Investigation of the genetic differences between bovine herpesvirus type 1 variants and vaccine strains

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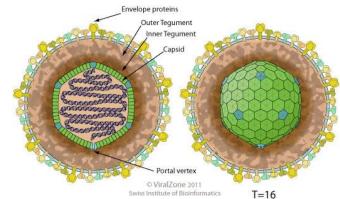
Bovine herpesvirus



- Bovine herpesvirus-1 (BHV-1)
 - Pathogen of Infectious Bovine Rhinotracheitis
- Infectious Bovine Rhinotracheitis (IBR)
 - Clinical signs: high fever, inflammation of nose, nasal discharge, conjunctivitis, abortion
 - Can predispose animals to secondary bacterial infections, such as shipping fever
 - Spread through nasal secretions, droplets, genital secretions, serum, and fetal fluids
- Cattle industry: suffers losses of more than \$500 million/year

Molecular basics

- Family: *Herpesviridae*
 - Subfamily: Alphaherpesvirinae
- Large, double-stranded DNA virus
 - Genome size: 136kb
- Consists of:
 - Core containing linear ds DNA
 - Icosahedral capsid
 - Envelope with viral glycoprotein spikes
- BHV-1: lifelong latent infection in TG of host
 - Virus reactivation: can infect others in the herd



BHV-1 Vaccine



- Efficacious BHV-1 vaccine used for years
 MLV or inactivated vaccine
- Recently, BHV-1 vaccine related abortion reported in increasing number of herds
- Pfizer: PregGuard (MLV Vaccines)
 - Abortion after Pfizer BHV-1 Vaccine during pregnancy
 - 2011: Wyoming
 - 2012: UC Davis (California), Texas A&M, and Cornell (New York)

BHV-1 Vaccine-related abortion

- Rise of vaccine-related abortion may be result of several factors:
 - 1. Emergence of new virulent strain of BHV-1
 - 2. Genetic recombination between wild type virus and BHV-1 vaccine strains
 - 3. Combination of environmental factors and reactivation of BHV-1 in latently infected herds

Question?

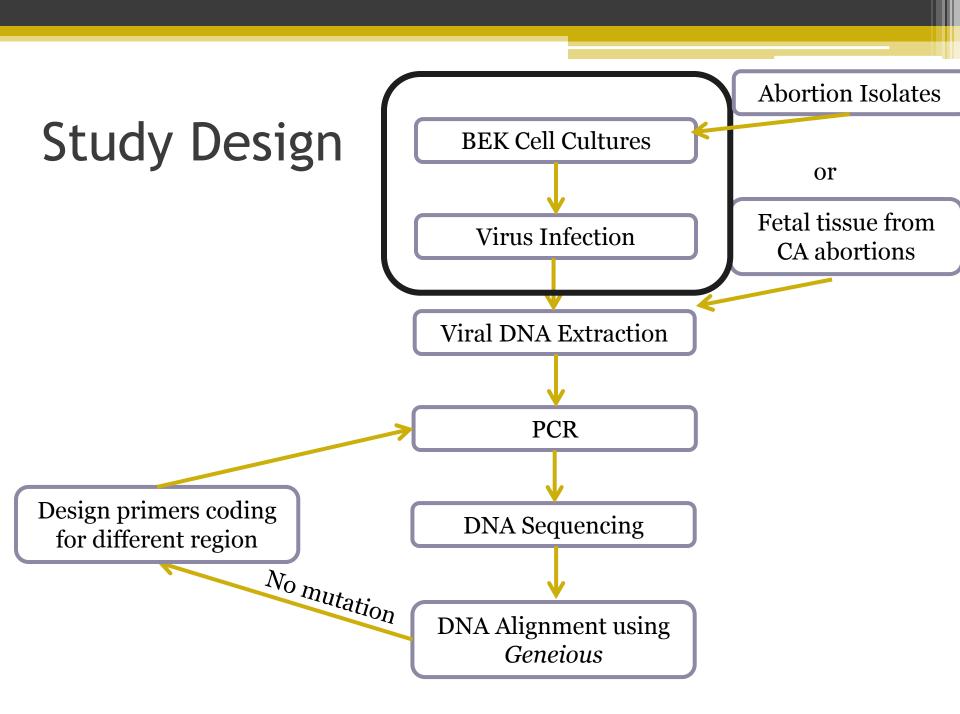
• Is the abortion caused by the vaccine?

Objectives

- 1. Sequence BHV-1 isolates from abortion cases and compare them to wild type BHV-1 virus and BHV-1 vaccine DNA genome
- 2. Establish strain specific nucleotide polymorphism (SSNP) profiles to assist diagnosis of BHV-1 infection

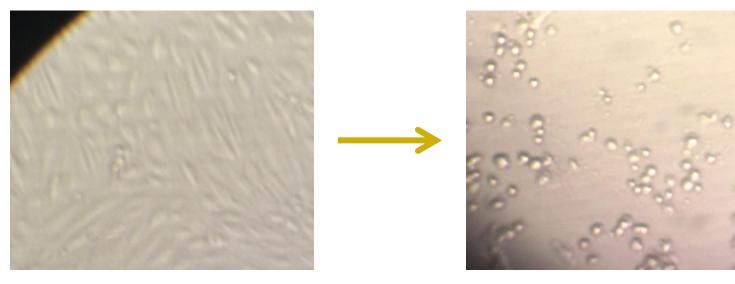
Approaches

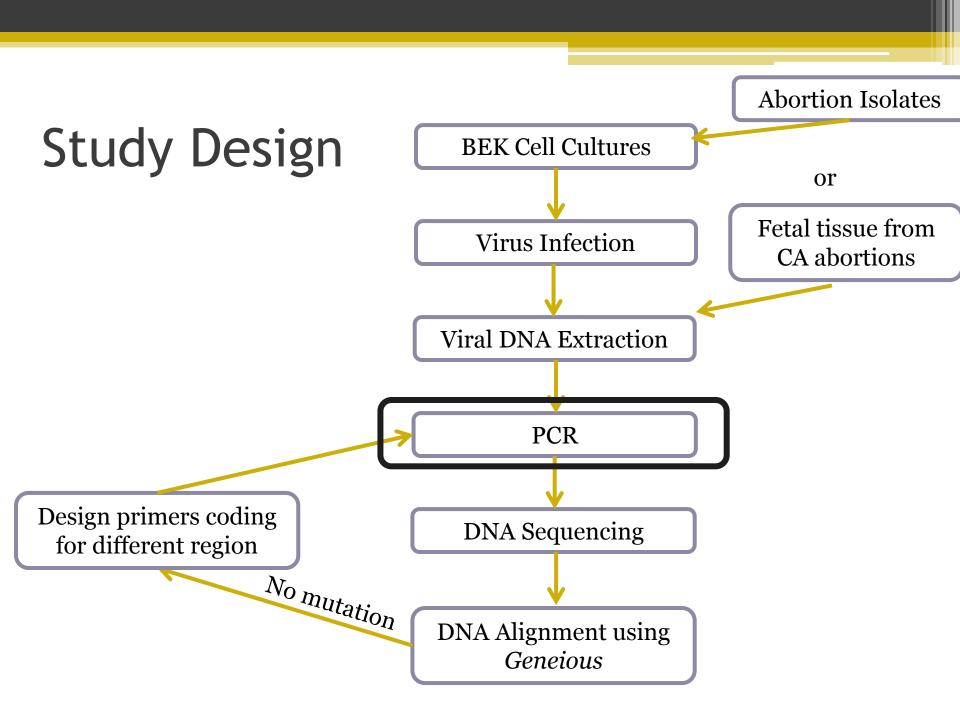
- TK, gE, and gG are unique genes in BHV-1 wild type and vaccine strains
- Compare the above genes between vaccine strains and abortion isolates by PCR-DNA sequence



BEK Cell Cultures & Virus Infection

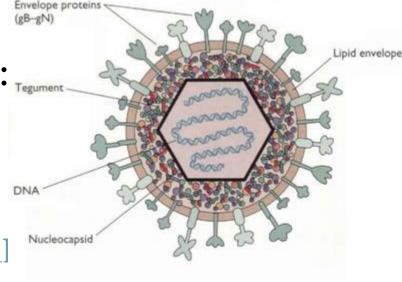
- Bovine Embryonic Kidney Cells: maintained monolayer in flasks
- Infected with virus isolate
- Examined for cytopathic effect (deterioration of monolayer cells)





Study Design: PCR Primers

- Amplified regions coding for:
 - Thymidine Kinase (TK)
 - Involved in viral virulence
 - **g**E
 - Required for direct cell-to-cell cell junctions
 - □ gG
 - Contributes to viral entry and attachment



Study Design: PCR Results

TK: R1 TK: R2 200bp 245bp 400bp 500bp 451bp MM 1 2 3 4 5

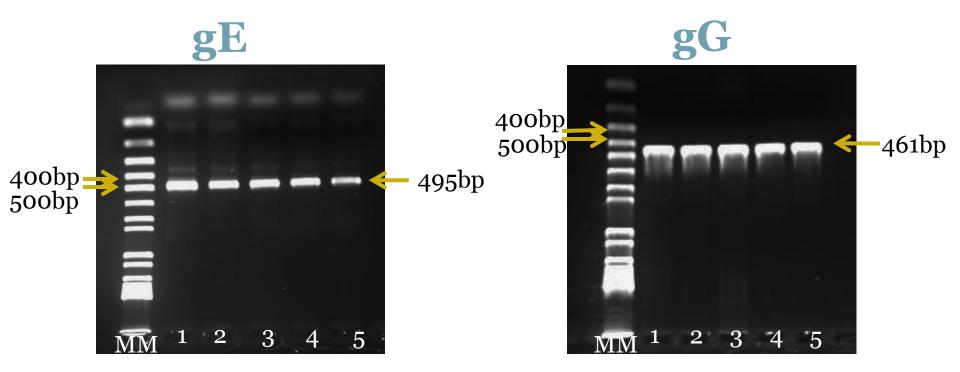
MM: Molecular Marker 1: T739073 2: T754-753 3: E754-753

- 4: T742-308
- 5: L6064-914

MM: Molecular Marker

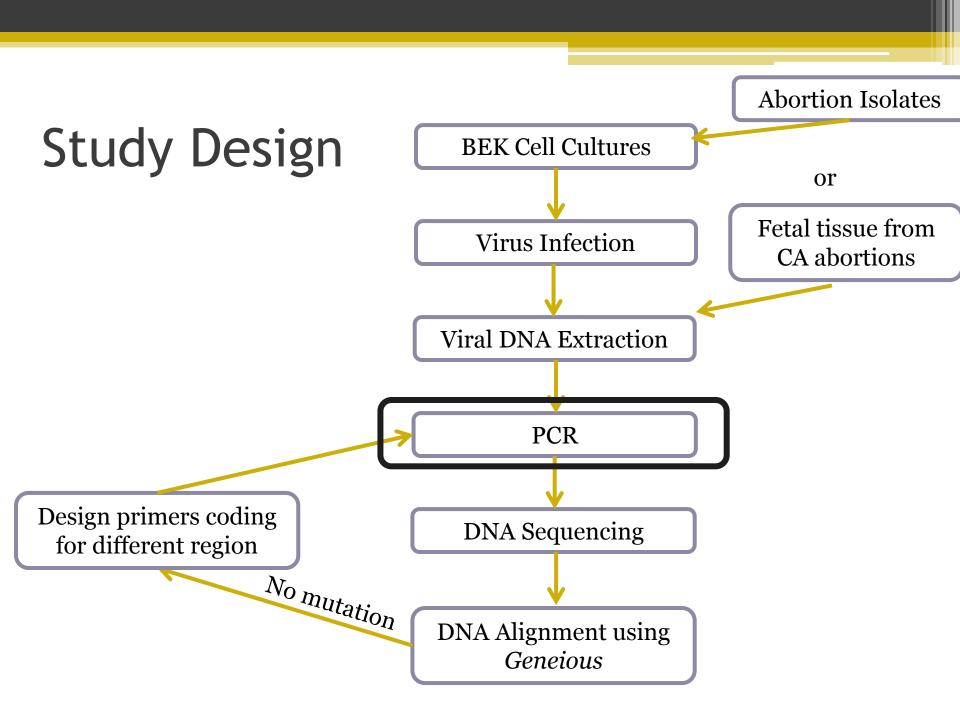
1: T596-042 2: T739-073 3: T754-753 4: E754-753 5: T742-308

Study Design: PCR Results



MM: Molecular Marker 1: PG-BHV-1 2: E737-501 3: T737-501 4: E739-051 5: T739-051 MM: Molecular Marker

1: L675-940 2: T519-200 3: T739-073 4: E739-051 5: T739051



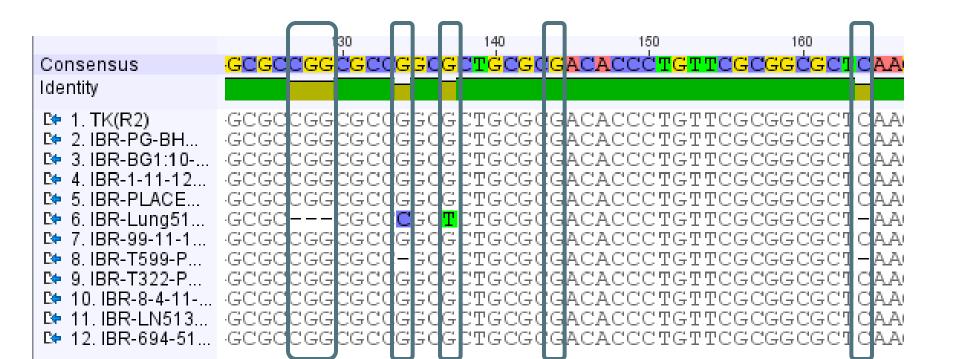
Results: TK R1

- Sequenced 35 isolates
- Substitution, Insertion, Deletion

				_				_					
Consensus		~	GCGC		90	C	-	C	-	CC	100	CC	L
Identity	-	-	30.30	-	GCC	9	30	9	2/2	1 L L	GG		
Tuentity		-		-		-		-					
🖙 1. TK(P1)			GCGC					G	ΞG		Contraction	100 million (100 million)	
C 2. IBR-1-11-12		C	GCGC	100 100			GΟ	G	ΞG			CG	
C+ 3. IBR-2LARY	CA	ÇI	GCGC	1	GCC			G	эG		GG	A 1947 A 1947 A	
C+ 4. IBR-4LARY	CA	9	SCGC	1.000	GCC		GQ	G	ΞG	CC	GG	the second second second	100 M
D* 5. IBR-6370-P D* 6. IBR-675-940	CA		3 / 3 / 3 / 3 / 3 / 3 / 3 / 3 / 3 / 3 /	T	G C C G C C	AG		CG	ΞĢ		GG	TACG	
C* 7. IBR-694-513	100 C C C	č	GCG0 GCG0	id	GCC	G		G	G G G		GG	1231-50	1.00
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C 9. IBR-8-4-11	A	10.0	FCGC	100	The second second		GC				GG	1.00	
C+ 10. IBR-A-P1	- C2103	1.01	GCGC		ĞČČ					CC			
C+ 11. IBR-A644-6	CAC	1.000	GCGC	1000	GCC					CC		1.1.1.1.1.1.1.1.1	C
C* 12. IBR-B-P1	CA	C	GCGC	C	GCC	A	GΟ	G	ΞG	CC	GG	CG	2
🖙 13. IBR-BG1:1	CA	C	GCGC	1 C	Contraction of the second s		GC	G	ΞG	CC	GG		
C+ 14. IBR-C-P1	CA	C	GCGC	1.	the second s			G	ΞG	CC	GG	CA	
C* 15. IBR-E596-0	3A)	A. C. C.	GCGC	1.	Contract and the second second		GQ	G	ΞĢ	CC	GG	CG	
C* 16. IBR-E739-0		C)	ECGO									CG	
C* 17. IBR-E737-5		C)	ECGO			G		26	22	CC	GG	CG CG	2
18. IBR-E754-7 19. IBR-L513			GCG(GCG(G C C G C C							CG	
C+ 20. IBR-L6046	EA	ž	GCGC	1.1.1.1.1	GCC	A	GC	G	3 G		GG		
C* 21. IBR-L6064	ÉA	2	GCGC	100 A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A	GCC	G		Ğ	GG		GG	2000 CAR	
C+ 22. IBR-LN513	AC	č	GCGC	1.1.1.1	ĞČČ			Ğ	ŝĞ		GG	100000000	
C* 23. IBR-LN604	CAC	G	GCGC	Ē	ĞCČ	A	ĜĈ	Ĝ	GG		GG	101311-000	1.00
C+ 24. IBR-PG-BH	CA	C	GCGC	C	GCC	G	GC	G	ΞG	CC	GG	CG	2
C* 25. IBR-PLAC		C	GCGC	C	GCC			G	ΞG	CC	GG	111 P. A. A.	
C 26. IBR-T322	CA			C	GCC			G			GG	1.11.11.11.1	1.00
C* 27. IBR-T519-2	CA		GCGC				GΟ		C - C - C - C - C - C - C - C - C - C -		GG	10000	10.000
28. IBR-T599			ECGO		GCC		GC	G	GG		GG	100000000	1 C C C C
29. IBR-E702	CA	21	ECGO	10.00	GCC	A	2010/11	G			GG		1.00
C+ 30. IBR-T702-2	CA	in a l	GCGC	1.000	in in in	100		G			GG		-
C+ 31. IBR-T737-5 C+ 32. IBR-T739-0	CAC	ž	GCGC GCGC	ia	acc	90	50	90	200	de	GG	CC	77
C 33. IBR-T739-0	1.000	č	aced	č	Gee	G	30	G		cc	Ge	ČG	17
C 34. IBR-T742-3		č	ECGO	č	G C C G C C	G	GC	G	$\frac{1}{3}G$	čč	GG	ĊG	
C+ 35. IBR-T754-7		č	GCG	č	ĞČČ	Ğ	ĞČ	G	ΞG	CC		ČĞ	1 A A A A A A A A A A A A A A A A A A A
C+ 36. IBR99-11	CA	100	GCGC	EC	ĞČČ		ĞČ					ĈĞ	
		-				-		-					-

Results: TK R2

- Sequenced 11 isolates
- Deletion, Substitution, Insertion



Results: gE

- Sequenced 31 isolates
- Substitution, Insertion, Deletion

	Π	310		320		ſ
Consensus	∎G.	CTĊTI	TIGO	GGATG	ACGAC	1
Identity						
🖙 1. gE(P3)	1G	ACTCTT	TTGO	GATG.	ACGA	1
🖙 2. IBR-1-11-12	AG	ACTCTI	TTGO	GGATG.	ACGA	1
🖙 3. IBR-2-Laryn	AG	ACTCTI	TTGO	GGATG.	ACGA	
C 4. IBR-4-Laryn		ACTCTI	TTGO	GGATG.	ACGA(1
C+ 5. IBR-519-200	AG	ACTCTI	TTGO	GATG.	ACGA	1
C+ 6. IBR-6370-P	100					I
C 7. IBR-644-644	AG	ACTCTI				
C* 8. IBR-675-940	AG	ACTCTI	TTGO	GGATG.	ACGA	
C 9. IBR-694-513	AG	ACTCTI	TTGO	GATG.	ACGA	
C+ 10. IBR-7212-P	AG	ACTCTI	TTGO	GGATG.	ACGA(
C+ 11. IBR-8-4-11		ACTCTI		GATG.		
C+ 12. IBR-99-11		ACTCTI	TTGO	GGATG.	ACGA	
🖙 13. IBR-A-P7		ACTCTI	TTGO	GATG.	ACGA	1
🖙 14. IBR-B-P7	1G	ACTCTT	TTGO	GGATG.	ACGA	
🖙 15. IBR-BG1-P	AG	ACTCTI	TTGO	GATG.	ACGA	1
C+ 16. IBR-C-P7	1G	ACTCTI	TTGO	GGATG.	ACGA	1
C 17. IBR-E-596	AG	ACTCTI	TTGO	GATG.	ACGA	1
C* 18. IBR-E-702	1G	ACTCTI	TTGO	GGATG.	ACGA	1
C+ 19. IBR-E-737	AG	ACTCTI		GATG.		
C 20. IBR-E-739	AG	ACTCTT	TTGO	GGATG.	ACGA	1
C+ 21. IBR-E754	AG	ACTCTI	TTGO	GGATG.	ACGA	1
🖙 22. IBR-L6046	AG	ACTCTT	TTGO	GGATG.	ACGA	
C 23. IBR-L6064	AG	ACTCTI	TTGO	GATG.	ACGA	
🖙 24. IBR-LN513	AG	ACTCTT		GATG.		
🖙 25. IBR-Lung5	AG	ACTCTI	TTGO	GATG.	ACGA	
🖙 26. IBR-T-596	AG	ACTCTT	TTGO	GATG.	ACGA	
🖙 27. IBR-T-702	AG	ACTCTI	TTGO	GATG.	ACGA	
C* 28. IBR-T-737	AG	ACTCTT	TTGO	GATG.	ACGA	
C 29. IBR-T-739	AG	ACTCTI	TTGO	GATG.	ACGA	
C 30. IBR-T322	AG	ACTCTT		GATG.		
C+ 31. IBR-T599		ACTCTI	TTGO	GATG.	ACGA	
C* 32. IBR-T739-0		ACTCTT	TTGO	GATG.	ACGA	

Results: gG

- Sequenced 34 isolates
- Deletion, Insertion

	ſ	350		360 370
Consensus	CCGC	A	FCGGGGCC	GAATCGCTGC TĠA
Identity				
🖙 1. gG(P4)	ACCGCC	A	GCGGGCCC	TGA
2. IBR-PG-BHV1_15	LCCGCC	A	GCGGGCCC	GAATCGCTGCTGA
C+ 3. IBR-BG1:10_1529	LCCGCC	A	GCGGGCC(GAATCGCTGCTGA
C 4. IBR-1-11-12-P9_1	ACCGCC	A	GCGGGCCC	GAATCGCTGCTGA
C 5. IBR-2Larynx-P9_1	ACCGCC	A	GCGGGCC	GAATCGCTGCTGA
C 6. IBR-4Larynx-P9_1	ACCGCC	A	GCGGGCCC	GAATCGCTGCTGA
C+ 7. IBR-519-200-P9_1	ACCGCC	A	GCGGGCC(GAATCGCTGCTGA
C 8. IBR-675-940-P9_1	ACCGCC	A	GCGGGCCC	GAATCGCTGCTGA
№ 9. IBR-675-940-P9_1	ACCGCC	A	GCGGGCCC	GAATCGCTGCTGA
C+ 10. IBR-694-513-P9	LCCGCC	A	GCGGGCCC	GAATCGCTGCTGA
C+ 11. IBR-739-073-P9	LCCGCC	A	GCGGGCCC	GAATCGCTGCTGA
C 12. IBR-8-4-11-P9_1	ACCGCC	A	GCGGGCCC	GAATCGCTGCTGA
C* 13. IBR-99-11-P9_15	LCCGCC	A	GCGGGCC	GAATCGCTGCTGA
🖙 14. IBR-A644-644-P	ACCGCC	A	GCGGGCCC	GAATCGCTGCTGA
C+ 15. IBR-E596-042-P				GAATCGCTGCTGA
C+ 16. IBR-E702-215-P	ACCGCC	A	GCGGGCCC	GAATCGCTGCTGA
🕩 17. IBR-E737-501-P	ACCGCC	A	GCGGGCCC	GAATCGCTGCTGA
C+ 18. IBR-E739-051-P	LCCGCC	A	GCGGGCCC	GAATCGCTGCTGA
C+ 19. IBR-E754-753-P	LCCGCC	A	GCGGGCCC	GAATCGCTGCTGA
🖙 20. IBR-L6046-914	ACCGCC	A	GCGGGCCC	GAATCGCTGCTGA
🖙 21. IBR-L6064-914	LCCGCC	A	GCGGGCC	GAATCGCTGCTGA
22. IBR-L6064-914	ACCGCC	A	GCGGGCCC	GAATCGCTGCTGA
C+ 23. IBR-LN513-P9_1				GAATCGCTGCTGA
C 24. IBR-LN6046-914	ACCGCC	A	GCGGGCC	GAATCGCTGCTGA
🖎 25. IBR-LN739-073	ACCGCC	A	GCGGGCCC	GAATCGCTGCTGA
🖙 26. IBR-Lung513-P9	LCCGCC	-	GCGGGCCC	GAATCGCTGCTGA
27. IBR-PLACENTA	LCCGCC			GAATCGCTGCTGA
🖙 28. IBR-T322-P9_15	ACCGCC	-	GCGGGCCC	GAATCGCTGCTGA
C* 29. IBR-T519-200P	ACCGCC	A	GCGGGCC	GAATCGCTGCTGA
30. IBR-T596-042-P	ACCGCC	A	GCGGGCCC	GAATCGCTGCTGA
C 31. IBR-T599-P9_15				GAATCGCTGCTGA
C* 32. IBR-T702-215-P	ACCGCC	A	GCGGGCCC	GAATCGCTGCTGA
🖎 33. IBR-T739-051-P			COMPANY AND COMPANY AND AND DO COMPANY	GAATCGCTGCTGA
C 34. IBR-T739-073-P				GAATCGCTGCTGA
🖙 35. IBR-T739-073-P				GAATCGCTGCTGA
🖙 36. IBR-T742-308-P				GAATCGCTGCTGA
C* 37. IBR-T742-308-P				GAATCGCTGCTGA
C 38. IBR-T754-753-P	CCCCC	0.81	PARADA	GAATCGCTGCTGA

Results: Wild Type vs. Isolates

		TX (26)	WY (3)	NY (1)	CA (5)	Bovine Shield (1)	PregGuard (1)	Total (37)	
TK	Insertion	24/24	3/3	1/1	5/5	1/1	1/1		
R1	Deletion				1/5			35/35	
	Substitution	4/24			5/5				
TK	Insertion					1/1		6/11	
R2	Deletion	2/5							
	Substitution	5/5				1/1			
gE	Insertion				1/5				
	Deletion				1/5			5/31	
	Substitution	4/22			1/5				
gG	Insertion	26/26	3/3	1/1	2/2	1/1	1/1	34/34	
	Deletion	2/26							
	Substitution				2/2				

Results: Isolates vs. Vaccine

		TX (26)	WY (3)	NY (1)	CA (5)	Total (35)
TK	Insertion					
R1	Deletion				1/5	9/33
	Substitution	4/24			5/5	
TK	Insertion					
R2	Deletion	2/5				5/11
	Substitution	5/5				
gE	Insertion				1/5	
	Deletion				1/5	5/30
	Substitution	4/22			1/5	
gG	Insertion				2/2	\frown
	Deletion	2/26			(4/32
	Substitution				2/2	

<u>TK R1 and gG</u>: most isolates identical to vaccine strains (which were different than the wild type)

<u>TK R2</u>: BoviShield Vaccine exhibited 2 mutations found in no other isolates, PregGuard Vaccine, or wild type

Results Summary

- <u>TK R1:</u> 100% of isolates different than wild type
 27.3% different than vaccine
- <u>TK R2:</u> 54.5% of isolates different than wild type
 <u>45.5% different than vaccine</u>
- **gE:** 16.1% of isolates different than wild type
 16.6% different than vaccine
- **gG:** 100% of isolates different than wild type
 12.5% different than vaccine

Conclusion and Discussion

- All the abortion isolates are different from the TK gene of wild types virus and many have similar TK gene sequence as the vaccine strain
- Not all the abortion isolates have the same genetic variation
- The abortion isolates may have been derived from the vaccine strain or other variant strains
- Mutations in TK, gE, and gG may lead these abortion isolates to be more virulent

Future Direction

- Examine the mutations in protein coding region and identify the epitope of the viral protein affected by those mutations discovered in our study
- Design primers to capture variations among different isolates

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