

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

Regional differences and the role of multiple serotypes in production

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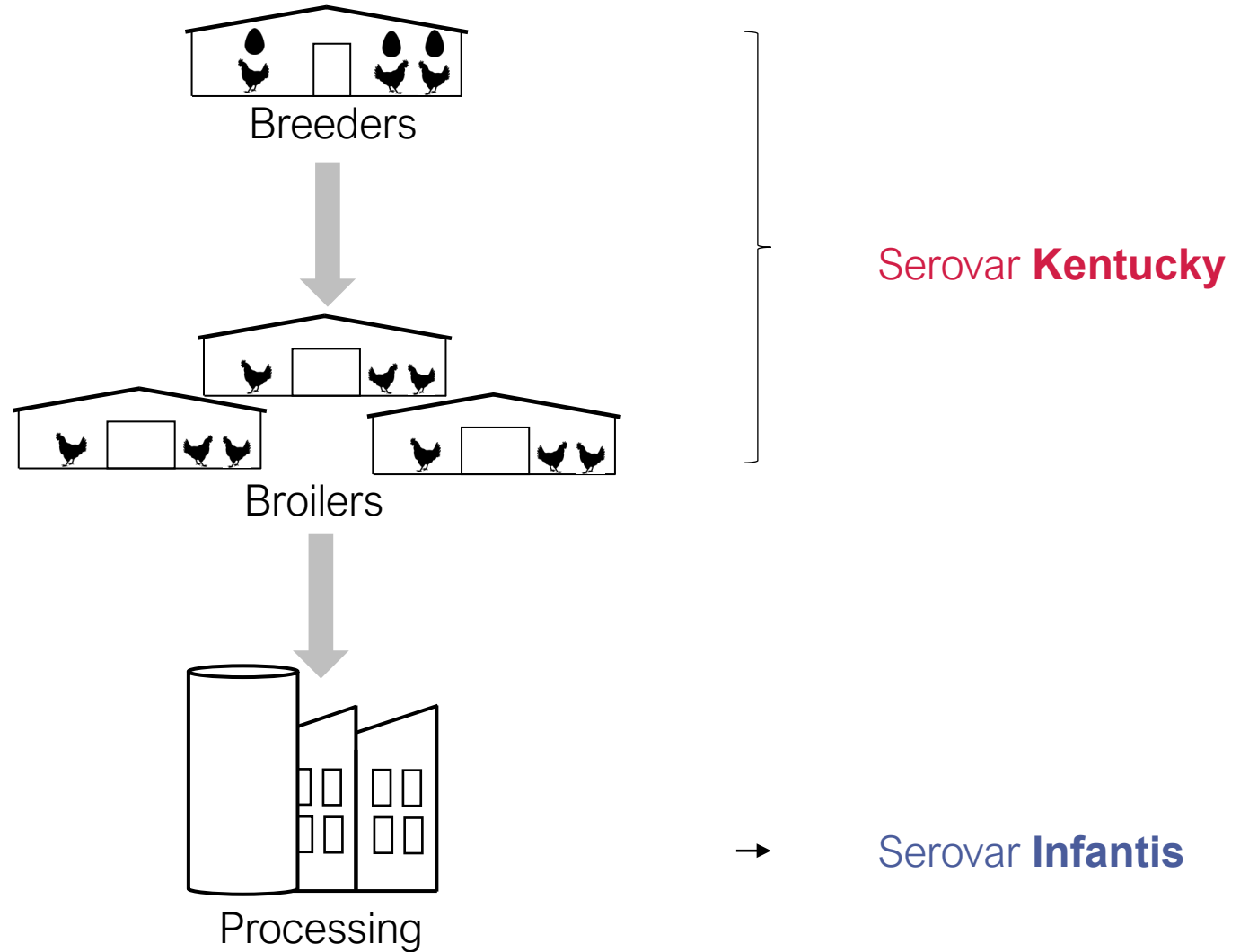
USDA-FSIS

Salmonella in poultry: Science and Research Round Table

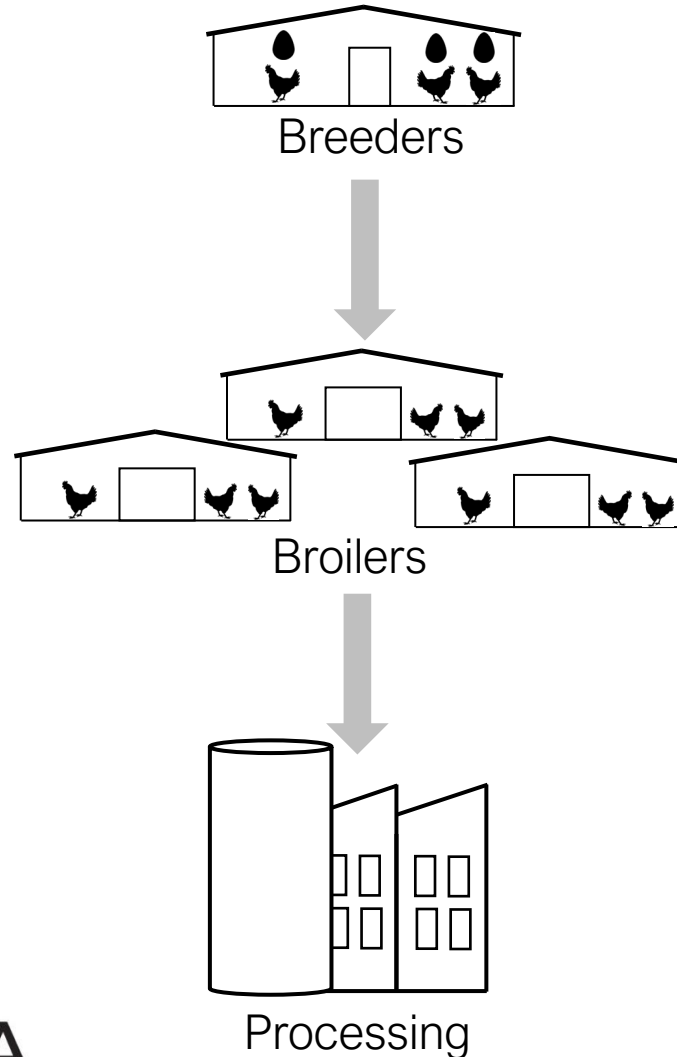


College of
Veterinary Medicine
UNIVERSITY OF GEORGIA

“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”



Serovar **Kentucky**



Funding:

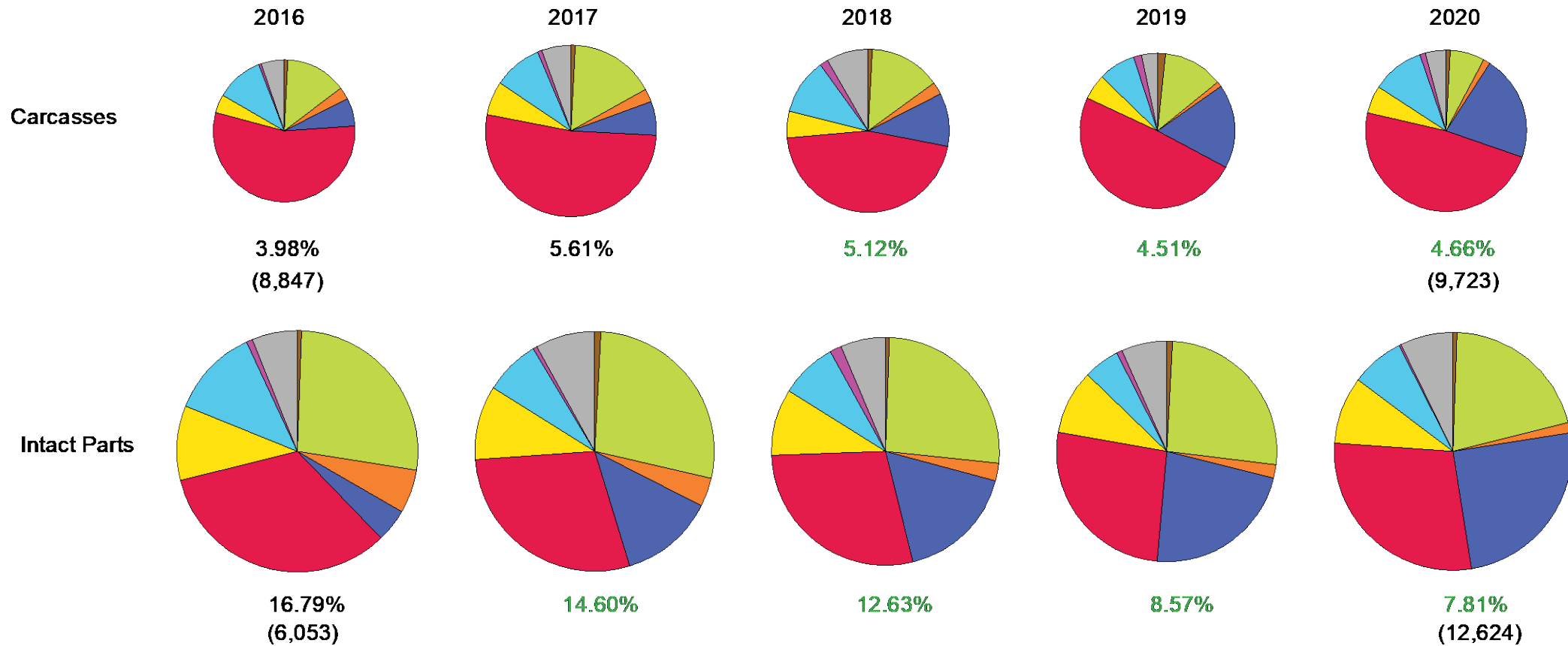


Serovar **Infantis**

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

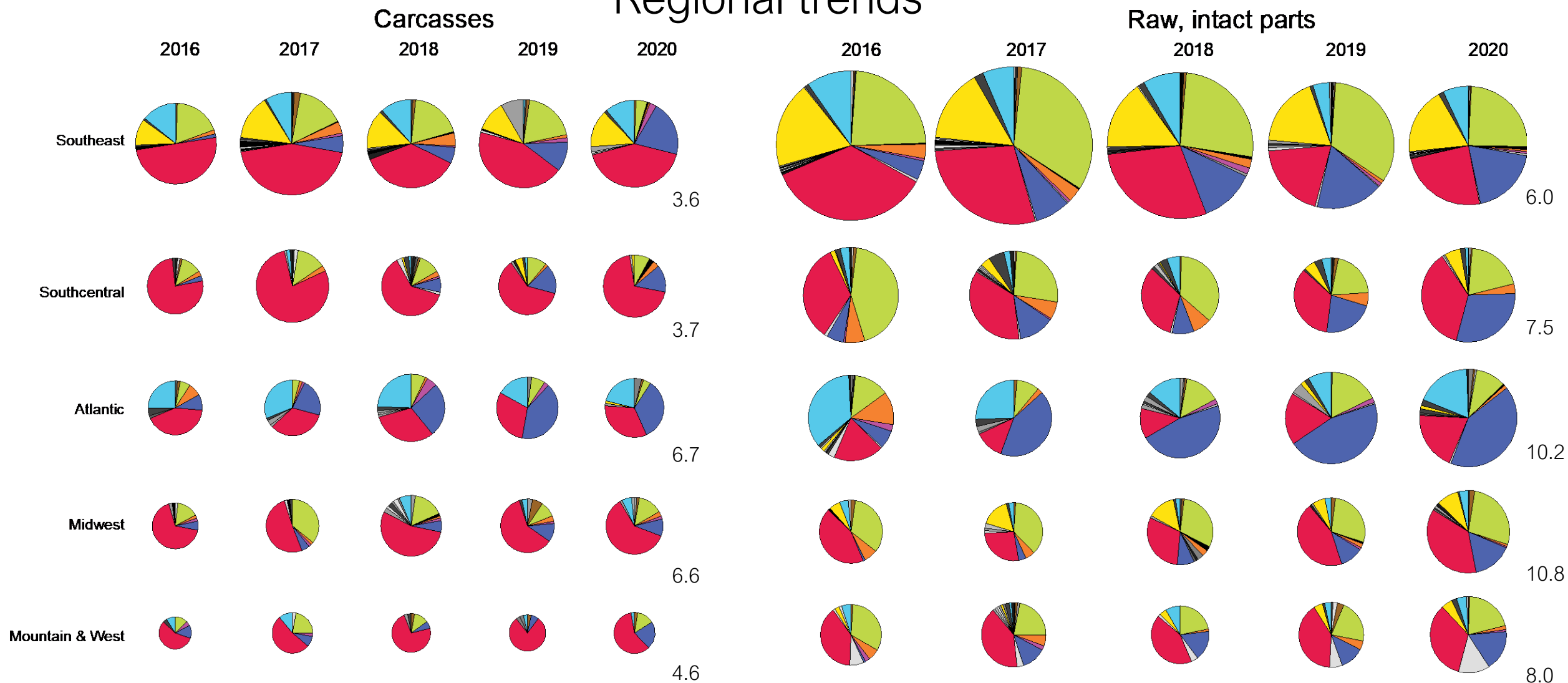
National trends



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

Data source: FSIS

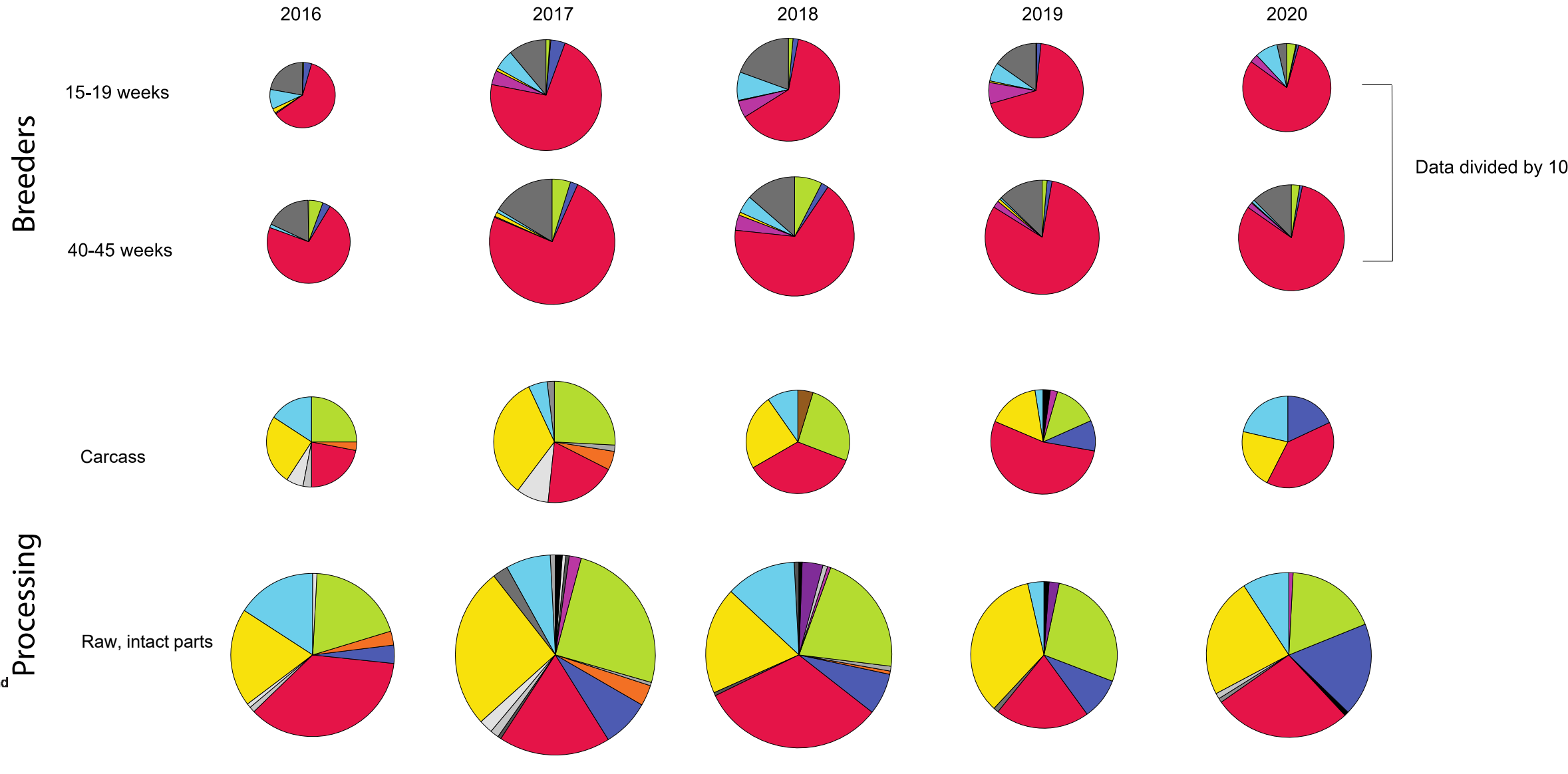
Regional trends



Serovar **Kentucky** higher in carcasses than parts
 Serovar **Enteritidis** higher in parts than carcasses
 Serovar **Infantis** increased in all regions
 Serovar **Heidelberg** decreased in all regions

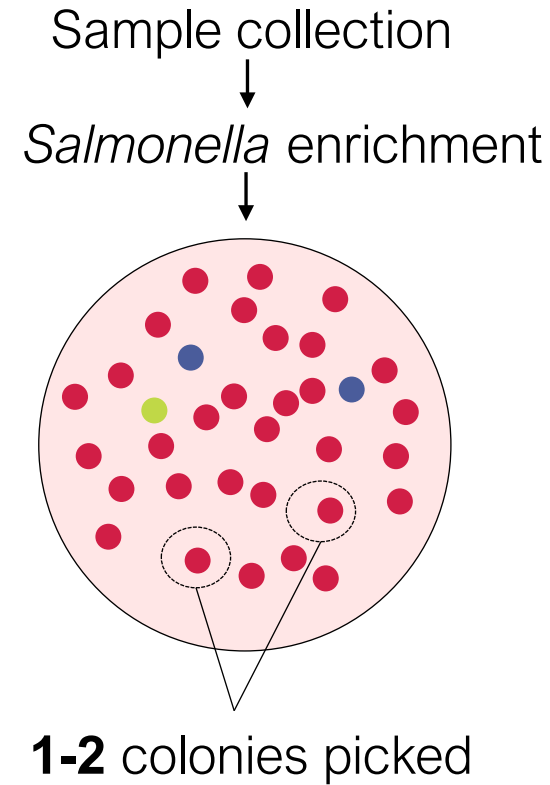
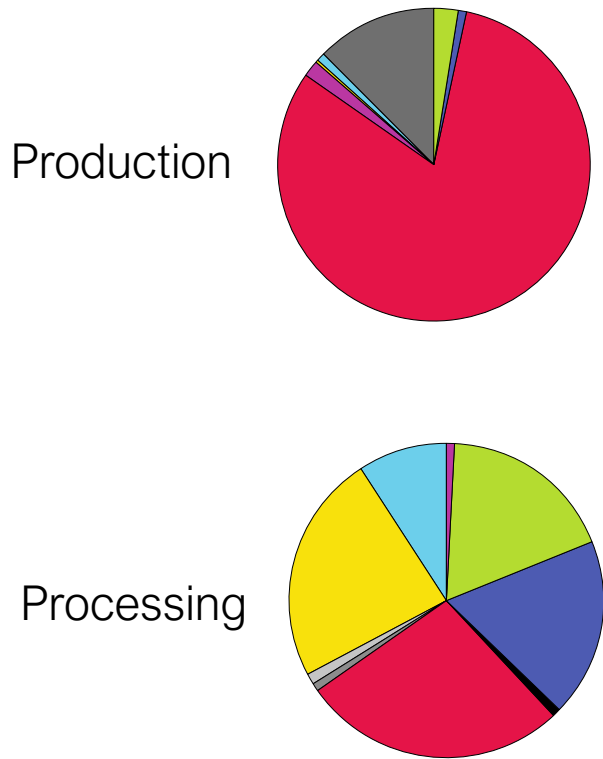
Higher **Infantis** and **Typhimurium** in the Atlantic region
 Higher **Schwarzengrund** in the Southeast region

Salmonella in breeders doesn't match Salmonella in the plant



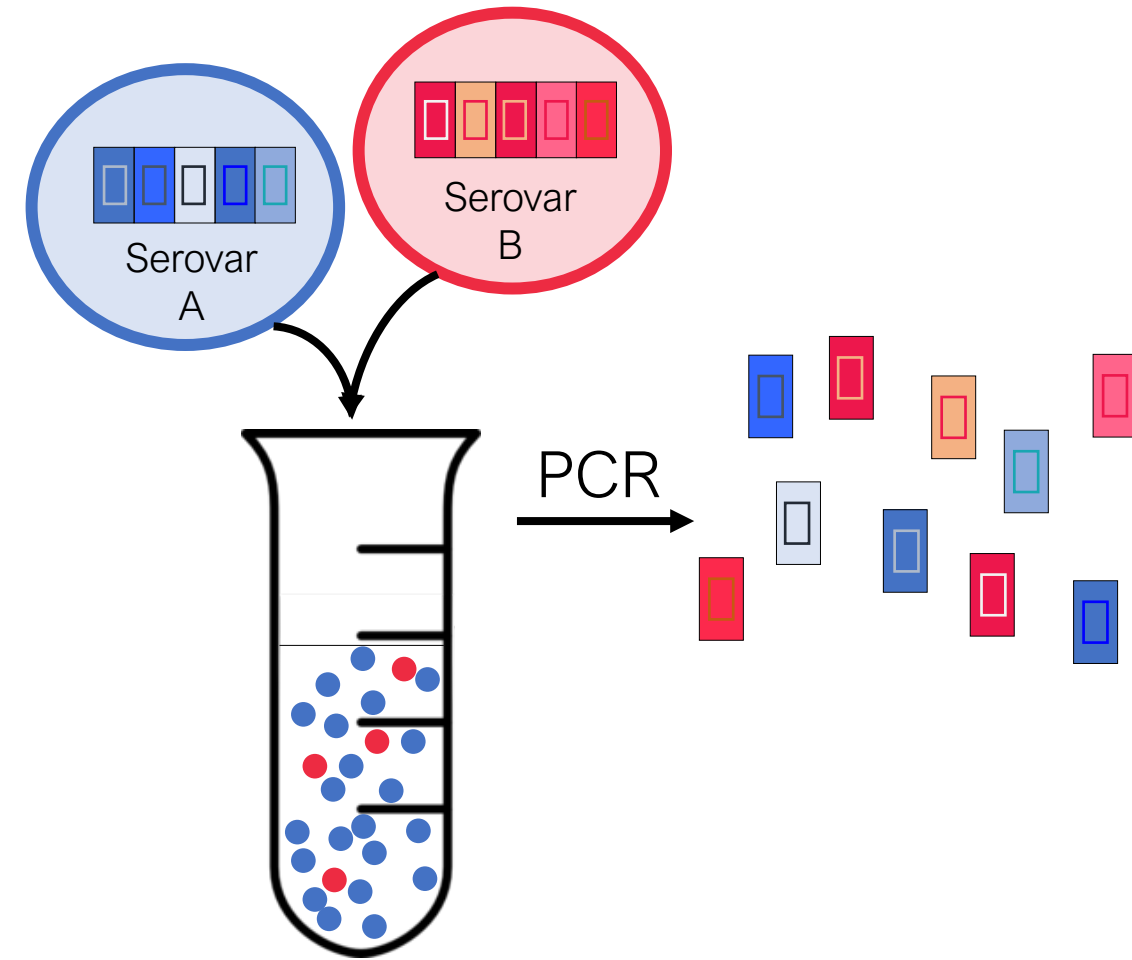
Is this because *Salmonella* surveillance is limited to finding the most abundant serovars?

Are low abundance serovars hidden by Kentucky?

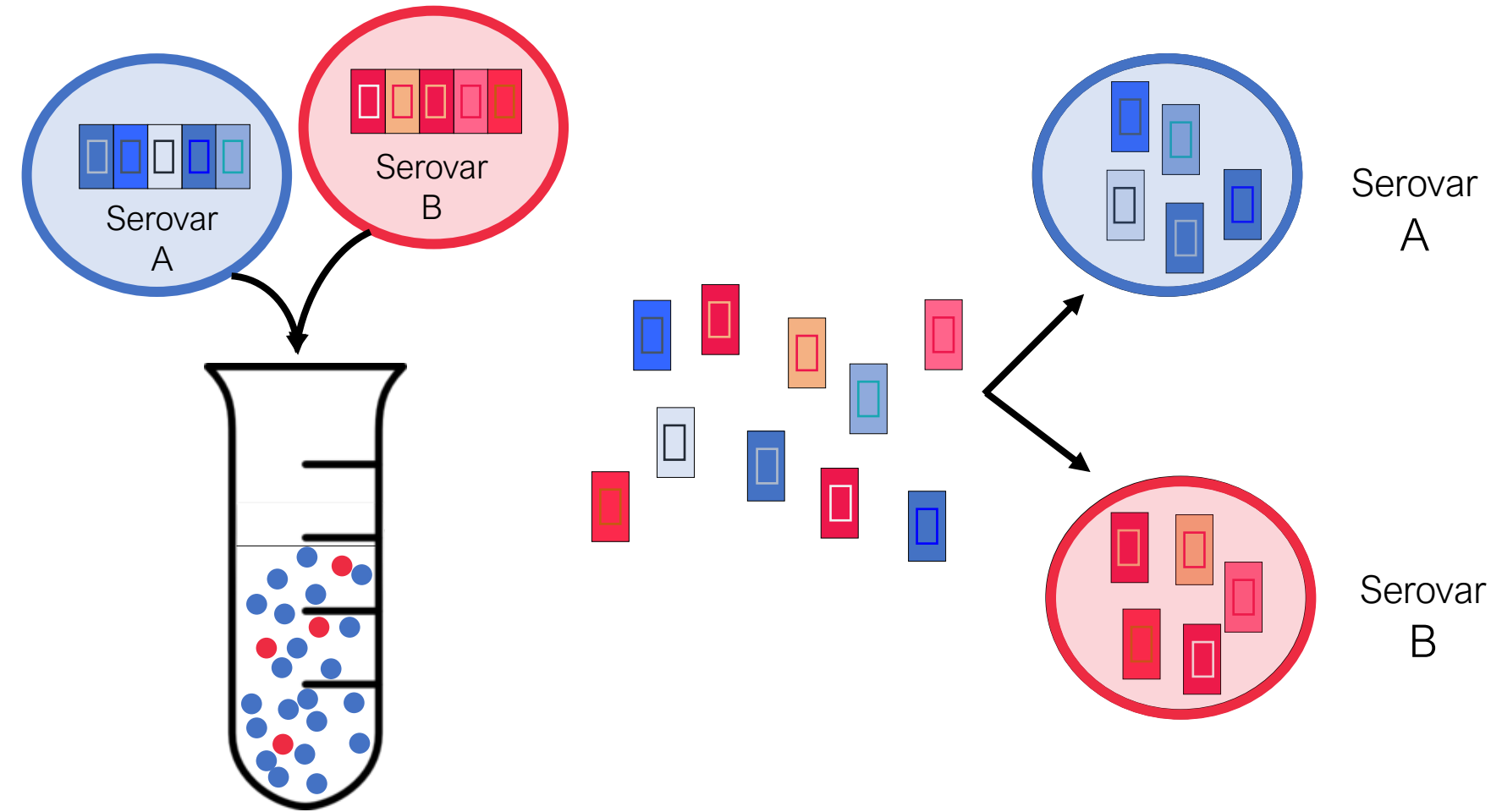


CRISPR-SeroSeq: amplicon-based sequencing tool to identify multiple serovars within a *Salmonella* population

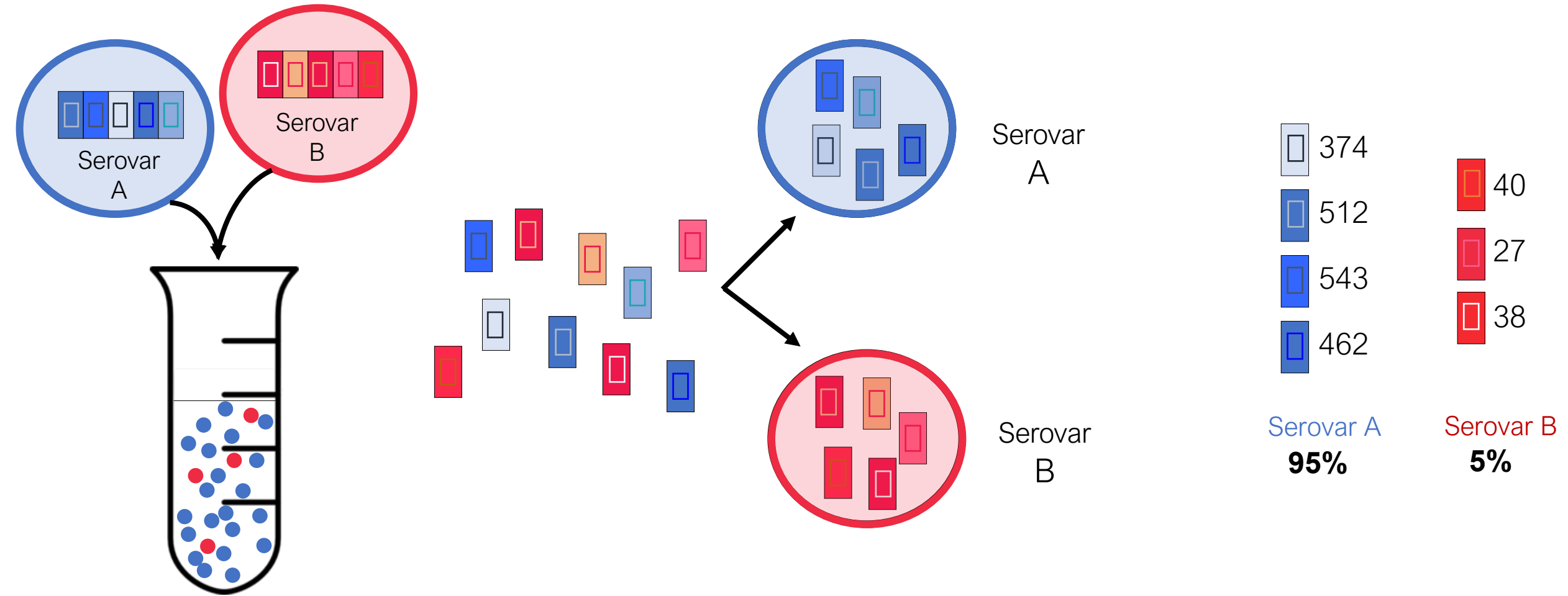
Using CRISPR-SeroSeq to profile serovar populations



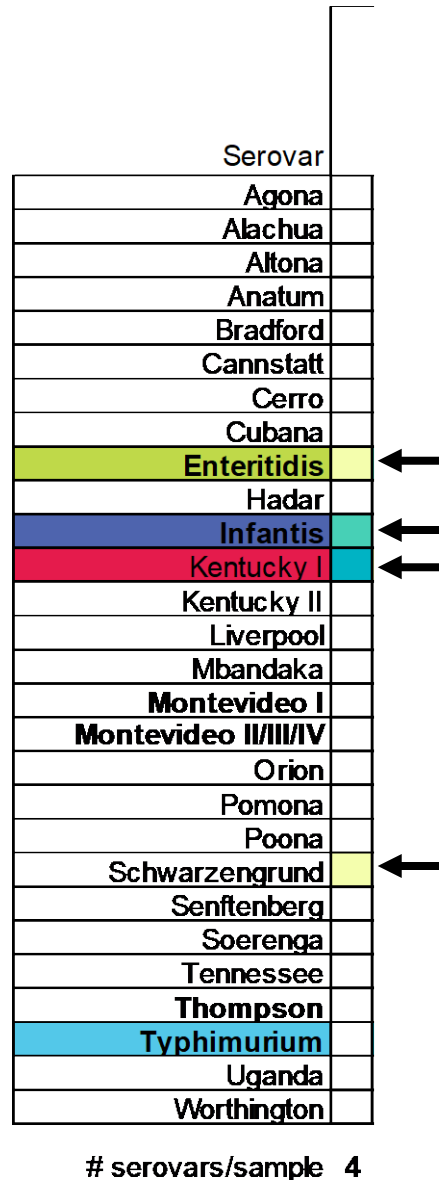
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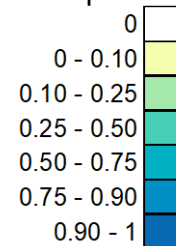


Multi-serovar *Salmonella* populations exist in one third of breeder flocks

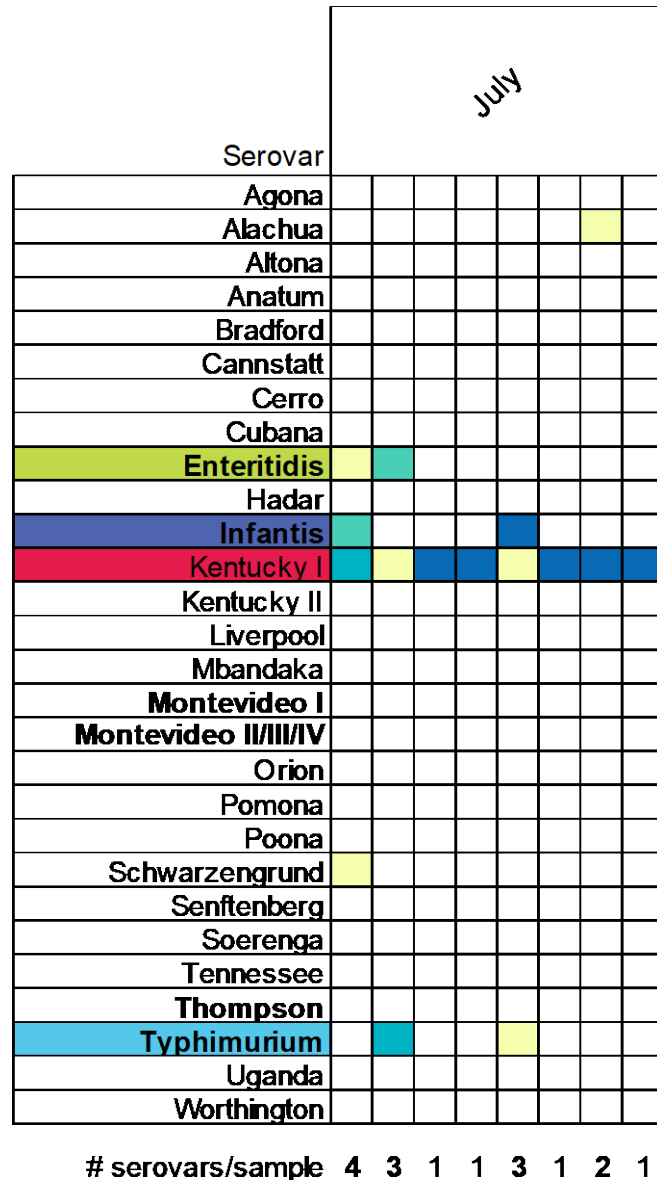


- Samples submitted to GPLN 7/20 - 6/21
- Collected samples each week on a different day
- Included 2-4 *Salmonella* positive samples per week (average)
- 134 samples analyzed using CRISPR-SeroSeq

Relative serovar
frequency

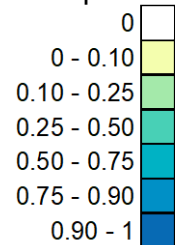


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- Every sample contained serovar Kentucky (8/8)
 - Half of the samples contained a single serovar (Kentucky)
 - Kentucky was the major serovar in 6/8 samples
 - Half contained multiple serovars (2-4 serovars)

Relative serovar frequency



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

Serovar	July							
Agona								
Alachua								
Altona								
Anatum								
Bradford								
Cannstatt								
Cerro								
Cubana								
Enteritidis								
Hadar								
Infantis								
Kentucky I								
Kentucky II								
Liverpool								
Mbandaka								
Montevideo I								
Montevideo II/III/IV								
Orion								
Pomona								
Poona								
Schwarzengrund								
Senftenberg								
Soerenga								
Tennessee								
Thompson								
Typhimurium								
Uganda								
Worthington								

serovars/sample 4 3 1 1 3 1 2 1

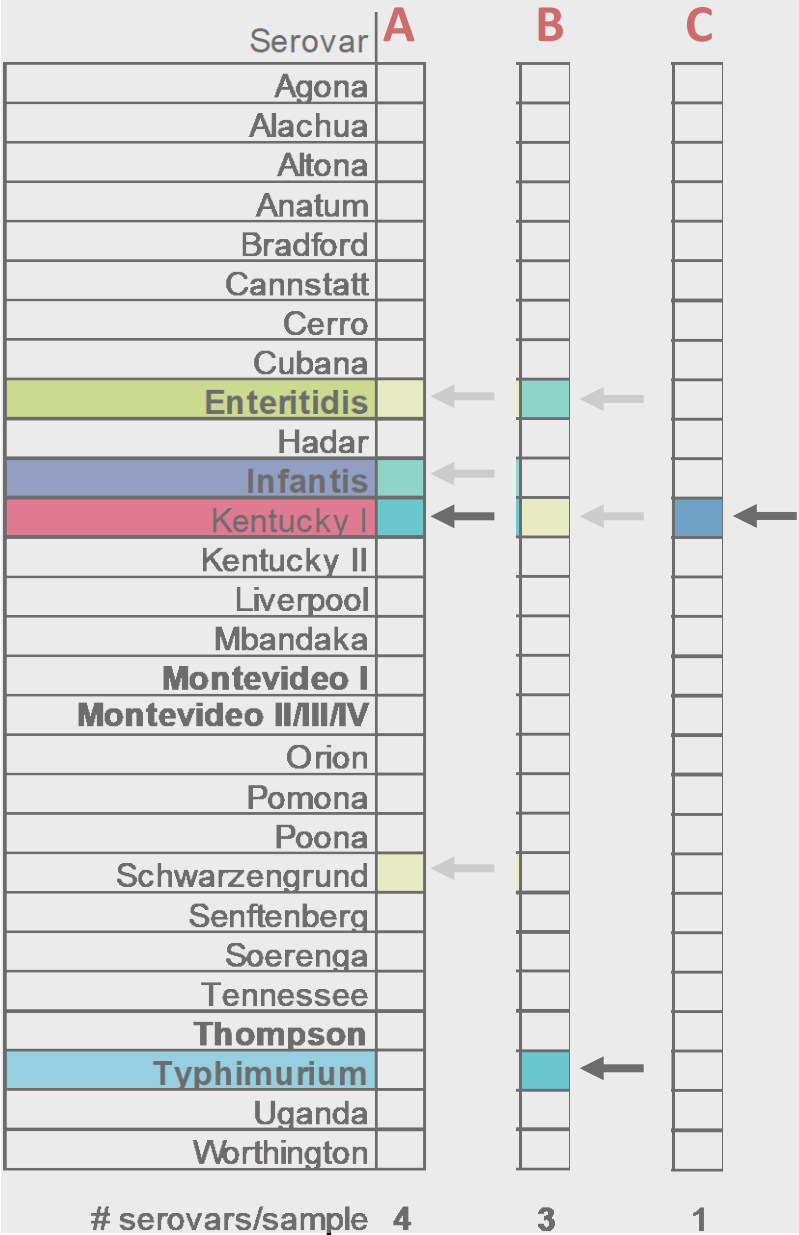
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July 2020 – June 2021

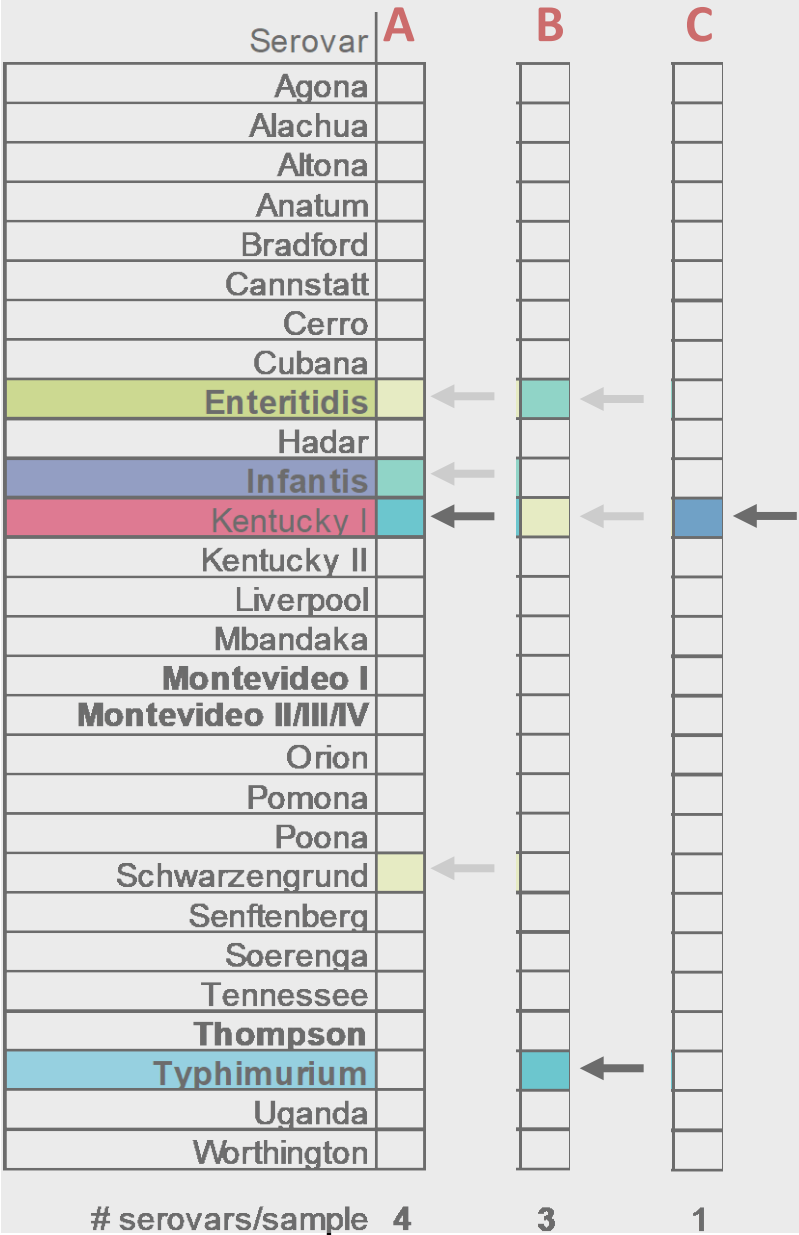
- 32% samples contain more than one serovar (average 1.6; range 1-11)
- 26 different serovars (5 in CDC top 10)

Kentucky is usually most abundant, Infantis is usually a minority

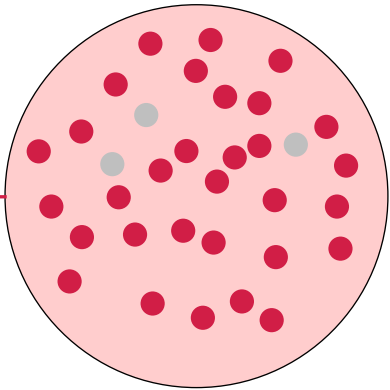


Serovar	Serovar prevalence across samples	Incidence of majority to minority (ratio)	Majority serovar in sample (%)	Minority serovar in sample (%)
Agona	2	1:1	50	50
Alachua	6	3:3	50	50
Altona	4	2:2	50	50
Anatum	3	1:2	33	67
Bradford	1	0:1	0	100
Cannstatt	1	0:1	0	100
Cerro	14	8:6	57	43
Cubana	2	0:2	0	100
Enteritidis	2	0:2	0	100
Hadar	1	0:1	0	100
Infantis	12	1:11	8	92
Kentucky I	104	93:11	89	11
Kentucky II	1	0:1	0	100
Liverpool	9	4:5	44	56
Mbandaka	12	3:13	25	108
Montevideo I	3	0:3	0	100
Montevideo II/III/IV	4	0:4	0	100
Orion	1	1:0	100	0
Pomona	1	1:0	100	0
Poona	1	0:1	0	100
Schwarzengrund	5	3:2	60	40
Senftenberg	1	0:1	0	100
Soerenga	4	1:3	25	75
Tennessee	5	0:5	0	100
Thompson	2	0:2	0	100
Typhimurium	9	5:4	56	44
Uganda	3	2:1	67	33
Worthington	2	2:0	100	0

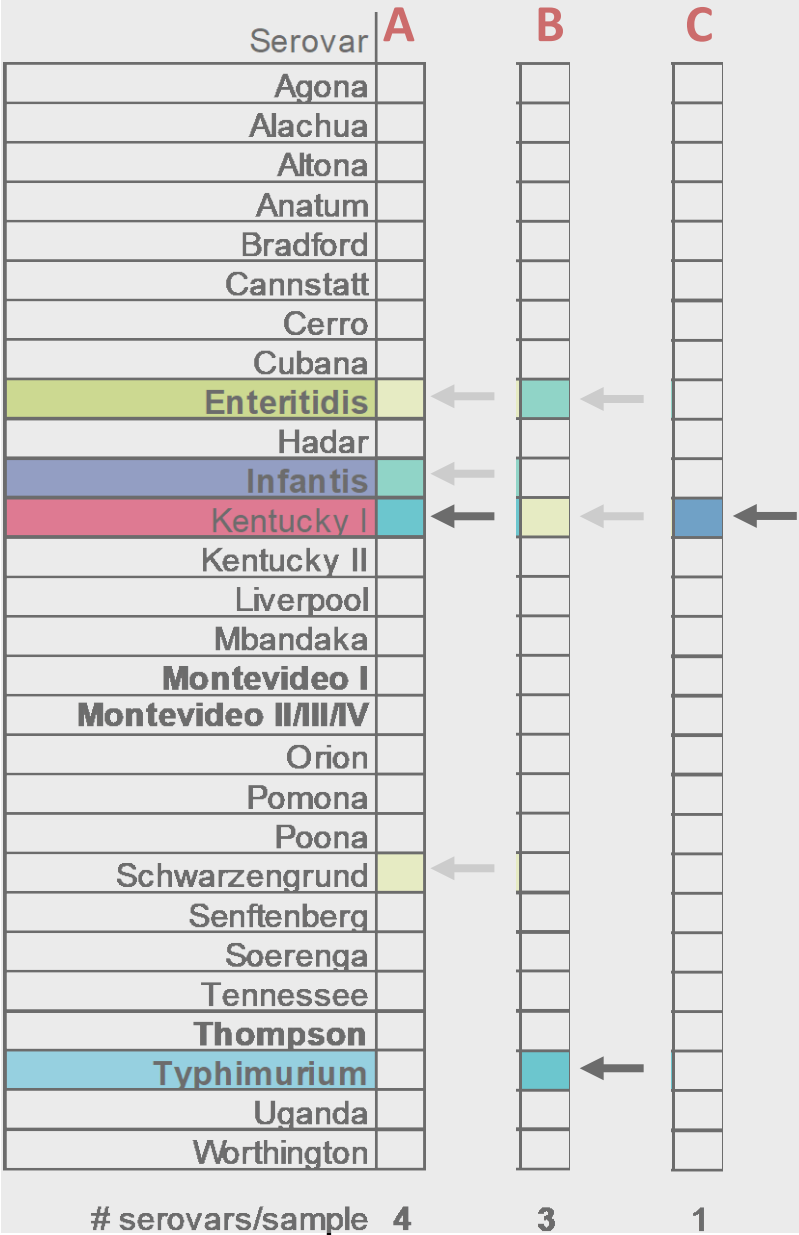
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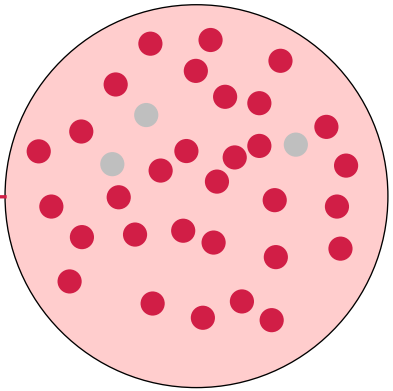
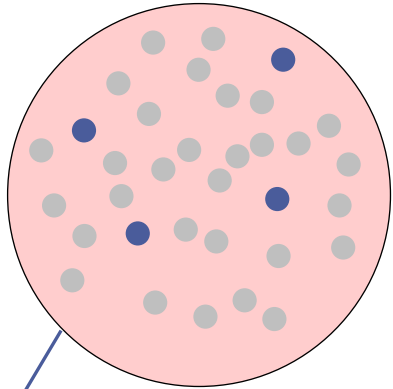
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Caveats

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

Summary

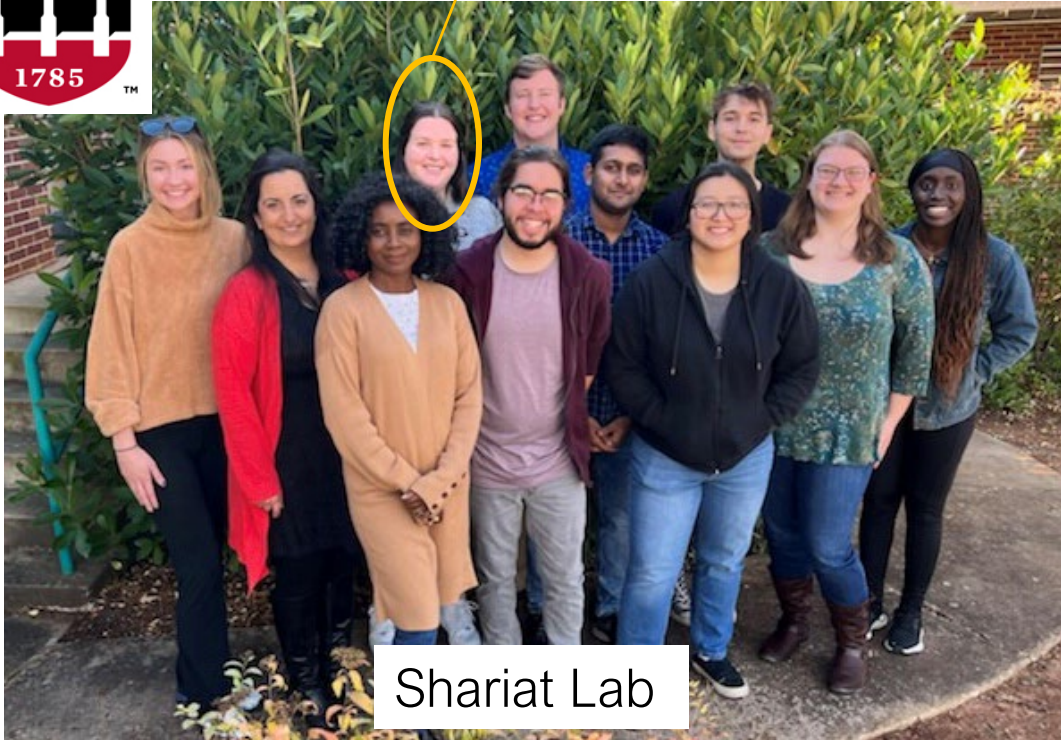
- *Salmonella* in live production does not match what we find in the plant
- *Salmonella* in poultry is complex; multi-serovar populations are one piece of the puzzle

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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PhD student



Shariat Lab



Doug Waltman



Poultry Diagnostic & Research Center

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