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**Writing Assignment 4 - Primary Article Review**

This primary article investigates the genetic basis of cattle's polled trait, which controls whether the animals have horns. In domesticated environments, polled or hornless animals are chosen for safety and because the polled gene is dominant, children of homozygous polled parents will be heterozygous. Certain breeds, such as black Angus, have uniform polling, but other breeds, like Holsteins, exhibit diversity. This study found other genetic variations that affect horn growth in addition to recognized mutations that produce polledness. In addition to known mutations that cause polledness, this research identified other genetic variations that impact horn development, including the Scurs mutation, which may be X-linked and present in heterozygous polled cattle.

Researchers discovered two overlapping haplotypes in the same chromosome region through gene mapping in Simmental and Holstein bulls. Comprehensive genome re-sequencing of different beef cattle breeds revealed a specific “indel” allele associated with polledness. This allele was found in most polled beef cattle but was absent in most polled Holsteins and in those with horn abnormalities. Re-sequencing of a homozygous polled Holstein confirmed that beef cattle without the “indel” allele still shared a haplotype common to Holsteins. This suggests that two historical mutations contributed to polledness in different cattle lineages. The “indel” allele likely originated in Angus and Galloway breeds, while the haplotype in Holsteins comes from an unknown source. The study also showed that some cattle could possess both haplotypes, indicating a shared genetic mechanism influencing horn development.

Similarly, the same re-sequencing method was applied to a homozygous polled Holstein cow. Interestingly, the beef cattle lacking the “indel” allele still exhibited the same haplotype found in polled Holsteins. This indicates that two distinct mutations occurred historically at different times and locations, both resulting in polled cattle. The “indel” variant likely originated in Angus and Galloway breeds before being introduced to others, while the haplotype seen in Holsteins has an unknown origin. The study also found that some cattle could carry both haplotypes. It was hypothesized that the overlapping nature of these haplotypes suggests they influence the same horn development pathway. The discussion revisits the possibility of the Scurs gene being X-linked; however, this remains unconfirmed and is merely speculative, based on the higher number of heterozygous males with scurs compared to females.

Additionally, breeds like the Yak demonstrate polledness without either Simmental or Holstein haplotypes in their genomes, suggesting that de novo mutations related to the polled gene can still arise. To further investigate, the study examined skin samples from fetuses at various developmental stages using mRNA sequencing, which revealed numerous “differentially expressed genes.” This sequencing clearly showed the presence of the “indel” variant in polled fetuses and its absence in horned ones, highlighting genes critical for horn development.

**Works Cited**

Wiedemar, N. et al. Independent Polled Mutations Leading to Complex Gene Expression

Differences in Cattle. *Plos One* **9**; <https://doi.org/10.1371/journal.pone.0093435>(2014).