Salmonella surveillance in United States broiler production, 2016-2020:

Regional differences and the role of multiple serotypes in production

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USDA-FSIS

Salmonella in poultry: Science and Research Round Table



College of Veterinary Medicine UNIVERSITY OF GEORGIA

"What we find in live production doesn't match what we find in the plant"



"What we find in live production doesn't match what we find in the plant"



Poultry Diagnostic & Research Center



Georgia Poultry Laboratory Network







Serovar Kentucky



Approach

- Analyze FSIS Salmonella monitoring data (2016-2020) Carcasses and raw, intact parts Nationally, regionally
- Compare FSIS serovar data from processing establishments with Salmonella breeder monitoring data in Georgia (2016-2020)
- Multi-serovar analyses of breeder samples

National trends



- Braenderup
- Enteritidis

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Siceloff et al., submitted

- Heidelberg
- **Infantis**
- Kentucky
- Schwarzengrund
- Typhimurium
- **I 4,[5],12**:i-
- Others

- Serovar Infantis has increased significantly in carcasses (6.5% to 21.2%) and parts (4.7% to 27.0%)
- The proportions of each serovar don't match between carcasses and parts
 - serovar Kentucky decreased in parts
 - serovar Enteritidis increased in parts

Serovar **Heidelberg** reduced in parts (6.2% to 1.4%)

Data source: FSIS



Siceloff et al., *submitted*

Data source: FSIS

Salmonella in breeders doesn't match Salmonella in the plant



Siceloff et al., submitted

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Data source: FSIS, GPLN
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Is this because *Salmonella* surveillance is limited to finding the most abundant serovars?



Are low abundance serovars hidden by Kentucky?



CRISPR-SeroSeq: amplicon-based sequencing tool to identify multiple serovars within a *Salmonella* population

Using CRISPR-SeroSeq to profile serovar populations



Using CRISPR-SeroSeq to profile serovar populations



Using CRISPR-SeroSeq to profile serovar populations



Multi-serovar Salmonella populations exist in one third of breeder flocks

Relative serovar

frequency

0 - 0.10

0.10 - 0.25

0.25 - 0.50

0.50 - 0.75

0.75 - 0.90 0.90 - 1



serovars/sample 4

- Samples submitted to GPLN 7/20 6/21
- Collected samples each week on a different day
- Included 2-4 Salmonella positive samples per week (average)
- 134 samples analyzed using CRISPR-SeroSeq

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- Every sample contained serovar Kentucky (8/8)
- Half of the samples contained a single serovar (Kentucky)
- Kentucky was the major serovar in 6/8 samples
- Half contained multiple serovars (2-4 serovars)

Relative serovar frequency 0 - 0.10 0.10 - 0.25 0.25 - 0.50 0.50 - 0.75 0.75 - 0.90 0.90 - 1

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July 2020 – June 2021

- 32% samples contain more than one serovar (average 1.6; range 1-11)
- 26 different serovars (5 in CDC top 10)

Kentucky is usually most abundant, Infantis is usually a minority

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Serovar			В		С			Serever			
Agona]]]		Seruvalanaa	Incidence of	Majority	Minority
Alachua		1 1					Serovar	prevelance	majority to	serovar in	serovar in
Altona		1 1						across	minority (ratio)	sample (%)	sample (%)
Anatum		1 1						samples			
Bradford		1 1					Agona	2	1:1	50	50
Cannstatt]]					Alachua	6	3:3	50	50
Cerro]]					Altona	4	2:2	50	50
Cubana]]					Anatum	3	1:2	33	67
Enteritidis]←]		-			Bradford	1	0:1	0	100
Hadar]]					Cannstatt	1	0:1	0	100
Infantis		←					Cerro	14	8:6	57	43
Kentucky I				-		-	Cubana	2	0:2	0	100
Kentucky II		1 1					Enteritidis	2	0:2	0	100
Liverpool		1 1					Hadar	1	0:1	0	100
Mbandaka		1 1					Infantis	12	1:11	8	92
Montevideo I		1 1					Kentucky I	104	93:11	89	11
Montevideo II/III/IV		1 1					Kentucky II	1	0:1	0	100
Orion		1 1					Liverpool	9	4:5	44	56
Domono		1 1					Mbandaka	12	3:13	25	108
Poopo	<u> </u>	· ·					Montevideo I	3	0:3	0	100
Schwarzongrund		-						4	0:4	0	100
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Semienberg	-						frequencióna	1	1.0	100	100
					<u> </u>			5	0.1	0	100
Tennessee								1	J.2 0:1	00	40
Inompson							– 0 - 0.10 erg	1	0.1	25	75
lyphimurium							– 0.10 - 0.25 <u>lga</u>	4 5	1.5	25	100
Uganda							- 0.25 - 0.50 ee	5	0.5	0	100
Worthington							0.50 - 0.75 on	2	0.2	56	100
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Siceloff et al., submitted

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Montevideo II/III/IV		†	_		_	Kentucky II	1	0:1	0	100
				-	_	Liverpool	9	4:5	44	56
Demono	-	+	_		_	Mbandaka	12	3:13	25	108
Pomona	-			-	_	Montevideo I	3	0:3	0	100
Poona				-	_	Montevideo II/III/IV	4	0:4	0	100
Schwarzengrund					_	Orion	1	1:0	100	0
Senttenberg			_	-	_	Relative seponationa	1	1:0	100	0
Soerenga	<u> </u>				_		1	0:1	0	100
Tennessee					_	0 grund	5	3:2	60	40
Thompson					_	- 0 - 0.10	1	0:1	0	100
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Uganda						- 0.25 - 0.50 ee	5	0:5	0	100
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Sobworzonaruna		-					Montevideo II/III/IV	4	0:4	0	100	
Schwarzengrund							Bolativo s er ovar	1	1:0	100	0	
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Caveats

- These are "trends"
- Missing piece of the puzzle: broilers
- Multi-serovar analysis only performed on breeders in Georgia

Summary

- Salmonella in live production does not match what we find in the plant
- Salmonella in poultry is complex; multi-serovar populations are one piece of the puzzle

Moving forward

- Implications for how/when we perform Salmonella monitoring?
- Integrators can use information derived from multi-serovar analysis to choose serovars for AV, complex biomapping/biosecurity



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