RNAs in the Acid Tolerance Response and Virulence of *Salmonella*

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*Calmonellaentericas*erovarTyphimurium is a major enteric pathogen **U** capable of causing severe gastroenteritis as well as systemic infections. The intestinal tracts of a diverse range of domestic and wild animals serve as a reservoir for Salmonella and consequently infection mainly occurs through the consumption of food and water contaminated with animal waste. This species is responsible for 93.8 million cases of gastroenteritis (80.3 million estimated food-borne), with 155,000 deaths (Majowicz et al., 2010). Salmonella spp. are able to survive a variety of stress conditions (pH, high osmolarity, low oxygen tension and bile salts) in their environmental niche, the gastrointestinal tract and the Salmonella containing vacuole(SCV) within macrophages, reflecting the adaptability of these pathogens. Following ingestion, Salmonella traverse the intestinal epitheliumutilizing a mechanism encoded by the horizontally acquired Salmonella Pathogenicity Island 1 (SPI1) type 3 secretion system (T3SS). In immunocompromised patients, Salmonella are able to cause typhoid like fever owing to their ability to replicate within macrophages. This survival is mediated by Salmonella Pathogenicity Island 2 (SPI2) genes encoding another T3SS(Fàbrega & Vila, 2013).

The adaptive response of Salmonella to acid stress conditions termed the Acid Tolerance Response (ATR) is vital to their ability to survive and ultimately cause infection. The ATR received attention through pioneering work by Foster and Hall (J. W. Foster & Hall, 1990; J. Foster, 1991, 1993) and defines a system that induces resistance to normally lethal pH, termed as acid challenge, following growth under mild acid exposure, termed as acid adaptation. This response could enhance survival of the bacteria in acidic foods as well as increase survival to harsher pH in the stomach and SCV. Depending on the growth phase, the ATR could be induced either during the log phase or the stationary phase both of which are functionally distinct. The log phase ATR was first described by shifting log-phase S. Typhimurium cells grown at pH 7.6, to mild acid (pH5.8, adjusted with hydrochloric acid) for one doubling and subsequent challenge at lethal pH (pH3.3, adjusted with hydrochloric acid). Subsequent studies utilized the same procedure while varying the pH values and exposure times for adaptation and challenge (J.

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Foster, 1993, Wilmes-riesenberg, Bearson, & Foster, 1996, (Baik, Bearson, Dunbar, & Foster, 1996; Bang, Kim, Foster, & Park, 2000). The stationary phase ATR was induced by growing overnight cultures to attain a final pH of 7.4 to 4.3 followed by challenge at pH 3.0(Lin, Lee, Frey, Slonczewski, & Foster, 1995). It was observed that stationary phase cells allowed to grow at a pH<5.0, showed significantly better survival than those adapted at higher pH values.

Salmonella have long served as model organisms for studying pathogenesis, virulence, gene regulation and evolution with most of the focus on proteins and their involvement. However, it is only of recent that Salmonella has come to the fore as a model organism for studying non-coding RNA mediated regulation. The diverse families non-coding RNAs may fall into include small RNAs (sRNAs) that are regulatory in nature, cis-regulatory elements (riboswitches and thermometers) and RNAs that bind to and interact with proteins. It is only in the last two decades that sRNAs have started to gain momentum as important regulators in diverse species. They range in size from 50 to 500 nucleotides, do not contain expressed open reading frames (ORFs) and are largely conserved in related species. They bring about their regulatory effects either by binding (cis or trans) to target mRNA and affecting their translation/stability, or by directly binding to proteins and modulating their activity (Altuvia, 2007). Translational repression is brought about by blocking of the ribosome binding site due to sRNA binding and activation, by unraveling of secondary structure that inhibit ribosome binding.

Both, acid tolerance and virulence are essential to the efficient survival and propagation of Salmonella in a host. Various protein coding genes involved in the ATR have also been shown to be essential for virulence such as the Mg²⁺ proton translocating ATPase encoded by atp. Consequently an atp mutant was found to be avirulent(Garcia-del Portillo, Foster, & Finlay, 1993). Similarly, atrC and fur mutants were found to be less virulent as compared to their wildtypes (Wilmes-riesenberg et al., 1996). Similar studies in Listeria monocytogeneshave shown that some acid tolerant mutants displayed increased virulence when compared to their wild-type(Hill, 1996).Additionally, the glutamate decarboxylase (GAD) system has also been shown to be important for both low pH survival and overall virulence. Similarly, several sRNAs have been shown to be involved in response to acid stress, with probable roles in virulence as well. For example, in E.colithe DsrAsRNA is a well known acid resistance regulator, with probable roles in virulence (Lease, Smith, Mcdonough, & Belfort, 2004). Other sRNAssuch as RprA, ArcZ and GcvB have also been shown to play similar roles with still more (IsrM, IsrC, IsrE) being implicated in virulence (Tracy, Gaida, & Papoutsakis, 2010). The link between the different acid tolerance systems and virulence should further be examined particularly in the case of enteric pathogens and with a focus on sRNA regulators involved. This would help provide a clear picture on the regulatory circuits that play roles in survival and pathogenesis.

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