Final Report to the Pennsylvania Soybean Board for Grant – R2011 – 002

Improving Swine Production and Profitability via Regional Control of the PRRS Virus

Pennsylvania farmers harvest approximately 495,000 acres of soybeans annually with an average yield of 43 bushel to the acre producing around 640,000 tons of beans per year. The Pennsylvania swine industry houses about 100,000 mother sows and feeds out over 2 million fat hogs a year. Together they require about 180,000 tons of soybeans to supply the soybean meal products commonly used in pig diets. Thus, ***Pennsylvania swine farms consume the equivalent of 28% of the soybeans produced in the state***, a significant share of the soybean market. It is important to soybean farmers that the sector behind this market share is maintained or exhibits growth.

The research described here addresses a vexing problem in swine production and health with an eye towards keeping the Pennsylvania swine farmers competitive and opening new doors for sustaining or expanding the number of pigs feeding on soybeans in the state of Pennsylvania. Porcine Reproductive and Respiratory Syndrome (PRRS) remains the swine industry's most costly health challenge and is responsible for over $600 million dollars a year in losses to US swine farmers (~$100 per inventoried sow). Emerging technologies such as geographical information systems and genetic fingerprinting provide new opportunities to control the devastating disease. Our research targets how these new tools can be applied to control the Porcine Reproductive and Respiratory Syndrome virus in Pennsylvania. First, we will describe our efforts to map the PRRS status of farms in Pennsylvania and then detail our analysis of the genetic fingerprints of this virus.

The Pennsylvania swine industry is dynamic with production sites changing and the control of existing sites also influx. Thus, a concerted effort is needed to keep our Geographical Informational Systems (GIS) database current. Producers and integrators were contacted to get updates on both the location of their animals as well as the PRRS status of these animals. In the last year, we also adopted a more complicated classification of our sites that is more consistent with the recommendation of the American Association for Swine Veterinarians and allows for our findings in Pennsylvania to be more readily compared to those in other parts of the country. This new set of classifications is detailed in Appendix 1.

In addition to the PRRS status of farm in our database, both the size of the farm and the type of production on that site is also recorded. This allows us to stratify our farms with respect to these three variables and better track how PRRS might be spreading through the Pennsylvania based what type of farm is impacted. Appendix 2 details our current knowledge about the PRRS status of different types of farms in Pennsylvania. An active effort is ongoing to reduce the number of unknown sites in the database.

We also have a geographic location for each farm in our data base and thus can map the PRRS status of each farm and look for spatial trends in the occurrence or spread of the disease. Appendix 3 shows our current PRRS map. These maps provide the basis for regional control strategies. We are meeting on regular basis with the Pennsylvania PRRS Regional Control Task Force to discuss area based strategies to control or eliminate the disease. The task force is comprised of several key members of the swine industry and is listed in Appendix 4.

In addition to simply knowing the PRRS status for different farms, in some instances we also have been able to recover the virus from that site that is causing the disease. The PRRS virus is a single stranded RNA virus that is predisposed to genetic mutation and thus there are many variants or strains of the virus that can be differentiated by an analysis of their genetic sequence. Comparison of the ORF-5 gene is used to generate a molecular fingerprint of each virus and the degree of homology between viruses is indicative of how closely related these viruses are. For instance finding two viruses with 98% homology or more at two separate sites suggests that they share a common source of the virus and provides some insight into how the virus is being transmitted. Area spread of the disease by aerosol transmission or other local vectors predicts that viruses isolated from geographically sites in close proximity should also be genetically related. We employed such molecular epidemiology to better understand how the PRRS virus is spread in Pennsylvania as a precursor to its control.

We have generated a database of over 55 unique PRRS virus sequences in Pennsylvania. The striking result is how unrelated the viruses are in Pennsylvania and suggests that we must be under constant bombardment from external sources with virus. The degree of relatedness of these different viruses can be seen in the dendogram displayed in Appendix 5. However, several clusters of viruses were also found within the database and provided the basis for additional analysis. We

used a sophisticated mathematical approach called the Mantel analysis to study if the geographical relatedness also predicts genetic homology. We also examined if other factors such as pig ownership and time predicted genetic homology. The findings of the Mantel analysis are summarized in Appendix 6. The size of the coefficient indicates the strength of the relationship between to factors and a probability of $p \leq 0.05$ confirms that the association can not be explained by random chance alone. As expected, the closer in time that two viruses where isolated the more likely they were to be genetically related ($r = 0.21$, $p<0.001$). However, perhaps unexpectedly there was a poor correlation between the geographic distance and genetic homology ($r=0.07$, $p=0.23$), suggesting that area spread is not a common route of transmission in Pennsylvania for PRRS. Perhaps equally unexpected was the finding that pig ownership was the best predictor of genetic homology ($r=0.33$, $p<0.001$) indicating that common viruses are moving within a production company and in some cases over great distances. Taken together our data suggest that the greatest risk of PRRS transmission in Pennsylvania is due to failures in internal biosecurity, where pigs, people or vehicles are moving viruses between farm independent of their geographic locations. These findings suggest that control of PRRS in Pennsylvania should focus on internal biosecurity procedures and elimination of the devastating virus might be a feasible objective.

Criteria for and summary of supporting evidence required for breeding-herd classification for PRRSV

Herd category	Criteria	Supporting evidence required
Positive Unstable (I)	Any virus detected on the site along with clinical signs consistent with PRRS. Herds that do not meet the criteria for any of the other categories (II through IV) are Category I by default.	None required. Non-tested herds are Category I by default. Detection of virus in any tissue and presence of clinical signs would confirm status.
Positive Stable (II-A)	Category II starts after a 90-day period of sustained lack of viremia in weaning-age pigs and no clinical signs of PRRS in the breeding herd. Herd has not initiated an elimination program.	Test serum from weaning-age pigs by PCR.* No positive results over a 90-day period (four consecutive negative herd tests sampling every 30 days or more frequently) and no clinical signs consistent with PRRS observed in breeding herd.
Positive Stable Undergoing Elimination (II-B)	Category II starts after a 90-day period of sustained lack of viremia in weaning-age pigs and no clinical signs of PRRS in the breeding herd. Herd has initiated an elimination program and intends to become Negative.	Test serum from weaning-age pigs by PCR.* No positive results over a 90-day period (four consecutive negative herd tests sampling every 30 days or more frequently) and no clinical signs consistent with PRRS observed in breeding herd.
Provisional Negative (III)	Category III starts 60 days after negative breeding replacements are first introduced during a herd rollover with diagnostic evidence that they remain uninfected.	Test serum from negative breeding replacements by ELISA.† No positive results, after ruling out false-positives, at least 60 days after the initial introduction of negative breeding replacements.
	If growing pigs are present at the same premises, a confirmation of negative exposure status in that subpopulation is also required.	Test serum from growing pigs by ELISA.† No positive results, after ruling out false-positives.
Negative (IV)	For herd rollovers, Category IV starts when all previously infected animals have been removed from the herd.	Test serum from adult breeding animals by ELISA.† No positive results, after ruling out false-positives, subsequent to completion of rollover. Confirmed by breeding-animal inventory lists from production records.
	Alternatively, Category IV starts 1 year after the herd was classified as Category III if all animals in the herd are seronegative by ELISA.	Test serum from adult breeding animals by ELISA.† No positive results, after ruling out false-positives, 1 year after the herd was classified as Category III. Individual animal records are not required for the alternative criteria.
	For herds established Negative as a new startup or by complete depopulation and repopulation.	Test serum from adult breeding animals by ELISA.† No positive results, after ruling out false-positives, at least 30 days after population of premises with negative breeding replacements.
	If growing pigs are present at the same premises, confirmation of a negative exposure status in that subpopulation is also required.	Test serum from growing pigs by ELISA.† No positive results, after ruling out false-positives.

Appendix E

Region	Pennsylvania	Density sows:	sq mi
Date	10/16/2012	Density pigs:	sq mi

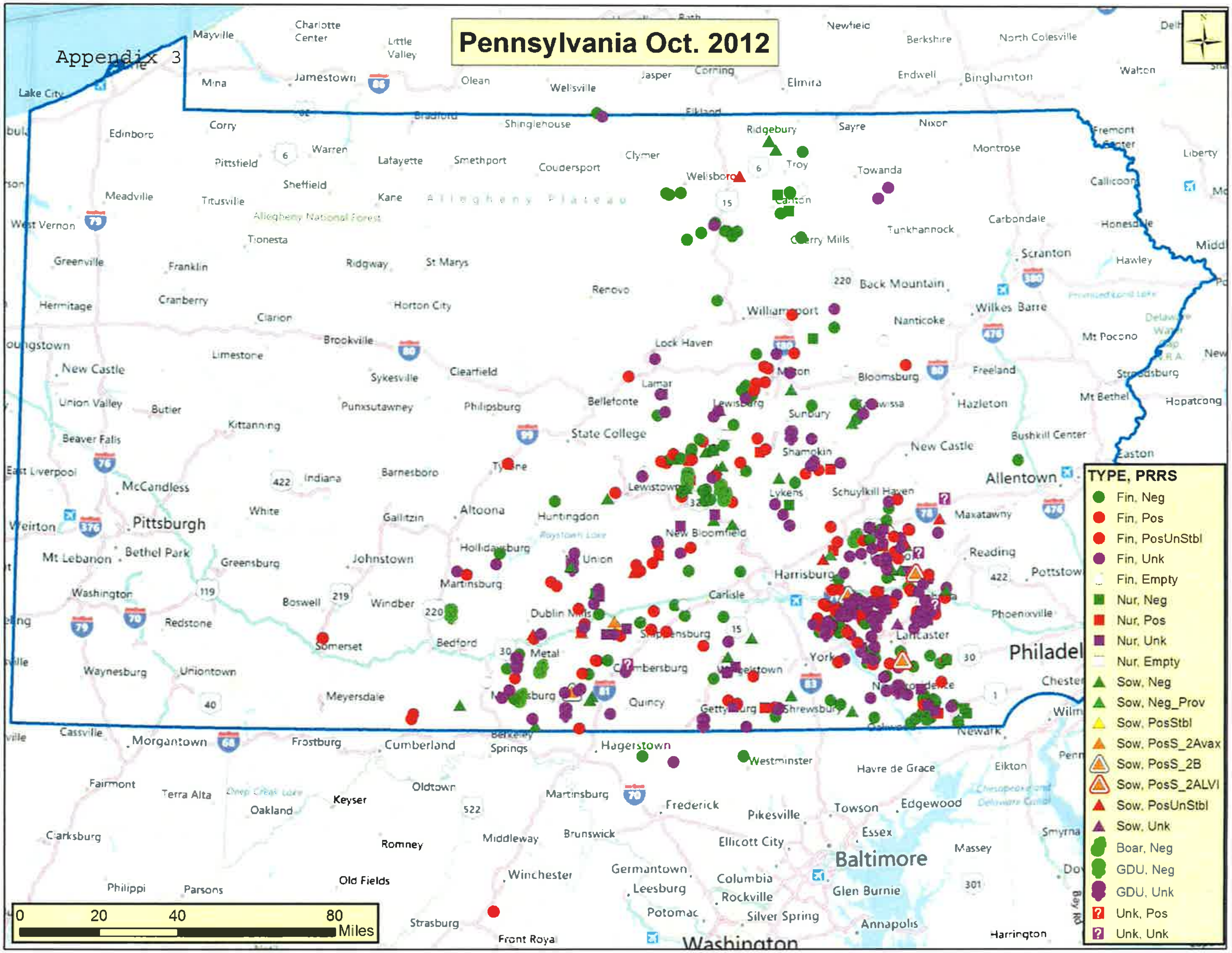
	Sow herd size							
	<=100	101-600	601-1500	1501-3000	>3000	Unknown		Total
Farrow to wean			12	10	3			25
Farrow to feeder			7	3				10
Farrow to finish			1			1		2
Show						1		1
Unknown		6	4	1		11		22
							All	60

	Sow herd size							
	<=100	101-600	601-1500	1501-3000	>3000	Unknown		Total
Unknown	1	0	1	0	0	2		4
Positive	0	0	3	6	0	2		11
Positive stable	0	0	5	2	1	0		8
Negative provisional	1	0	1	1	0	0		3
Negative	0	5	14	5	2	9		35
							All	61

	Nurseries (no sows or pigs >10 wks)										
	<=1200		1201-2400		2401-4800		>4800		Unknown		
	Source		Source		Source		Source		Source		
	inside region	outside region	inside region	outside region	inside region	outside region	inside region	outside region	inside region	outside region	Total
Unknown	2		6				1		1		10
Positive					11	5	2	1			19
Positive stable											0
Negative provisional											0
Negative					3	1	6		1		11
Total	2	0	6	0	14	6	9	1	2		All 40

	Finishing or Wean to finish										
	<=1200		1201-2400		2401-4800		>4800		Unknown		
	Source		Source		Source		Source		Source		
	inside region	outside region	inside region	outside region	inside region	outside region	inside region	outside region	inside region	outside region	Total
Unknown	22		28		30		4		5	5	89
Positive	4	3	19	15	17	3	4	1		29	66
Positive stable											0
Negative provisional											0
Negative	7	1	32	9	17	7	2	1	2		78
Total	33	4	79	24	64	10	10	2	7	34	All 267

Appendix 3


Pennsylvania Oct. 2012
TYPE, PRRS
Fin, Neg
Fin, Pos
Fin, PosUnStbl
Fin, Unk
Fin, Empty
Nur, Neg
Nur, Pos
Nur, Unk
Nur, Empty
Sow, Neg
Sow, Neg_Prov
Sow, PosStbl
Sow, PosS_2Avax
Sow, PosS_2B
Sow, PosS_2ALVI
Sow, PosUnStbl
Sow, Unk
Boar, Neg
GDU, Neg
GDU, Unk
Unk, Pos
Unk, Unk
0 20 40 80
Miles

Pennsylvania PRRS Regional Control Task Force

Voting Members

Scott Hoffer(Murphy Brown)
Richard Kreider (Hershey Ag)

Kurt Good (Good's Livestock)

Barry Geib(White Oak Mills)

Drew Derstein (Deerstone Ag)

Scott Bailey (Wenger Feeds)

Keith/Jason Kurtz (Keystone Mills)

Aaron Ott (Country View Family Farms)

Mac Magee (Commercial Concepts)

Tom Pastor (PIC)

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Technical Advisors

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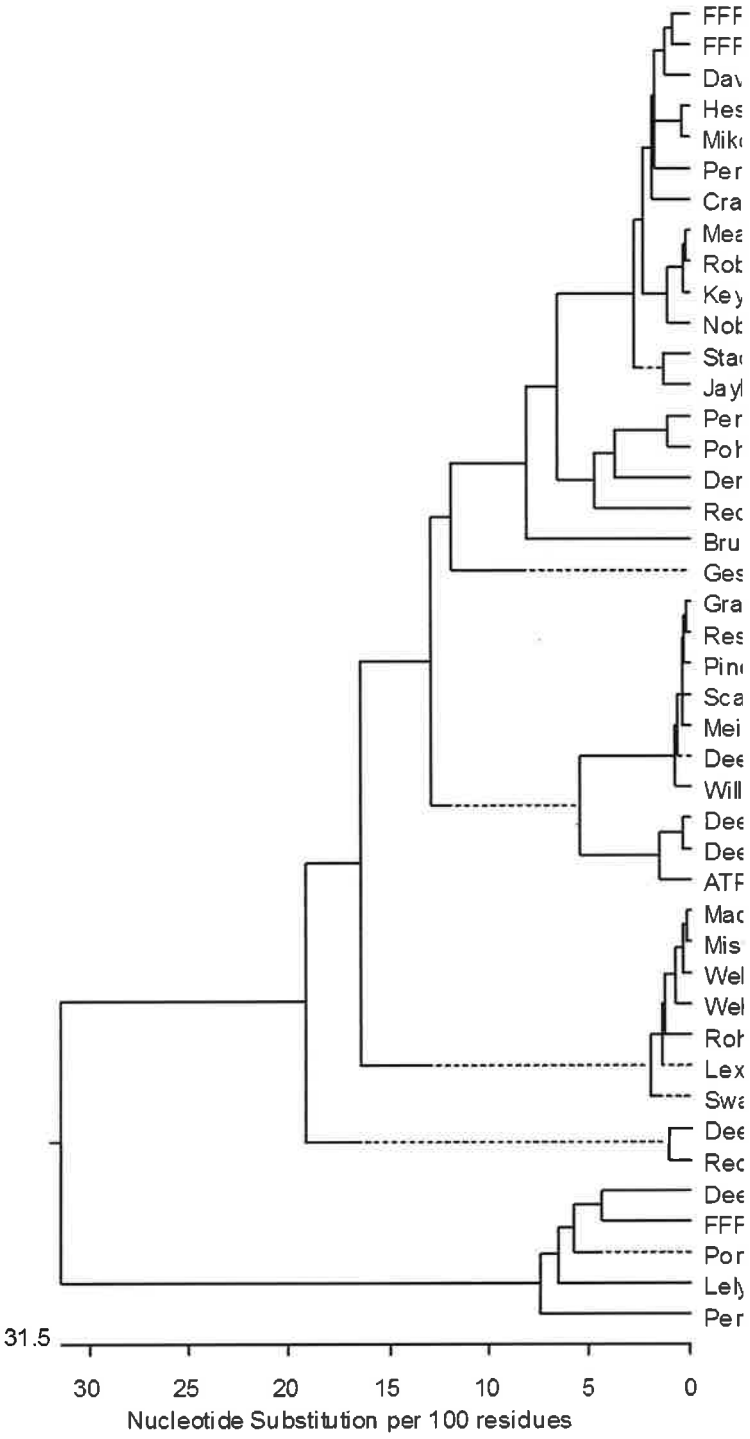
Dr. Jessica Risser (Country View Family Farms)

Dr. Jeremy Pittman (Murphy-Brown)

Dr. Ines Rodriquez (University of Pennsylvania)

Dr. Keith Zimmerman (River Valley Animal Health)

Appendix 5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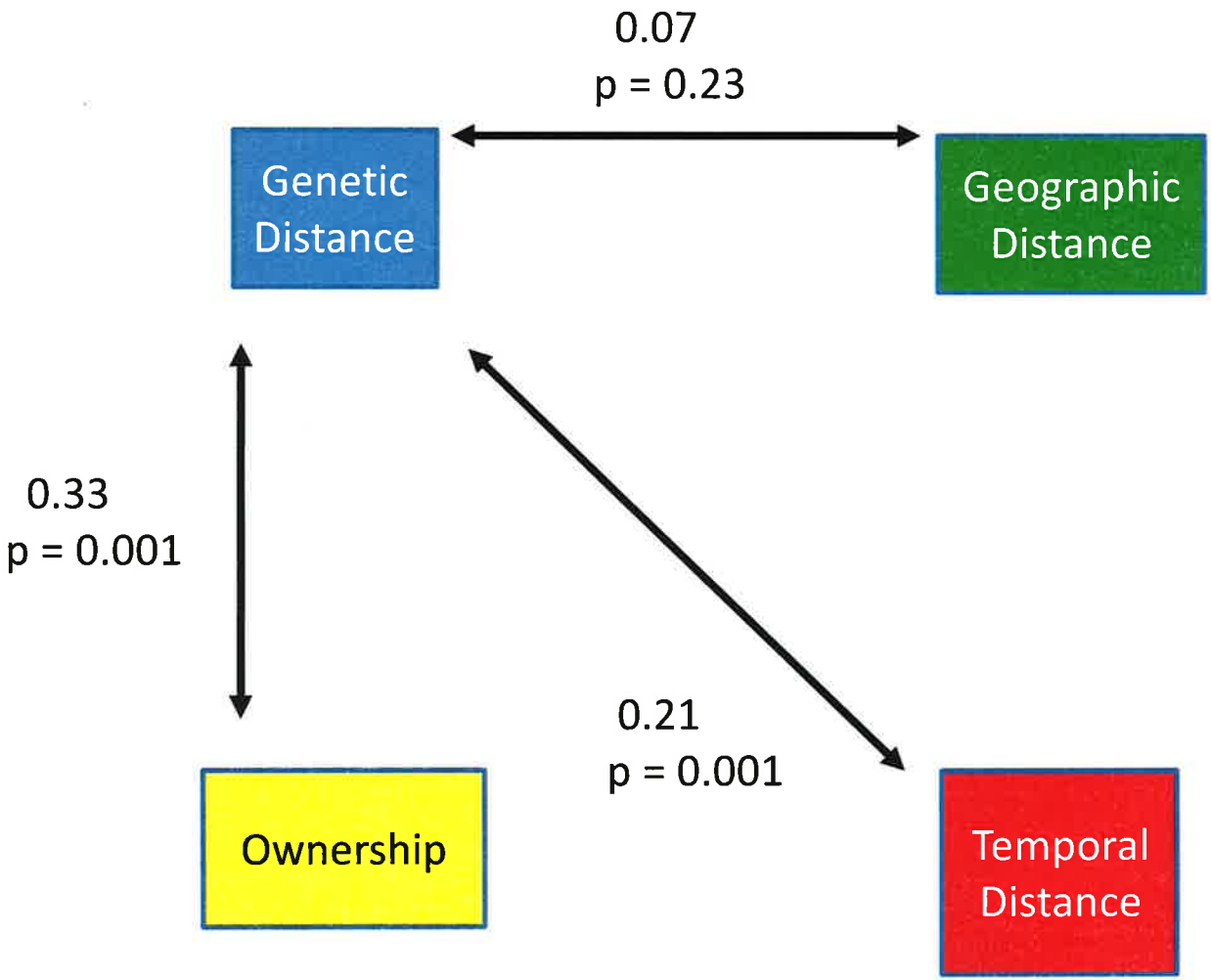
FFF
Dav
Hes
Mik
Per
Cra
Mea
Rob
Key
Nob
Sta
Jay
Per
Poh
Der
Rec
Bru
Ges
Gra
Res
Pin
Sca
Mei
Dee
Will
Dee
Dee
ATF
Mac
Mis
Wel
Wel
Roh
Lex
Swa
Dee
Rec
Dee
FFF
Por
Lel
Per
31.5
30
25
20
15
10
5
0
Nucleotide Substitution per 100 residues


0.07
p = 0.23
Genetic Distance
Geographic Distance
0.33
p = 0.001
0.21
p = 0.001
Ownership
Temporal Distance