Prevalence of Scrapie resistance genes in Cal Poly Pomona's Dorset and hair sheep flocks

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Abstract

Scrapie is a lethal degenerative condition, in which a sheep is exposed via ingestion or skin cuts to an infective protein prion Scrapie (PrP), ultimately leading to spongiform encephalopathy. Scrapie prions bind to natural and normal cellular prions, inducing them to misfold into the malignant prion form. This process repeats itself in a chain reaction; eventually prions accumulate in tissues and cause severe neurological illness in sheep, and inevitably death. Sheep genetics plays a role in resistance to the disease, with codon 171, coding for certain amino acids, glutamine (Q) or Arginine (R), which inhibits the ability of PrP to interact with healthy proteins. If the sheep genome codes for QQ, then the sheep is susceptible for Scrapie. If it codes for QR, then the sheep is somewhat resistant, while RR sheep are highly resistant to PrP. This research will collect skin samples from two sheep populations at Cal Poly Pomona. Dorset sheep herd, which was selected for the PrP resistance gene. And Hair sheep herd, which was not selected for the resistance gene. The research attempted to determine whether the sheep's PrP resistance genotype is dependent on its breed and selection process. The research utilized TypiFix™ sample collectors, which collected a skin sample from the sheep's ear and analyzed in an of site lab. The results showed a significant difference (in both P-value and Chi-square) between the Dorset and Hair sheep herds genotypic and allele PrP resistance frequency.

Introduction

Scrapie is a fetal neuro degenerative disease, which affects both sheep and goats. The condition caused by Scrapie is called spongiform encephalopathy, and it is caused by the accumulation of proteins that were induced to fold into a malignant form. Scrapie prions (PrP) are virulent proteins which causes this process to occur. Once a PrP attaches to a natural cellular prion and changes its confirmation to a virulent PrP form, the body natural enzymes become unable to lyse it. These proteins accumulate in neural tissues, and over time, causes severe neurological illness in sheep, and inevitably death. A Scrapie outbreak in any herd is a serious event, one which can cause a farmer his entire herd.

Sheep genetics plays a vital role in their ability to whitened and resist naturally occurring Scrapie infections, such as codon 136, 141 and 171. However, codon 171 is responsible for a much more drastic effect on sheep Scrapie resistance properties. Codon 171 can code for glutamine (Q) or Arginine (R), and It is sheep with this allele that indicates resistance and increase survivability rate. Sheep which carry the R gene, heterozygous or homozygous, have a significant chance to survive the disease. Some sheep breeds are typically selected for the resistance gene, while other do not. By preforming a simple skin sample extraction from sheep's ears, it is possible to analyze their genetic makeup, which will indicate if the sheep has the Scrapie resistance gene R.

This research attempts to find if there is a significant difference in Scrapie resistance gene prevalence between the Cal Poly's Dorset Sheep (which has been selected for the gene) and Hair Sheep herds (Which was not selected for the gene).

Materials and methods

29 Dorset sheep and 10 Hair sheep were chosen for the experiment. Most of the Dorset sheep herd was selected for genetic analysis, as such, their selection was not random. The 10 Hair sheep were selected randomly by collecting samples from the first 10 sheep that entered the squeeze.

Protocol:

1. Sheep are selected by staff, based on desirable traits already possessed by herd.
2. Research group is herded to an enclosed shoot (squeeze) where they could be handled one at a time, and in safety for both the handler and animal.
3. Subject is held safely by one dedicated handler, while a dedicated collector handles the TypiFix™.
4. Skin sample is taken from subjects via TypiFix™ sample collector.
   A. Prepare one sample collector and one plug.
   B. Slide plug over onto the pin of pliers as far as it will go.
   C. Make sure that the plug resides on the tip of the pliers without sliding off.
   D. Inset sample container deep into cavity holder (under the retainer clip)
   E. Device is ready as long as the tip is aligned with the center of the container's circle.
   F. Clear ear area of any dirt or moisture. Area should be clean and dry.
   G. Place collector around the subject's ear, with the plug above the ear and the collecting well below the ear.
   H. Squeeze quickly and firmly! (white cap has no more function, but it need not be taken off)
   I. If the subject shakes its head, collector must allow himself to follow the motion to avoid tearing at the ear.
   J. Sample is ready to be sent to lab for results.
4. Results are analyzed and summarized.

Figure 1: TypiFix™ collector unit and sample wells


Figure 2: Sheep squeeze, allow for animal safe restrain


Figure 3: A Dorset sheep right before data collection

Results

Out of the 29 Dorset sheep sampled, 17 possessed homozygous R gene, 11 possessed heterozygous QR gene, and 1 possessed homozygous Q gene. Out of the 10 Hair sheep sampled 1 possessed homozygous R gene, 6 possessed heterozygous QR gene, and 3 possessed homozygous Q gene. Furthermore, the Dorset sheep herd had a total population allele prevalence frequency of .78 for the R allele, and 0.22 for the Q allele. In contrast, the Hair sheep herd had a total population allele prevalence frequency of 0.40 for the R allele, and 0.60 for the Q allele.

A contingency table calculation was preformed for both genotypic allele population differences between the two herds:

- Genotypic difference
  - P-value = 0.007633
  - χ^2 = 9.75065
- Allele population difference (Yates correction was applied for a 2X2 table with DF=1)
  - P-value = 0.004682
  - χ^2 = 7.998375

Genotypic frequency	Dorset sheep genotype	Frequency	Hair sheep genotype	Frequency
RR	17	0.59	1	0.10
QR	11	0.38	6	0.60
QQ	1	0.03	3	0.30
Total	29	1	10	1

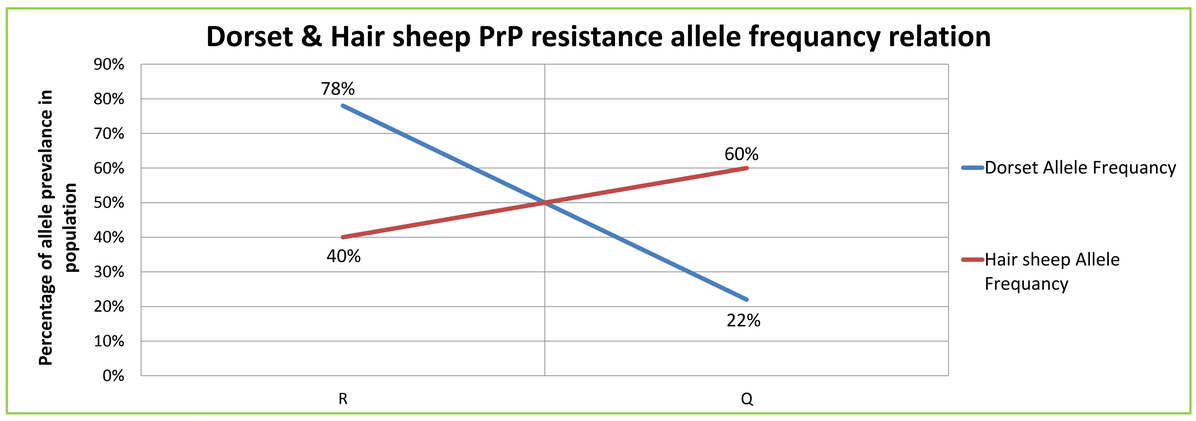
Table 1: Genotypic frequency table of both the Dorset and Hair sheep herds

Genotypic contingency table	RR	QR	QQ	
Dorset	17	11	1	29
Hair	1	6	3	10
	18	17	4	

Table 2: Genotypic contingency calculation of p-value and χ^2

Allelic population contingency table	R	Q	
Dorset	45	13	58
Hair	8	12	20
	53	25	

Table 3: Population for single allele contingency calculation of p-value and χ^2



Graph1: Allele population frequency, graph indicates an inverse relation between the Dorset and Hair sheep herds

Discussion & Conclusions

An analysis of both of the sheep herds, as displayed by Graph 1, suggests a significant difference between the two by an inverse relation. The Dorset sheep herd revealed a high prevalence of PrP resistance allele in its population. In contrast The hair sheep population displayed a minimal amount of PrP resistance allele. Table 1 aggregates the genotypic data of the two herds, the Dorset herd had a 59% genotypic ration of RR carriers, 38% of QR carriers and 3% of non resistant QQ carriers. This means that 97% of the Dorset herd is resistant to PrP to some degree, with the majority (59%) almost completely. On the other hand, the Hair sheep herd had a 10% genotypic ration of RR carriers, 60% of QR carriers, and 30% of RR non resistant carriers. This indicates that approximately 70% of the Hair sheep herd is somewhat resistant to PrP. However, this time, most of the herd (60%) is only partially resistant. In addition, a large amount of Hair sheep (30%) are non resistant to PrP.

In order to calculate the results and establish if the differences between the two herds are significant, two contingency tables were constructed. One for the genotypic ration between the herds, and one for the allelic population ration of the two herds. For the genotypic ratio, the P-value = 0.007633 and χ^2 = 9.75065. Furthermore, for the allelic population ratio, the P-value = 0.004682 and χ^2 = 7.998375. , both results, and in both cases, indicate that the differences between the groups are significant. Hence the research concludes that Cal Poly Pomona Sheep Herd's PrP resistance gene is dependent on the sheep breed.

It is possible that low sample population used to gather data from the hair sheep herd caused a bias in the final results. A future comparative test between equal and large numbers of Hair and Dorset sheep should be conducted in order to confirm that these results are significant.

Biliography

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