

Whole Genome Sequencing as a Tool to Understand the Epidemiology of *Salmonella* in Integrated Poultry Companies.

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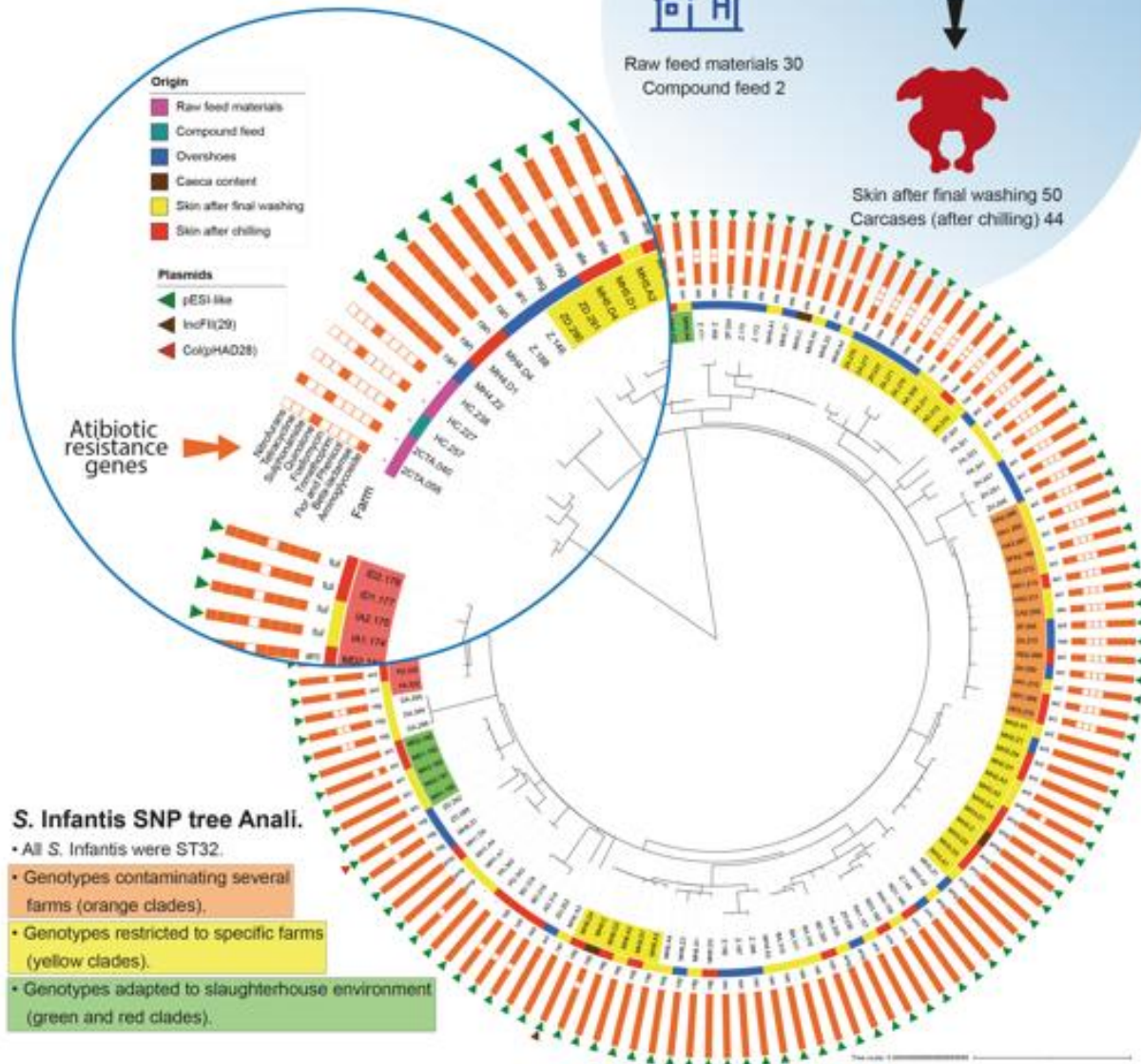
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Methodology

- DNA extraction and purification.
- Whole-genome sequencing, MiSeq platform (CDC PulseNet, 2018).
- Bioinformatics analyses (MLST typing, serovar prediction SNP tree analysis, identification of disinfectants and antimicrobial resistance genes, virulence genes, and plasmids).



Highlights

- *S. infantis* was the most prevalent serotype (77%).
- *S. infantis* from feed mill is not related to the rest of the collection.
- Complex patterns of resistance to antibiotics and disinfectants can be identified with this analysis.
- pESI-like plasmids can enhance the fitness of specific strains in poultry integrations.
- Analysis of *Salmonella* with WGS allows traceability of strains within integrations and planification of effective interventions to control this pathogen.

Genome-derived resistant patterns of other serovars

Serovar	ST	AMR Pattern	No. of isolates (%)	Origin (n)
Albany	292	AQ	1 (0.6)	Overshoes
Amsterdam	2090	AQ	18 (10.3)	Raw feed materials
Havana	588	ARQS	2 (1.2)	Skin after chilling
		ABPRMQST	1 (0.6)	Overshoes
14,[5],12:-	19	ARQST	1 (0.6)	Skin after chilling
		ABS	1 (0.6)	Turkey house
Javiana	1674	AQ	1 (0.6)	Overshoes
		ABQ	1 (0.6)	Transport paper
Liverpool	1959	AQ	9 (5.1)	Raw feed materials (8), Overshoes (1)
Muenchen	83	AQT	1 (0.6)	Overshoes
Saintpaul	50	A	1 (0.6)	Skin after chilling
Soerenga	1659	ABPRMST	1 (0.6)	Overshoes
Uganda	684	AQ	1 (0.6)	Compound feed
		AQ	1 (0.6)	Overshoes
Total of isolates			40 (22.9)	

Serotype Type (ST), Aminoglycoside (A), Beta-lactam (B), Plasmid (P), Trimethoprim (S), Macrolide (M), Quinolone (Q), Sulfonamide (S), Tetracycline (T).

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