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INTRODUCTION:

Salmonella remains a significant health concern causing millions of cases of foodborne illness annually. The CDC estimates Salmonella bacteria causes 1.35 million infections, more than 26,000 hospitalizations, and over 400 deaths in the United States each year. Food is the source of a majority of these illnesses.

While there are established performance standards set by the USDA to reduce the prevalence of Salmonella in poultry, there has been no significant reduction in the number of human infections from Salmonella in poultry products.

The USDA and the food industry work to find a balance to continue to offer wholesome, nutritious meat products while reducing the risk of illness from Salmonella for humans. The established performance standards measure the prevalence of Salmonella, but the risk of human illness is associated with the amount of Salmonella in a product and its virulence.

There is a need in the poultry and beef industry for a rapid method to identify the risk of Salmonella in food samples based on virulence or pathogenicity, instead of prevalence alone.

PURPOSE:

- 1. Development of a real-time PCR assay to detect *Salmonella* in relevant food samples based on genes associated with pathogenicity as researched by USDA.
- 2. Evaluate the performance of the assay in detecting the pathogenicity of samples previously characterized by USDA as highly pathogenic Salmonella (HPS).
- 3. Demonstrate the inclusivity and exclusivity of the assay.

REGISTERED TRADEMARKS

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The lyophilized PCR assay was developed to detect three HPS targets and Salmonella spp. In order to check the results regarding PCR inhibition, an internal control was added as a fifth target. The assay was tested on FSIS Salmonella-positive enrichments and isolates prepared by USDA from each of the four major commodities: chicken, turkey, pork, and beef.

In this study, 30 turkey samples, 36 chicken samples, 33 pork samples, and 30 beef samples were evaluated using the newly developed real-time PCR assay.

Pure, RNA-free DNA of Salmonella Enteritidis and Salmonella Dublin was quantified by droplet dPCR (dPCR; Stilla, naica[®] instrument) and used in a POD approach to estimate the absolute LOD_{95%}. DNA concentrations of 25, 5, 2.5, 0.25, and 0.025 copies/reaction were tested in 32 replicates each.







Development of a Multiplex Real-time PCR Assay for the **Detection of Highly Pathogenic** Salmonella enterica (HPS) in Beef, Poultry and Pork

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METHODS:

The USDA Agriculture Research Service (USDA-ARS) conducted a study to characterize differences in virulence gene content among Salmonella serovars most commonly linked to outbreaks and human illness, and serovars more commonly found as commensals associated with food animals. Primers and probes for the PCR assay were selected based on the virulence genes and targets researched by USDA-ARS and shared via a CRADA. A gel-based PCR assay was developed by USDA-ARS, and a real-time lyophilized PCR assay was developed by Hygiena[®].

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COMPARISON OF USDA ARS GEL-BASED PCR WITH REAL-TIME ASSAY FOR ISOLATES:

Table 2. Comparison of Turkey Samples (n = 30)											
	HPS-BHPS-AHPS-XSalmonella spp.										
Agreement	30	30	28	30							
Deviation	0	0	2	0							
Accuracy [%]	100.0	100.0	93.3	100.0							

Table 4. Comparison of Chicken Samples (n = 36)									
	HPS-B HPS-A HPS-X Salmonella sp								
Agreement	35	36	36	36					
Deviation	1	0	0	0					
Accuracy [%]	97.2	100.0	100.0	100.0					

Table 3. Comparison of Beef Samples (n = 30)											
	HPS-BHPS-AHPS-XSalmonella spp.										
Agreement	30	29	30	30							
Deviation	0	1	0	0							
Accuracy [%]	100.0	96.7	100.0	100.0							

Table 4. Comparison of Pork Samples (n = 33)											
	HPS-BHPS-AHPS-XSalmonella spp.										
Agreement	33	33	33	33							
Deviation	0	0	0	0							
Accuracy [%]	100.0	100.0	100.0	100.0							

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RESULTS:

ity (Absolute Limit of Det	tection (LOD _{95%})	1.00	
Table 1. LOD _{95%} in Copies	s/reaction	0.90- 0.85- 0.80- 0.75-	
HPS-B	3.08	0.70- 0.65- 9 0.60-	
HPS-A	3.42	е 0.50- 0.45- 0.40-	
HPS-X	3.82	0.35- 0.30- 0.25-	
ella spp.	3.66	0.15 0.15 0.05 0.05 0.00 0.1	LOD _{95%} = 3.08
LOD _{95%} = 3.42 10 copies nominal	LOD _{95%} = 3.82	1.00 0.95 0.90 0.85 0.80 0.75 0.70 0.65 0.70 0.65 0.70 0.65 0.70 0.65 0.70 0.65 0.70 0.65 0.70 0.65 0.70 0.05 0.00 0.000000	LOD _{95%} = 3.66 10.0 100.0
is Number of positive vs total num	mber of samples; DNA Concentr	ation [copies/µL; (copies/	(reaction)] (CV [%])
16/16: 32 29 (0 41) 16/16: 34	(3) $(2.3)59 (1.30) 13/16: 33.82 (1.04)$	4/16:36.43 (0.51)	0/16: -
16/16; 32.82 (0.23) 16/16; 34.	96 (0.83) 15/16: 36.14 (1.34)	2/16: 36.96 (0.10)	0/16: -
16/16; 30.81 (0.27) 16/16; 32.	78 (0.94) 13/16; 33.82 (1.04)	3/16; 36.12 (2.53)	0/16; -
16/16; 32.02 (0.42) 15/16; 34.	76 (1.00) 15/16; 35.34 (0.78)	4/16; 36.37 (0.69)	0/16; -
16/16; 29.36 (0.34) 16/16; 29.3	22 (0.36) 16/16; 29.37 (0.29)	16/16; 29.51 (0.50)	16/16; 29.91 (0.23)
Number of positive vs total nur	nber of samples; DNA Concentr	ation [copies/µL; (copies/	(reaction)] (CV [%])
1 (25) 0.2	(5) 0.1 (2.5)	0.01 (0.25)	0.001 (0.025)
16/16; 30.93 (0.47) 16/16; 32.5	85 (0.71) 16/16; 33.86 (0.89)	3/16; 35.77 (0.62)	0/16; -
16/16; 31.72 (0.30) 16/16; 33.4	45 (0.58) 14/16; 34.44 (0.67)	2/16; 34.93 (0.24)	0/16; -
16/16; 29.80 (0.69) 16/16; 32.	16 (0.60) 14/16; 32.87 (0.65)	2/16; 32.77 (0.61)	0/16; -
16/16; 31.33 (0.62) 16/16; 33.	70 (0.77) 13/16; 34.98 (0.86)	4/16; 35.95 (0.82)	0/16; -
16/16; 30.20 (0.83) 16/16; 30.9	09 (0.62) 16/16; 30.17 (0.75)	16/16; 30.11 (1.12)	16/16; 30.20 (0.77)

RESULTS:

Table 5: Comparison of gel-based PCR vs. real-time PCR assay for specificity study

		Original primer sets [% posit		% positive]	ve] HPS real-time PCR kit [% positive]				Original primer sets [% positive]			HPS real-time PCR kit [% positive]					
	Number									Number							
Serotype	tested	HPS-B	HPS-A	HPS-X	HPS-B	HPS-A	HPS-X	S. spp.	Serotype	tested	HPS-B	HPS-A	HPS-X	HPS-B	HPS-A	HPS-X	S. spp.
4,[5],12:i:-	2	100	100	100	100	100	100	100	Manhattan	3	33	100	100	33	100	100	100
Abaetetuba	1	0	0	0	0	0) 0	100	Mbanaka	1	0	100	0	0	100	0	100
Aberdeen	1	0	100	100	0	100	100	100	Meleagridis	1	0	100	0	0	100	0	100
Abony	2	0	100	100	0	100	100	100	Mississippi	1	100	100	100	100	100	100	100
Agona	1	0	100	0	0	100	0 0	100	Montevideo	7	0	14	0	0	14	0	100
Anatum	3	0	0	67	0	0	67	100	Muenchen	1	0	0	100	0	0	100	100
Bardo	1	100	100	100	100	100	100	100	Münster	2	0	0	0	0	0	0	100
Bareilly	2	0	0	100	0	(100	100	Napoli	1	0	0	100	0	0	100	100
Blockley	4	100	100	100	100	100	100	100	Newport	6	0	100	100	0	100	100	100
Bovismorbificans	2	0	100	100	0	100	100	100	Oranienburg	1	0	0	0	0	0	0	100
Brandenburg	3	0	0	0	0	(0 0	100	Paratyphi	4	0	0	0	0	0	0	100
Brenderup	1	100	100	100	100	100	100	100	Paratyphi B	9	11	22	33	11	22	33	100
Cerro	2	0	0	0	0	(0 0	100	Paratyphi C	1	100	100	0	100	100	0	100
Choleraesius	1	100	100	100	100	100	100	100	Reading	3	0	33	33	0	33	33	100
Concord	1	0	100	100	0	100	100	100	Rissen	1	0	100	0	0	100	0	100
Cottbus	1	0	0	100	0	(100	100	S. bongori	2	50	100	0	50	100	0	100
Crossness	1	0	100	100	0	100	100	100	S. enterica subsp. arizonae	10	0	0	0	0	0	0	100
Cubana	1	. 0	100	0	0	100	0 0	100	S. enterica subsp. diarizonae	8	13	0	0	13	0	0	100
Derby	3	0	33	0	0	33	3 0	100	S. enterica subsp. enterica	6	33	67	33	33	67	33	100
Dublin	8	88	100	88	88	100	88	100	S. enterica subsp. houtenae	7	0	0	100	0	0	100	100
Enteritidis	3	100	100	100	100	100	100	100	S. enterica subsp. indica	2	50	0	0	50	0	0	100
Gallinarum	3	100	100	100	100	100	100	100	S. enterica subsp. salamae	8	13	13	0	13	13	0	100
Gallinarum-Pullorum	3	100	100	100	100	100	100	100	Saintpaul	3	0	100	100	0	100	100	100
Hadar	5	60	100	100	60	100	100	100	Senftenberg	14	0	100	0	0	100	0	100
Havana	1	100	100	0	100	100	0 0	100	Stanley	1	0	100	0	0	100	0	100
Heidelberg	6	0	100	100	0	100	100	100	Stanleyville	1	0	100	0	0	100	0	100
Hvittingfoos	1	0	100	100	0	100	100	100	Tennessee	1	0	100	0	0	100	0	100
Infantis	11	0	100	100	0	100	100	100	Thompson	2	100	100	100	100	100	100	100
Johannisburg	1	100	0	0	100	0	0 0	100	Typhimurium	5	100	100	100	100	100	100	100
Kentucky	1	0	100	0	0	100	0 0	100	Uganda	2	0	0	100	0	0	100	100
Krefeld	1	0	100	0	0	100	0 0	100	Virchow	2	0	100	100	0	100	100	100
Lille	1	. 0	100	0	0	100	0 0	100	Waycross	1	0	0	0	0	0	0	100
Litchfield	1	100	100	100	100	100	100	100	Weltevreden	2	100	0	100	100	0	100	100
Livingstone	4	0	50	25	0	50) 25	100	Westhampton	1	0	100	0	0	100	0	100
London	1	0	100	100	0	100	100	100		204							

SIGNIFICANCE:

The results demonstrate that highly pathogenic Salmonella can be quickly detected in meat and poultry using this next-generation method for Salmonella detection. This approach to Salmonella testing can enable the industry to make risk-based decisions about their product by offering an indication of when product has more infectious potential. It would help achieve the objective of simultaneously reducing the number of illnesses caused by Salmonella while continuing to provide consumers with nutritious and affordable meat.

REFERENCES:

The research presented was conducted by scientists with the USDA-ARS US Meat Animal Research Center (USMARC). A Cooperative Research and Development Agreement (CRADA No. 58-3040-1-009) is established between USDA and Hygiena[®] LLC for the development of the HPS markers into a real-time assay intended for the BAX[®] System.

Disclaimer

Names are necessary to report factually on available data; however, the USDA neither guarantees nor warrants the standard of the product, and the use of the name by USDA implies no approval of the product to the exclusion of others that may also be suitable. USDA is an equal opportunity provider and employer.

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INCLUSIVITY & EXCLUSIVITY

Specificity studies yielded 100% inclusivity on 204 Salmonella serovars (Table 5) and 100% exclusivity on 53 closely related species of Enterobacteriaceae.

The data from the specificity study with serovars from the in-house culture collection also show 100% agreement with the USDA-ARS gel-based PCR.

https://www.cdc.gov/salmonella/index.html

2. Response to Questions Posted by the Food Safety and Inspection Service: Enhancing Salmonella Control in Poultry Products, Journal of Food Protection, 87, 2024

https://www.fsis.usda.gov/sites/default/files/media_file/documents/NACMCF_Salmonella_2023.pdf