Understanding contagious transmission of *Mannheimia haemolytica* in feedlot calves by leveraging whole genome sequencing of a unique isolate collection

Emily R. Snyder, Elaine M. Bird, Stacey R. Lacoste, Cheryl L. Waldner

OBJECTIVE

The goal of this project is to evaluate the contagious spread of *Mannheimia haemolytica (Mh)* between cattle in a feedlot setting, by utilizing whole-genome sequencing to analyze genetic relationships of *Mh* between contiguous pens of cattle.

METHODS

- Deep nasopharyngeal swabs were collected at arrival, 13 DOF, and 36 DOF from 4 pens of fall 2020 placed calves in a Saskatchewan research feedlot, with 100 calves per pen (400 calves total)
- Cattle received a 5-way BRD vaccine with *Mh* toxoid, clostridial vaccine, and metaphylaxis with tulathromycin
- All calves were sampled at Day 0 and Day 13, and 10 calves per pen were sampled at Day 36
- 489 total *Mh* isolates were found on culture
- Whole genome sequencing was performed on all isolates with Illumina NovaSeq 6000 SP PE150
- Genomes were assembled with Shovill and annotated with Prokka 1.14.6. Resistance genes were identified using ABRicate.
- Alignments were constructed with CSI Phylogeny, using USMARC strain 191 as a reference, to identify genetic relationships between isolates.

RESULTS

- At arrival there were a total of 154 isolates, spread between 56 different clusters.
- At 13 DOF, there were a total of 307 different isolates, spread between 26 different clusters.
- In each pen, one cluster became dominant by 13 DOF.
- At 36 DOF, only 10 calves per pen were sampled. Total number of *Mh* isolates was 28, in 10 clusters.
- There were 8 different resistance genes identified. Classes include aminoglycosides/cyclitols, macrolides, sulfonamides, and tetracyclines
- Clusters F and G had a "resistance profile" characterized by genes *mphE*, *msrE*, *and sul2*
- Clusters E and LL had a "resistance profile" characterized by genes *strA*, *aphA1*, *strB*, *estT*, *sul2*, and *tetH*

CONCLUSION

This study provided additional evidence to show that selection for and expansion of a dominant strain of *Mh* appears to be a not uncommon occurrence in cattle entering feeding operations.

A **single clone** of *Mannheimia haemolytica* becomes **dominant** within a pen just 13 days after arrival.

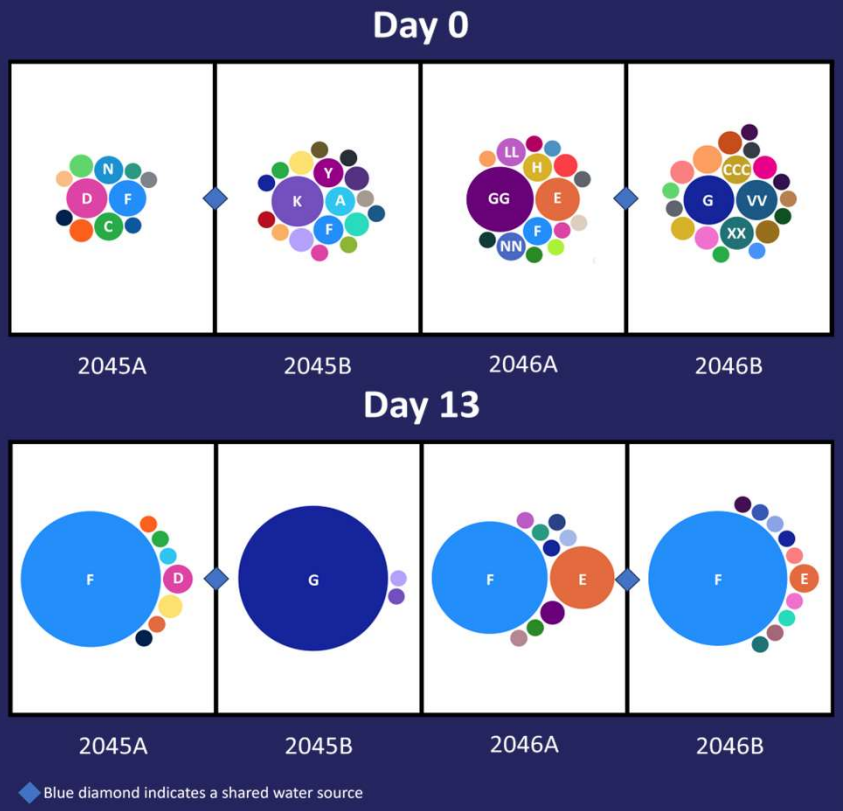

Fig. 1 and 2. Cluster distribution of *Mannheimia haemolytica* isolates collected from all cattle at 0 and 13 DOF.

Table 1. Calves shedding *Mannheimia haemolytica* as identified by whole-genome sequencing, by pen and sampling time. Each pen contains 100 calves in total.

	Time Point No. isolates (%)		
Pen	1 DOF	13 DOF	36 DOF
2045A	26 (26)	77 (77)	8 (80)
2045B	36 (36)	83 (83)	7 (70)
2046A	46 (46)	68 (68)	6 (60)
2046B	46 (46)	79 (79)	7 (70)

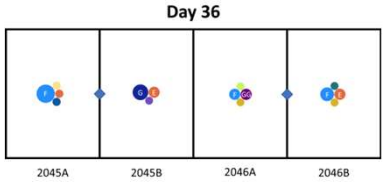

Fig. 3. Cluster distribution of *Mannheimia haemolytica* isolates collected from 10 cattle per pen at 36 DOF.

Table 6. Resistance gene distribution by cluster within pens at 0 DOF. Clusters without resistance genes are not shown. No resistance genes were identified from isolates from pen 2046B on day 0.

		Pen (Total No. isolates)					
		2045A (26)	2045B (36)	2046A (46)			
		Cluster (No. isolates)					
Class	Gene	D (6)	F (5)	F (3)	E (7)	F (3)	LL(3)
Aminoglycosides	*strA*	0	0	0	7	0	3
	aphA1	0	0	0	7	0	3
	strB	0	0	0	7	0	3
Macrolides	*mphE*	1	5	3	0	3	0
	msrE	1	5	3	0	3	0
	estT	0	0	0	7	0	3
Sulfonamides	*sul2*	1	5	3	7	3	3
Tetracyclines	*tetH*	0	0	0	7	0	3

Table 7. Resistance gene distribution by cluster within pens at 13 DOF. Clusters without resistance genes are not shown.

		Pen (Total No. Isolates)							
		2045A (77)		2045B (82)	2046A (67)			2046B (79)	
		Cluster (No. isolates)							
Class	Gene	E (1)	F (67)	G (80)	E(14)	F (44)	LL(1)	E (3)	F (67)
Aminoglycosides	*strA*	1	0	0	13	0	1	3	0
	aphA1	1	0	0	13	0	1	3	0
	strB	1	0	0	13	0	1	3	0
Macrolides	*mphE*	0	67	80	1	44	0	0	67
	msrE	0	67	80	1	44	0	0	67
	estT	1	0	0	14	0	1	3	0
Sulfonamides	*sul2*	1	67	80	14	44	1	3	67
Tetracyclines	*tetH*	1	0	0	13	0	1	3	0

UNIVERSITY OF SASKATCHEWAN
Western College of Veterinary Medicine
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