Salmonella enterica: a surprisingly well-adapted intracellular lifestyle

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INTRODUCTION
Salmonella enterica serovar Typhimurium (S. Typhimurium) is an important human gastrointestinal pathogen with an invasive and facultative intracellular lifestyle (Neidhardt, 1996; Eisenreich et al., 2010). Among the various habitats that can be colonized by Salmonella, the adaptation to life inside the host cell is of specific interest, since this ability is considered as crucial for systemic infections with fatal outcome. The World Health Organization estimated 1.4 million cases of non-typhoidal Salmonella infections with fatal outcome. The World Health Organization estimated 1.4 million cases of non-typhoidal Salmonella infections. Furthermore, these cause 580 deaths annually even in the United States (World Health Organization, 2005). Infections are often associated with selected subgroups as elderly or patients suffering from HIV and connective tissue disorders (Cummings et al., 2010).

Throughout the intracellular life, Salmonella remains in a membrane-bound compartment, which is termed Salmonella-containing vacuole or SCV. The SCV is probably a unique compartment that is formed by the combined action of a large number of bacterial virulence factors (Figure 1). Virulent Salmonellae are able to modify this vacuole in order to escape killing in the endocytic pathway, and to proliferate within host cells (Haraga et al., 2008). The ability to survive and replicate within host cells is closely related to the systemic pathogenesis of Salmonella in a murine model of typhoid fever. Mutant strains defective in intracellular replication due to auxotrophies are also attenuated in virulence in an animal murine model of typhoid fever (Fields et al., 1986). Salmonella is able to rapidly multiply in various eukaryotic cell lines, but the proliferation appears to be far less rapid within cells in tissues of infected hosts, indicating a more restrictive situation in vivo (Mastroeni et al., 2009). The SCV is commonly considered as a nutritional deprived environment, and this notion is based on the phenotypes of auxotrophic strains, analyses of bacterial reporter strains, and microarray analyses. However, the fact that Salmonella replicates within the SCV indicates the successful adaptation to this intracellular environment.

Despite the remarkable increase in understanding of the cellular microbiology of Salmonella infections and the molecular functions of virulence factors required for intracellular life, the nutritional basis of life of Salmonella within the SCV is still not completely understood.

Understanding how Salmonella survives and thrives within this compartment and how nutrients are acquired is not only essential for the understanding of the intracellular lifestyle, but might as well open new avenues to therapeutic interference with Salmonella infections.

METHODS AND APPROACHES TO GET INSIGHTS INTO INTRACELLULAR NUTRITION
To target metabolism of intracellular Salmonella, several approaches have been established covering in vitro approaches from analyzing simple growth behavior in full or minimal medium and changes in morphology (Paterson et al., 2009), intracellular replication ability (Bowden et al., 2009, 2010) to more complex transcriptome analysis (Eriksson et al., 2010) or 13C-isotopolog profiling analysis (13C-IPA; Götz and Goebel, 2010) in a cell culture model. Experiments to test if a gene of interest contributes to virulence are mainly done in macrophage cell lines as strains unable to replicate within macrophages proved to be avirulent (Fields et al., 1986). In addition, epithelial cell infection models.
The intracellular replication ability of Salmonella isolated from infected mice (recovered from cecum and spleen) has been performed (Becker et al., 2006) providing information about the essential metabolic enzymes and pathways. Data on metabolite levels would provide important complementary information, but are often difficult to obtain for intracellular bacteria and require complex experimental setups. Another complementary approach is proteome analysis, a modern technique to directly determine enzyme type and amount as well as modifications (e.g., regulatory phosphorylation of metabolic enzymes).

The fact that there may be differences between results obtained by in vitro and in vivo approaches does not render data from in vitro experiments questionable. The data may very well be reliable (i.e., reproducible) and of importance for understanding of a limiting number of specific factors. The differences in results from in vivo analyses can best be explained by the presence of a large number of additional factors (immune responses, different concentration gradients of nutrients in different tissues, cytokines, etc.) that are often interrelated and affect pathogen survival and replication in host tissue. For example, comparing experimental evidence including proteomics, metabolomics, and survival data on mutants with in vivo and in vitro conditions, conflicting results can be observed for mutant strains of Salmonella with defects in enzymes of the tricarboxylic acid (TCA) cycle. The mutant strains showed even increased replication in a murine RAW macrophage cell line, but were highly reduced in virulence in an animal model (Bowden et al., 2010).

As they are easier to study and analyze, cell culture models for Salmonella infections will remain the essential basis for the understanding of the cellular and molecular changes and mechanisms of the intracellular bacterial nutrition. Cell culture experiments are less complex and laborious than animal experiments and offer the possibility to study such important aspects of intracellular nutrition as access of Salmonella to host cell nutrients or to nutrients in extracellular medium. Attenuation of certain mutant strains can be directly linked to the lack of a certain metabolite in the extracellular medium. For example, comparing experimental data on metabolite levels would provide important complementing information about the essential metabolic enzymes and pathways.
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**FIGURE 2** | Principles of isotopolog profiling with labeled \([U-^{13}C_6]\) glucose. The fate of labeled glucose via different metabolic routes can be followed by isotopolog profiling in analyzing resulting metabolites or products (in this case amino acids). An example is given for the biosynthetic routes of the two aspartate isotopologs \(^{13}C_2\)-aspartate and \(^{13}C_3\)-aspartate (represented by orange and blue arrows, respectively) and the origin of a \(^{13}C_3\)-alanine. Isotopolog studies are described in Eisenreich et al. (2006), Eylert et al. (2008), and Eylert et al. (2010). \(^{13}C\)-atoms are marked in red and indicated by an asterisk.

Listeria and Salmonella enterica use glucose as a carbon source, with differences in their metabolic pathways. For example, Listeria the enzyme 2-oxoglutarate dehydrogenase is missing (Glaser et al., 2001; Eisenreich et al., 2006), so oxaloacetate is formed by carboxylation of \(C_3\) compounds like pyruvate and the anaplerotic enzyme pyruvate carboxylase becomes crucial (Schar et al., 2010). De novo synthesized listerial amino acids are Ala, Asp, Glu, Ser, Thr, Val, and Gly (Eisenreich et al., 2010), indicating that other amino acids are taken up in the host cell cytoplasm (Schauer et al., 2010).

For comparison, Legionella pneumophila, a gram-negative intracellular pathogen and causative agent for Legionnaire’s disease, was long time supposed to feed solely on amino acids while residing in the host alveolar macrophages (Tesch and Miller, 1981). Indeed, the amino acids Cys, Gln, Ser, and Arg are efficiently used as carbon and energy sources in vivo (Wieland et al., 2005). However, recent studies highlight that also glucose is metabolized by Legionella during infection of eukaryotic cells. In contrast to Salmonella, Legionella predominantly degrades glucose by the 2-keto-3-deoxy-phosphogluconate pathway (KDPGP) and only in small quantities by glycolysis. The non-oxidative branch of PPP also accounts for small amounts of glucose catabolism (Harada et al., 2010). \(^{14}C\)-IPA further revealed that there is no evidence for a functional glyoxylate bypass (Eylert et al., 2010), confirming earlier models built on genome sequence analysis (Cazalet et al., 2004). Furthermore, \(^{13}C\)-IPA results indicate that a complete and active TCA cycle occurs in Legionella and that the inability to synthesize amino acids \textit{de novo} is only valid for Ile, Leu, Val, Phe, Met, Arg, and Tyr.

**COMPUTATIONAL AND SYSTEM BIOLOGICAL ANALYSES OF THE METABOLISM OF INTRACELLULAR SALMONELLA**

A number of recent studies highlight the importance of system biological modeling of Salmonella during infection (Romain, 2009b; McDermott et al., 2011). Besides the genome information, the analysis of the pathogen proteomes during infection provides
an important basis for infection research, as well as for devising novel control strategies including antibiotics and vaccines (Bunnemann, 2009a). On this, independent models for Salmonella metabolism are built (Becker et al., 2006; AbuOun et al., 2009; Raghunathan et al., 2009; Eisenreich et al., 2010). In such models the flow of metabolites is modeled in terms of pathways. Enzyme chains are calculated such that metabolites are balanced, i.e., consumed and produced in equilibrium, this is called flux balance analysis (FBA). If such a chain of metabolic enzymes cannot be dissected any further, this is named an elementary mode. Helpful software tools include the COBRA Toolbox (Schellenberger et al., 2011) and YANAsquare (Schwarz et al., 2007) which can compile available biochemical and genome data systematically and calculate flux distributions by FBA or elementary mode analysis (EMA). Specific tools such as the KEGG browser (Schwarz et al., 2007) simplify the direct import of available biochemical data into metabolic network reconstructions even on genome-scale basis. Furthermore, metabolic gaps and dubious annotations for enzymes of central metabolism often occur and therefore different genome annotation software and comparisons are strongly recommended to improve the network reconstruction (Gaudermann et al., 2006).

Recently, a community effort towards a knowledge-base and mathematical model of S. Typhimurium strain LT2 has been initiated, resulting in the BiGG knowledge-base of Salmonella metabolism (Thiele et al., 2011). A consensus metabolic reconstruction was obtained from two independently developed (Ruppin et al., 2010) metabolic reconstructions for S. Typhimurium. The joined reconstruction effort included, furthermore, the development and implementation of a community-based workflow for annotation and corrections including incorporation of thermodynamic information (to decide on reversible and irreversible reactions). By this, metabolite transporters and reactions are more accurately identified and considered. Higher reliable consensus models improve, furthermore, the potential of multi-target drug therapy approaches for specific strains though of course the host response is another important factor to consider.

Our metabolic modeling approach calculating elementary flux modes on central carbon and amino acid metabolism in S. Typhimurium indicates that the anaplerotic reactions around phosphoenolpyruvate (PEP) to oxaloacetate are pivotal and occur in many flux modes. For modeling growth on glucose as the sole C-source, PEP carboxylase (ppc) plays a central role in directing the flux from the TCA cycle. However, disruption of PEP carboxylase can be partly compensated by alternative routes in the network regarding carbohydrate metabolism. A ppc-deficient mutant showed no reduced virulence in vivo (Tchawa Yimka et al., 2006), indicating the availability of further C-sources such as amino acids which, through transaminase reactions, also can feed into the TCA cycle. This would give support to a model that contains both glucose and amino acids as C-sources. Here, the flux through PEP carboxylase decreases and the flux through PEP carboxykinase (pckA) increased, compared to a medium with only glucose. PEP carboxykinase catalyzes a reaction in the opposite direction of the normal flow cycle, i.e., increasing the flow from oxaloacetate to PEP. The direct conversion of oxaloacetate to aspartate cannot be easily compensated by alternative flux modes. Transaminase activity can be compensated, for instance, loss of two transaminases (aspC and tyrB) is required before aspartate auxotrophy appears. Moreover, aspartate can also be acquired from the host. However, the production and availability of oxaloacetate is critical, requiring increased PEP carboxylase activity or a reversal of the flow from oxaloacetate to aspartate. This and similar other modeling results suggest that amino acid metabolism is easier impaired and more critical in the SCV than in intracytoplasmic survival (Schauer et al., 2010).

Flux balance analysis and EMA calculate metabolic pathways but the integration of experimental "omics" data allows to better determine metabolic flux strengths (Coevert et al., 2004). Tools have thus recently been developed that help to integrate experimental data into metabolic models such as YANAsquare (Li et al., 2011) fit experimental flux measurements, enzyme activities, gene expression data (Cecil et al., 2011), as well as extracellular metabolite ratios to computational predictions.

Due to the intracellular lifestyle, the host provides further nutrients by transporters (Figure 3). Overall, there is an intensive exchange of metabolites during growth in the host cell. Game theoretical approaches treat such interdependencies in a novel mathematical way showing advantages as well as limitations for any specific survival strategy (bacterial pathogen) or opposing strategy from the host (Ruppin et al., 2010; Schauer et al., 2010b, 2011). This becomes even more important as the robust Salmonella metabolism including its redundant, overlapping pathway organization limits possibilities for new antimicrobials interfering with its metabolic processes (Becker et al., 2006). Moreover, the potential of central carbon metabolism as a target for microbial defense depends on the environmental factors of the specific niche and the genetic and phenotypic traits of infecting bacteria. For instance, in dormant sub-populations, or “persisters,” the uptake of glucose, mannitol, or fructose implies a direct influence in preparatory steps of glycolysis. This potentiates the killing by aminoglycosides (Allison et al., 2011). Thus, for an iterative refinement of computational modeling the integration of transporter reactions (Raghunathan et al., 2009) and a strain-specific analysis (Li et al., 2011) is crucial. In this regard, a global gene expression analysis of S. Typhimurium (Harvey et al., 2011) during colonization of the chicken’s cecal lumen and cecal mucosa demonstrates very specific Salmonella metabolic adaptations to its environment. For comparison, differences in expression of transporters and in the usage of C-sources regarding three specific niches (cecal lumen, mucosal wall, and the SCV in macrophages and epithelial cells) are illustrated in Figure 3.

**THE ROLE OF CENTRAL CARBON METABOLISM PATHWAYS DURING INTRACELLULAR SURVIVAL**

Salmonella is in fact a pathogen with a very broad and versatile metabolism and as already seen by its comparatively large genome, is a generalist among gram-negative bacteria (Figure 4). For instance, Salmonella can easily metabolize glucose combining various pathways to supply both energy and amino acids and the same applies for most nutrient sources.

Furthermore, the combination of different pathways guarantees a fine-tuned balance of internal metabolites. Due to this redundancy it is not easy to block growth of Salmonella by...
The role of catabolism of glucose

There are three routes for the catabolism of glucose: (i) glycolysis, (ii) the PPP, and (iii) the Entner-Doudoroff pathway also known as the KDPGP. The two latter pathways for glucose utilization seem to be of lesser importance for *Salmonella*. A *Salmonella* mutant strain deficient in *zwf* (encoding glucose-6-phosphate dehydrogenase), catalyzing the first step of both PPP and KDPGP, and a double mutant strain in *gnd* (PPP) and *edd* (KDPGP), or a double mutant in *gnd* (PPP) and *edd* (KDPGP) are not attenuated in proliferation in the murine macrophage cell line RAW 264.7 (own unpublished results). Nevertheless, it was reported that a *zwf* mutant shows reduced virulence in a mouse model of systemic infection (Lundberg et al., 1999). This group refers to the importance of NADPH production in the PPP which is used as electron donor for reductases required for oxidative stress response. However, we think that in our cell culture models the superoxide levels should be less high than in the mouse infection model and this may explain the decreased need for such reductases and for NADPH. Other important PPP products like ribose used for nucleoside synthesis can still be produced by the non-oxidative part of PPP. We suggest that PPP and KDPGP play no important role if glucose is the major substrate. Isotopolog profiling experiments in CaCo-2 cells showed that the internalized glucose is mainly converted by glycolysis and/or KDPGP pathway and excluded PPP as a major route for glucose catabolism (Götz and Goebel, 2010). *Salmonella* studied in epithelial cell lines are significantly less challenged with reactive oxygen intermediates (ROI) and reactive nitrogen intermediates (RNI) responses, hence, the generation of NADPH would be less important than in an animal model. In particular, the activity of the PPP may become
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**FIGURE 4** | Salmonella central carbon metabolism. Shown are genes and enzymes of the central carbon metabolism covering glycolysis, PPP, KDPG cycle, Entner–Doudoroff pathway, oxidative carbon fixation, TCA cycle, and anaplerotic reactions. Boxes represent metabolites, arrows indicate enzyme reactions. Metabolites and enzymes are colored according to the color of their pathway name. Arrows are directed according flux direction under glucose metabolism but may vary under different conditions. Detailed information on importance of the illustrated pathways in intracellular infection is outlined in the text including behavior of an array of different enzyme mutations. 1,3pg, 1,3-bisphospho-D-glycerate; 2pg, 2-phospho-D-glycerate; 3pg, 3-phospho-D-glycerate; 6pg, 6-phospho-D-gluconate; αkg, α-ketoglutarate; ac-coa, acetyl-CoA; cit, citrate; dha, dihydroxyacetone phosphate; e4p, D-erythrose-4-phosphate; f1,6bp, fructose-1,6-bisphosphate; f6p, D-fructose-6-phosphate; fum, fumarate; gap, D-glyceraldehyde-3-phosphate; glyox, glyoxylate; icit, isocitrate; kdpg, 2-dehydro-3-deoxy-D-gluconate-6-phosphate; mal, (S)-malate; mg, methylglyoxal; pep, phosphoenolpyruvate; pyr, pyruvate; r5p, D-ribose-5-phosphate; ru5p, D-ribulose-5-phosphate; s7p, D-sedoheptulose-7-phosphate; suc, succinate; suc-coa, succinyl-CoA; x5p, D-xylulose-5-phosphate.

Important if Salmonella is challenged with higher degrees of oxidative stress.

The significance of glucose as one of the major C-sources, and glycolysis as the main route for utilization has recently been shown (Bowden et al., 2009). Extending the set of glycolysis mutant strains analyzed by Bowden et al. (2009), work in our group showed that eno, fba, pgk, gapA, or tpiA deficient strains are strongly attenuated in intracellular replication and survival in RAW 264.7 cells (unpublished results). In case of a tpiA mutant it was demonstrated that reduced growth in rich medium (lysogeny broth, LB) and decreased fitness in mice seems to depend on accumulation of the toxic electrophile methylglyoxal from accumulated dihydroxyacetone phosphate by reaction of the methylglyoxal synthetase (Paterson et al., 2009). Overproduction of methylglyoxal as a result of tpiA mutation for E. coli has been shown before (Cooper and Anderson, 1970; Cooper, 1984) and although the concentration is lower in the tpiA mutant of Salmonella, it still leads to reduced growth in medium and lower fitness in mice (Paterson et al., 2009). Mutant strains deficient in eno, fba, gapA, or pgk show similar growth characteristics in medium containing just traces of glucose or other C-sources ending up in glycolytic intermediates, e.g., in LB or minimal medium containing ribose. None of these mutant strains was able to grow in these media, but growth was observed on minimal medium with glycerol or PEP.
The TCA cycle plays an important role as a source for precursors for anabolic pathways, e.g., amino acids, and reducing agents used as electron donors in the respiratory chain or for biosynthesis. Due to this central role, it is obvious that in the last years research efforts were stimulated by these questions (Eisenreich et al., 2010; Götz and Goebel, 2010). However, to what extent can the SCV be reached from outside? Are there macrophage-specific strategies of adaptation? A number of recent efforts were stimulated by these questions (Eriksson et al., 2003; Becker et al., 2006; Bowden et al., 2009; Götz and Goebel, 2010) and gene knockout strategies as well as metabolite measurements and modeling were applied to better understand Salmonella life inside the cell.

Limitation of magnesium, phosphate, and iron occur as genes for their uptake are up-regulated in Salmonella during infection. By gene expression analysis it could also be shown that glycolysis, KDPGP, and TCA cycle are highly expressed in SCV of macrophages and epithelial cells (Hautefort et al., 2008). In contrast, gluconeogenesis is not required for a full virulent phenotype in mice (Tchawa Yimga et al., 2006).

The role of the TCA cycle and anaplerotic reactions

The TCA cycle provides a platform for the metabolism of all sugars used during infection. The environmental and nutritional conditions encountered by Salmonella within the SCV are still a matter of debate. In the process of SCV formation an acidification of the intravacuolar environment takes place (Rathman et al., 1996). Salmonella metabolism during infection adapts to this intracellular lifestyle in the host cell. It is regulated by different transcription factors (Eisenreich et al., 2010; Götz and Goebel, 2010). However, to what extent can the SCV be reached from outside? Are there macrophage-specific strategies of adaptation? A number of recent efforts were stimulated by these questions (Eriksson et al., 2003; Becker et al., 2006; Bowden et al., 2009; Götz and Goebel, 2010) and gene knockout strategies as well as metabolite measurements and modeling were applied to better understand Salmonella life inside the cell.

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In a number of reports, the nutrient-poor, underfed conditions of the SCV were stressed (Eriksson et al., 2003; Ibarra et al., 2009). This applies even more for the early phases of the infection. Furthermore, detailed studies suggest that intracellular Salmonella deploys specific mechanisms to redirect vacuolar transport to make use of host-derived nutrients (Rahile et al., 2006; Drecktrah et al., 2007; Rajashekar et al., 2008).

Direct comparison of intracellular lifestyles of bacterial pathogens such as Salmonella and Legionella that reside within a membrane-bound compartment, to those with survival and replication within the cytoplasm of host cells is of interest. For the latter, survival depends on the availability of cytoplasmic host cell metabolites and tight regulation is necessary such as by the pathogenicity factor PhoP in Listeria (Fukert et al., 2008) to survive surprisingly poor nutritional conditions (Eriksson et al., 2003; Ibarra et al., 2009). For the Salmonella lifestyle in the SCV, also strong metabolic adaptations are necessary, in particular regarding how abundant nutrients and ions, however, carbohydrates are not that limiting. The survival under these different conditions of intracellular life in the host cell indicates successful adaptation to different metabolic limitations.

The expression of virulence factors by Salmonella does not come without a price. For example, in a recent study retarded growth of S. Typhimurium cells expressing the type III secretion system 1 (T3SS-1) compared to the minus phenotype was observed and the effects on growth kinetics were modeled (Sturm et al., 2011). Growth retardation was at least partially attributable to the expression of the T3SS-1 effector and/or translocation proteins. In spite of this growth penalty, the T3SS-1(+)-subpopulation increased from <10% to approximately 60% during the late logarithmic growth phase of an LB batch culture. As shown by experimental data and mathematical modeling, this was attributable to an increasing initiation rate of expression of T3SS-1 genes, in response to environmental cues accumulating during this growth phase. The key is here to mathematically describe the whole system, correctly quantify responses and obtain results from the model which agree with observation. Such models and methods can, furthermore, also be transferred to better understand other genetic variations pertaining, for instance, to effector proteins and estimate the cost of virulence regarding growth and metabolism. Such systems biology approaches to Salmonella lifestyle and pathogenicity are expected to grow (Helaine et al., 2010).

Furthermore, a number of technical developments contributed to the understanding of bacterial metabolism during infection. The modeling of genome-scale metabolic networks is now feasible, originally pioneered by the Palsson group (Price et al., 2004a). However, even with strong computational power at hand, detailed modeling requires additional methods to handle the combinatorial explosion of different pathways concerned, for instance, by dividing the metabolic network (Schuster et al., 2002) or sampling averages over high numbers of different modes (Price et al., 2004b). Furthermore, a number of recent developments tackle new software solutions for metabolic modeling including modifications of extreme pathway analysis (Kalten et al., 2009; Schuster et al., 2010a). Moreover, the analysis of isotopolog data profits from advances in software development (Nanchen et al., 2007). Achieving gene knockout combinations experimentally has been advanced technically (Datsonko and Wanner, 2000; Gerlach et al., 2009) and this has been complemented by in silico prediction studies on gene knockouts agreeing well with these experiments. This can also be applied to study survival during infection (Raghunathan et al., 2009).

**IMPLICATIONS AND CONCLUSIONS**

Pathogenicity can arise from a bacterial specialization where intrinsic cellular functions are especially adapted to the host’s environment such as in exclusive human pathogens like Mycobacterium tuberculosis (Moller and Hoal, 2010), Neisseria gonorrhoeae (Cass and Seifert, 2012), N. meningitides (Cass and Seifert, 2012), and Mycoplasma pneumoniae (Dumke et al., 2011). In contrast, Salmonella is a surprisingly successful intracellular pathogen that is less specialized but rather a generalist with an extraordinary metabolic versatility. Furthermore, E. coli, Pseudomonas spp., Klebsiella spp., and further bacteria are common pathogens with a similar metabolic background which are not highly specialized for a specific host environment.

To underline this, a broad spectrum of central carbon metabolism routes constitutes the repertoire of the Salmonella lifecycle (Figure 4). Glucose, the predominant C-source during SCV colonization can either be degraded in the glycolytic pathway or the KDPG route, the former one preferentially used. The TCA cycle as the major biosynthetic origin of precursor and provider of reductive agents is complete and is supported by important anaerobic reactions that lead the metabolic flux to the TCA cycle, mainly by the PEP carboxylase. However, this enzyme can be compensated by other flux modes as shown by EMA. In systemic infections, the PPP generates NADPH required for reductases in oxidative stress response. Salmonella is well-equipped to rapidly adapt to various environments during the passage through the host’s body.

The flexible metabolic abilities of Salmonella make it challenging to elucidate targets to inhibit metabolic functions during infection. The pathogen efficiently modifies its unique vacuolar compartment for its benefits. Additionally, the transport of nutrients to the SCV in response of Salmonella effector proteins is currently under investigation. Host-pathogen metabolism is intertwined.

Is there an Achilles’ heel of Salmonella metabolism in infection? To answer this we suggest a combination of a thorough analysis of central metabolic enzymes such as mutant phenotypes of glycolytic enzymes with systematic analysis such as transporter expression profiles, strain-specific analysis, and projecting those on the very specific environmental conditions under study. Thus, the loss of pyruvate dehydrogenase may have an influence on the expression of virulence genes important for ROI defense. Further, mutants with a defect in the TCA cycle showed reduced virulence in a murine infection model. In Salmonella, the TSS-2 is responsible for translocation of over 20 virulence proteins into the host cell cytoplasm (Haraga et al., 2008). SFA is probably the most prominent among these effectors in maintaining the integrity of the SCV and induction of extensive networks of tubular membrane compartments including Salmonella-induced...
filaments and recently identified further tubular compartment (Schoeder et al., 2011).

Future work will take up the challenge of this surprisingly well-adapted pathogen by looking more closely at the host-pathogen interaction, not only regarding metabolic interactions for further pathways including secondary metabolism, iso-enzymes, and intercellular links between pathways (including supplementation experiments), but also regarding the regulatory and immune response from the host, for instance, potential immune modifiers as novel approaches to boost host response in severe infections by Salmonella. Infections disease burden in developing countries will doubtlessly profit from improved hygiene and clean water supply but also protective nutrient additives (e.g., vitamins; golden rice, and similar recent developments) and regarding trace elements such as selenium. Challenges in industrialized countries include persistent infection which can again be coped with metabolic approaches relying, for instance, on elicitors of growth which in turn make the previous persist Salmonella vulnerable to standard antibiotics. In general, the exploration of the link between metabolism and infection has to be explored further to improve medical options against Salmonella.

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