



Review Paper

Prevalence of *Salmonella* spp. in raw vegetables and fruits and their plant contamination routes: a review

Hiral S. Raval^{*} and Alkesh I. Shah

Department of Zoology, B.P. Baria Science Institute, Navsari, Gujarat, India
hiralraval31@gmail.com

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Abstract

Raw vegetables and fruits are essential ingredients of healthful nourishment and necessity for salad vegetables and fruits have become greater than before as vegetables and fruits act as antioxidants and immune boosters. In conflict to their health profits, it is observed by scientists that utility of raw vegetables and fruits have also been connected with the risk of disease if consume draw. Some *Salmonella* spp. contain virulence plasmid (pSV) which encodes *spv* operon are capable to adhere with plant surfaces by using T3SS and vigorously infect the core of plants by defeating immune response of plants as equally as animal cells, *Salmonella* spp. defeat plant defence mechanisms, shows that *Salmonella* possess a variety of infection strategy including *agfD* gene which is responsible for infecting variety of host from different kingdoms, which arise questions of *Salmonella* host specificity. The purpose of review study is to discuss and gain depth knowledge of routes and infection pattern of *Salmonella* with contrast to plant physiology, microbiological physiology, environmental interrelationship, crop processing, crop handling mechanisms along with crop cultivation methodology that provides opportunity for contamination will lead us to develop foolproof reliable policies, trustworthy standard operating procedures and infallible technologies for reducing the risk of contamination.

Keywords: *Salmonella* prevalence, plant contamination, host specificity, immune response, virulence plasmid.

Introduction

Raw vegetables and fruits are significant factors of a nourishing as well as stable diet; their ingestion is promoted by health authorities of many countries to protect citizens from diseases. Though, vegetables and fruits, which are consumed raw, are increasingly being known as crucial vehicles for spreading of human pathogens which are conventionally connected with foods from an animal source. In spite of extended prominence of raw crops as a agent for *Salmonella* spp., there is presently inadequate awareness about where in the resource sequence contamination arises or about the appliance through which human pathogens colonize and persist on or in vegetables and fruits. It is also potential that the testified rise in the number of sicknesses linked with ingestion of fresh crop echoes a factual rise in contamination¹.

Sivapalasingam² had observed that the fraction of food-borne outbreak-related sicknesses linked with raw crops raised from 1% to 12% within a duration of two decades. He had also observed *Salmonella* was frequently recorded bacterial pathogen, guilty for nearly half of epidemics due to bacteria. Extensive variety of crop vehicles have been linked to *Salmonella* spp. contamination along with this he had recorded fluctuations in crop treatment and distribution exercises which may also have enlarged hazard of enhanced broad epidemics.

Bacteria were guilty of 60% in crop linked epidemics in the USA for almost two decades².

In 2007, *Salmonella* was found around 0.3% from crop related specimens analyzed in the European Union, had been surveyed by Westrell³. Enormous researches on the prevalence of *Salmonella* spp. from vegetables and fruits were operated in the UK, Ireland, Germany, and the Netherlands in 2007 surveyed by Westrell³. Numerous epidemics related to ingestion of tomatoes have been studied by Hedberg⁴, Cummings⁵, Gupta⁶ and melons studied by Gayler⁷, Mohle-Boetani⁸, Bowen⁹, Munnoch¹⁰. Pagadala¹¹ in 2015 reported that human infections connected with ingestion of raw vegetables and fruits have been predictable as a potential for transmission of *Salmonella* spp. Centres for Disease Control and Prevention reported raw vegetables and fruits were vehicles for a large multistate outbreak of *Salmonella*¹².

Schikora¹³ observed *Salmonella* spp. is the foremost reason for food contamination and these bacteria can magnificently colonize animals, humans, and plants. *Salmonella*-related with spinach and green vegetable salad affected at least 430 individuals in northern Europe studied by Denny¹⁴. Nonetheless, findings had shown that ¼ of food poisoning epidemics could be related to the ingestion of *Salmonella* spp. Infected vegetables or fruits¹⁵. In precise, *Salmonella* spp. Infected

tomatoes were found to spread multistate and worldwide epidemics¹⁶⁻¹⁹. Kumar²⁰ found that 7.8% of salad vegetables sheltered by *Salmonella spp.*

In this manuscript, I review the existing data and promising imminent improvements in this progressively considerable field of food protection.

Salmonella-plant contamination routes

Hamilton²¹ had suggested water is expected to be a significant resource of contamination in the crop cultivation area and found that probable sources are overspill from adjacent animal fodders and irrigation from an infected source. The hazard linked with consuming water from a variety of supplies that fluctuate in bacteriological quality for irrigation of crop has been evaluated and the necessity for amended strategies realized by Tyrrel²². They also indicate a poorer possibility of spreading *Salmonella spp.* from contaminated water by drip irrigation against a greater possibility by overhead nozzle systems^{21,22}.

Nevertheless, Sivapalasingam²³ during his study observed irrigation is not the alone described path of infection connected to water. Usage of water in postharvest handling has similarly participated a task of contamination. An epidemic of infections with *Salmonella spp.* was correlated to ingestion of mangoes treated with hot water for preventing fruit flies²³.

Pathogens may be relocated to the atmosphere by the appliance of inefficiently processed or raw animal composts suggested by Beuchat²⁴, Roever²⁵, Natvig²⁶, Santamaria and Toranzos²⁷. The faeces of wild animals can similarly ensure a cause was observed by Rice²⁸ and Ackers²⁹. Jay³⁰ had studied the derives yielded by Pulsed-Field Gel Electrophoresis and Multilocus Variable Number Tandem Repeat Analysis (MLVNTRA) and concluded the *Salmonella spp.* participating in the epidemic corresponded those from isolates regained from regional undomesticated pig and livestock faeces.

Insects are similarly a probable cause of contamination, flies have been revealed to immediately transfer bacteria to plant leaves or fruits was observed in an individual experiment carried out by Iwasa³¹, Sela³² and Talley³³. Recommended sources of contamination of vegetables and fruits involved the usage of dropped fruit that has remained in interaction through contaminated soil, water, sewage or manure, use of contaminated water, and contamination at the point of consumption reported by Vojdani³⁴.

Though we are not enough rich with knowledge of contamination routes till date, this encourages us to do some revolutionary research in this field which may lead us to improve present agricultural practices especially organic farming, if we succeed in this then it will almost solve said problem of contamination and we may able to challenge the ecological fitness of *Salmonella* to overcome any future epidemics resulted by this organism.

Mechanism of Salmonella adhesion to plant

Beuchat and Scouten³⁵ reported adhesion is mandatory for colonization and consequent spread of pathogens by the eatable fragments of plants, once adhere it is too challenging to eradicate the pathogens from contaminated vegetables and fruits through ordinary washing. *Salmonella spp.* can colonize seeds observed by Mahon³⁶, Winthrop³⁷, sprouted seeds reported by O'Mahony³⁸, leaves reported by Campbell³⁹, Horby⁴⁰, and fruit observed by Mohle-Boetani⁹, Guo⁴¹ of a variety of plant species.

Barak et al.⁴² in 2005 reported that the *agf* B encoded pilus curli show a crucial role in adhesion *Salmonella spp.* Though, they similarly observed *agfB* removal did not inhibit leaf attachment entirely, demonstrating that additional adhesins expected to show responsibility. Barak⁴² in 2005 concluded 65% of the *Salmonella spp.* genes recognized as possibly participating in bacterial adhesion to plant tissue have no earlier stated utility, which indicates the significance of studying bacterial interrelations among subordinate hosts, such as plants, subsequently many *Salmonella spp.* genes might show a superior role in persistence in nature or on subordinate hosts than they perform in virulence in animals.

Remarkably, in 2006 Gibson et al.⁴³ reported curli, cellulose, and capsule are controlled by *AgfD* which might show a foremost function in ecological suitability of *Salmonella spp.* In 2007 further experiments carried out by Barak et al.⁴⁴ have revealed that the *yihO* encoded O antigen capsule and the *bcs* A encoded cellulose synthesis also show a function in adhesion of *Salmonella spp.* *AgfD*, which was also recognized to play not just a dominant function to adhere to plant exteriors, but similarly for ecological suitability and pathogenicity of the bacteria concerning animals^{44,45}.

In 2007 Jonas et al.⁴⁶ observed curli and cellulose have remained unfailingly noticed to establish a cellular matrix, which grants development of biofilms and certain genes recognized to code for the *agfB* and for the universal shock organizer *rpoS* which controls the assembly of curli, cellulose and other adhesins that are significant for animal pathogen city also. In *Salmonella spp.* *rpoS*, the common shock governor, is a universal mechanism obligatory for *Salmonella spp.* pathogen city in animals, Which shows a prominent function in biofilm development⁴⁷, like in the regulation of *agfD*⁴⁸, another adhesins⁴⁹, and supplementary genes^{49,50}.

Salmonella spp. genes mandatory for pathogen city in animals are similarly mandatory for adhesion to plant tissue. These consequences enhance tactics for bacterial capability in involvement with eukaryotic hosts that are developing in animal and plant pathogens^{51,52} by indicating that curli and gene yields controlled by *rpoS* are mandatory for *Salmonella spp.* adhesion to plant tissue.

The dissimilarity between host-restricted and generalist *Salmonella spp.* is the existence of the *Salmonella* virulence

plasmid (*pSV*). A small fraction of the *Salmonella spp.* contain *pSV* which encodes the *spv* operon, which shows a function in the manifestation of the virulence to specific hosts⁵³⁻⁵⁷. Despite numerous common properties shared by the *pSVs* of diverse serovars, each plasmid appears to be specific to its bacterial host, showed by a distinctive plasmid size in different serovars⁵⁸. Injury of the *spv* region destroys the virulence phenotype of the serovars in their animal hosts^{54,55,59}.

Beside this the insertion of a *pSV* to a serovar that is inherently lacking it does not rise the virulence assets of the strain⁶⁰⁻⁶², indicating that another chromosomally encoded components are causative agents for the virulence phenotype. Latest experiments have proved that *Salmonella* can interact precisely with plants, showing that plants can function as unconventional hosts⁶³. Numerous raw vegetables and fruits have been involved in *Salmonella* infection, most frequently lettuce, sprouted seeds, melons, and tomatoes⁶⁴.

It is observed by scientists numerous aspects participating in infection of animals are also obligatory for effective contamination of plants, including T3SS that modify host cell responses, and suppression of the host immune response^{65,66}. A. schikora⁶⁶ in 2011 concluded that *Salmonella* propagation in plants do not modify pathogen city for animal cells and plants react to *Salmonella spp.* Damage through initiation of protective genes. Heals observed T3SSs are mandatory for virulence for animals and plants. Experiments on the invasion of tomato plants have revealed that *Salmonella* can colonize rising fruits. When tomato plants were inoculated by inoculating stems or scrubbing flowers with *Salmonella*, the bacteria continued viable throughout fruit development, surviving within the ripened fruit^{41,67}.

It is hence appropriate confirmation that the genetic apparatus of *Salmonella*, earlier assumed to be animal specific, shows a significant function in infection of animals and plants alike. *Salmonella spp.* had shown a relationship between the ability to yield bio films and the adhesion to leaves, yielding the toughest biofilms and exhibiting the utmost proficient adhesion to lettuce leaves⁶⁸.

Salmonella spp. was found to form biofilm-like structures on the exterior of roots, favourably colonizing areas adjacent evolving horizontal roots and injured tissues^{69,13}. Recently, three reports showed the probable entrance objectives of bacteria to the internal layers of leaves⁷⁰⁻⁷² and it was suggested that trichomes are most favoured colonization part of plants⁷⁰. It was revealed that *Salmonella* uses stomata as an entrance objective in a direction to invade lettuce leaves⁷².

Investigations on different vegetable and fruit plants revealed noteworthy variances in the sensibility to *Salmonella* contamination^{70,73}, indicating a significant role of plant inherent immunity in amending the response to contamination by these bacteria. *Salmonella spp.* frequently found to use T3SS

supported inoculation of effect or proteins in a mandate to modify host composition and defeat the immune system. It is observed during experiments that the *Salmonella* relies on T3SS for infection of plants^{74,75}.

Plant and *Salmonella* interactions

Once *Salmonella spp.* colonize plant exteriors, they must escape or nullify the protection procedures of plants. Plants have a huge variety of sensors which permit them to distinguish and originate mechanisms to govern *Salmonella spp.* propagation¹. Iniguez⁶⁹, Schikora¹³ reported *Salmonella spp.* colonizes various parts of plants and encourages a host response. Removal of genes from *Salmonella spp.* which encode flagellar and T3SS machinery diminished plant reaction and in equivalent strengthened the colonization⁶⁹.

Above studied consequences recommend that though plants could be proficient to modify colonization by human pathogenic *Salmonella spp.*, plants are not able to identify them as potentially unsafe and thus do not commence defence mechanisms to inhibit colonization¹. It is observed after inoculation, *Arabidopsis* reacts to *Salmonella spp.* by a quick stimulation of defence reactions, involving the stimulation of protein kinases MPKs which was observed via the expression of a numerous defence genes, such as pathogenesis-related genes PR2 and PR4¹³.

Beside this mutation in either MPK6 or MPK3 provide plants additional sensitive to *Salmonella*, indicating to the significant character of MAPK signalling cascades¹³. The latest investigation assessed indications of symptoms such as wilting and chlorosis in *Arabidopsis* plants later the invasion by diverse *Salmonella spp.* has two discrete T3SSs^{76,77}.

Recently, Heffron et al.⁷⁸ had recognized the cytoplasmic complex which is the grouping platform for T3SSs which controls the suitable order for protein secretion which permits the chronological distribution of translocases earlier the secretion of the original effectors. Along with they explained the character of precise chaperones in the identification and charging of effectors into the assorting complex⁷⁸.

Even though numerous experiments recommend that the procedures used by *Salmonella spp.* to contaminate animal and plant hosts might be analogous, the function of *Salmonella* T3SS effectors throughout plant contaminations persists uncertain. Numerous effectors focus MAPK cascades, which are significant mechanisms of immune reaction in animals and plants⁷⁹⁻⁸¹.

The issue is authentic to consider that the virulent characters of T3SS components are preserved between animal and plant hosts, offering *Salmonella spp.* with proficient apparatuses for dominating the host immune systems⁸². These consequences recommend that *Salmonella* rely on the T3SS throughout plant contamination and aggressively dominate immune responses⁸².

Conclusion

Salmonella spp. hold expertise to colonize larger host variety and distinct modifications. There are notable data to defence the hypothesis that plants are used as unconventional hosts by animal pathogenic *Salmonella spp.*, till date our knowledge is limited about many raised unanswered questions for the processes of plant colonization through these organisms. Genomic estimations are just unique technique toward a definition of the plant related roles of precise genes and ideal molecular skills might still reveal procedures for plant colonization.

Conventional genetic procedures that allow a phenotype to a genotype have formerly fabricated abundant records on bacterial composition. But the image is less pleasant whilst abundant dynamics are alarmed in the phenotype, for instance amongst bacterial bio films. The task for upcoming effort will remain to scrutinize the expression reports of numerous factors in situ in order to untangle the complication, main target for upcoming research must be to enhanced recognize the interrelations among stanimal-linked bacteria and host plants.

Beside this A depth knowledge of routes and infection pattern of *Salmonella* with contrast to plant physiology, microbiological physiology, environmental interrelationship , food and crop processing and food and crop handling mechanisms along with food and crop cultivation methodology that provide opportunity of contamination will lead us to develop foolproof reliable policies, trustworthy standard operating procedures and infallible technologies for diminishing the danger of contamination of fresh vegetables and fruits so human can live disease-free and fear-free life.

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