
to stress and changes in the environment. These sRNAs post-
transcriptionally modulate gene expression, mostly through
base-pairing with target mRNAs, thereby regulating relative levels of translation or decay [59]. In addition, messenger RNAs themselves can act as direct sensors of the physical or metabolic state of the cell via their 5’-untranslated (5’-UTR) region that undergoes structural changes upon metabolite binding (riboswitch). The conformational alteration of the mRNA structure affects the expression of the downstream transcript [60]. Altogether, these RNAs are widespread in bacteria and regulate metabolic pathways, carbon source utilization and the composition of the membrane [61]. Moreover, their direct or indirect involvement in the regulation of virulence genes and host-pathogen relationship is becoming more and more clear [62,63].

With regard to the implication of these sRNA on Brucella metabolism or virulence, this is almost “terra incognita.” Nevertheless, owing to the recognized role of Hfq in facilitating the action of sRNA and the importance of this RNA binding protein in Brucella adaptation [64] the chances are high that Brucella RNA regulation will be brought to the center stage as has recently been the case for other intracellular bacterial pathogens such as Listeria monocytogenes [65,66] or Legionella pneumophila [67]. Nevertheless some basic questions, concerning the functioning of Brucella metabolism, still remain to be investigated:

What parts of the central metabolic network are functional, and under which conditions?

Why is erythritol a preferred carbon source for Brucella?

How is catabolite repression (if any) mediated in Brucella?

Why is erythritol a preferred carbon source for Brucella under which conditions?

What is the metabolic network and/or its regulation responsible of the host specificity of Brucella strains?

And to a greater extent, how has the intracellular lifestyle of Brucella influenced the design of its metabolic network?

Undeniably, we are looking at bacterial physiology and host bacteria interactions is rapidly evolving in the «omics» era. In the near future, new approaches such as metabolomics [68] or 13C-isotopologue-profiling analysis [2] will lead to an increased understanding of the Brucella metabolic plasticity both in vitro and during cellular infection. This will yield new insights on Brucella virulence and will, potentially, open new prophylactic avenues.

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