

Genetic Marker Exploration for Livestock Vertebral Traits

Subjects: **Genetics & Heredity**

Contributor: Muhammad Zahoor Khan , Wenting Chen , Bingjian Huang , Xiaotong Liu , Xinrui Wang , Yihong Liu , Wenqiong Chai , Changfa Wang

In livestock breeding, the number of vertebrae has gained significant attention due to its impact on carcass quality and quantity. Variations in vertebral traits have been observed across different animal species and breeds, with a strong correlation to growth and meat production. Furthermore, vertebral traits are classified as quantitative characteristics. Molecular marker techniques, such as marker-assisted selection (MAS), have emerged as efficient tools to identify genetic markers associated with vertebral traits.

livestock

vertebral traits

meat production

genetic markers

1. Introduction

The meat production industry encounters challenges in augmenting carcass and meat quality attributes, significantly influencing consumer preferences and demand amid the global upsurge in meat consumption [1][2]. Key attributes encompassing body morphology, skeletal architecture, vertebral characteristics, muscular development, tenderness, and adipose deposition in livestock species hold paramount significance in governing both meat quality and quantity [3][4][5][6][7][8][9].

In the domain of livestock breeding, the pursuit of augmenting traits related to body size has emerged as a central objective, particularly in China, due to its substantial influence on meat production and carcass traits [10][11][12]. Recent research underscores the economic significance of vertebral count in determining carcass length, weight, and body size traits [10][11][12][13]. Variations in body size have emerged within and between domestic animal species or breeds during livestock evolution [14]. Notably, the number of thoracolumbar vertebrae plays a crucial role in carcass characteristics, particularly carcass length [15]. Across different pig breeds [16], sheep breeds [17], donkeys [10][18], and yaks [19], variations in the number of thoracolumbar vertebrae have been observed. This trait has been considered a selection criterion in commercial animal breeding due to its strong correlations with growth and meat production, exhibiting high heritability (0.60–0.62) and a positive correlation with body length [15].

China has made significant advancements in livestock genetic improvement, particularly in pig breeding [20]. However, enhancing breeding efficiency and accuracy remains a challenge. Molecular marker techniques, such as marker-assisted selection (MAS), have emerged as a rapid and effective approach [21][22][23]. MAS relies on the linkage between phenotypic traits and molecular markers within the genome, enabling the swift and accurate identification of individuals with desired traits, thus improving breeding efficiency. Identifying candidate genes and

their polymorphisms associated with vertebral traits holds scientific and economic significance, providing markers for genetic enhancement in livestock.

The influence of genetic factors and signaling pathways on multi-vertebrae traits in livestock is a complex and multifaceted area of research. Several studies have shed light on the genetic underpinnings of these traits, with a focus on genes such as *PLAG1*, *VRTN*, *PRKG2*, *MMP4*, *NR6A1*, *LTBP2*, *DCAF7*, *NCAPG-LCORL*, *ActRIIB*, and *TGFβ3*, as well as their associations with specific vertebral characteristics in various livestock species, especially pigs, donkeys, and sheep. Consistently, Yan et al. [10] and Liu Z et al. [18] emphasized the quantitative nature of these traits, indicating that they are influenced by multiple genes and intricate biological signaling pathways. This highlights the polygenic nature of multi-vertebrae traits, where numerous genetic factors interplay to determine the final outcome. The genes *PLAG1* and *NCAPG-LCORL*, originally known for their roles in human height, carcass weight, and body length, have emerged as key players in livestock vertebral traits, underscoring their pleiotropic effects [24]. Furthermore, specific mutations in genes like *ActRIIB* and *TGFβ3* have been linked to variations in vertebral number in sheep and pigs, respectively. Liu J et al. [25] identified a point mutation in intron 4 of the *ActRIIB* gene in Small-Tailed Han sheep associated with vertebral number variation. Similarly, Yue J et al. [26] reported that the mutation g.105179474 G > A in the *TGFβ3* gene was associated with rib and thoracolumbar vertebrae numbers in pigs, highlighting the genetic diversity that can underlie these traits. In Beijing Black pigs, Niu N et al. [27] identified a significant link between variant-g.19034 A > C of the *VRTN* gene and multiple thoracic vertebrae numbers, further exemplifying the genetic complexity of vertebral traits in sheep and pigs.

Donkeys are a comparatively less explored area in this context and have shown promising insights. Shi et al. [28] reported significant associations between specific genetic loci, *HOXC8* g.15179224C > T and g.15179674G > A, with lumbar vertebrae length and the number of lumbar vertebrae. This highlights the potential for genetic selection and breeding strategies to influence vertebral traits in donkeys, similar to other livestock species. Nevertheless, the existing body of literature to date has exclusively focused on the investigation of genetic markers associated with vertebral traits in donkeys, sheep, and pigs. However, it is noteworthy that comprehensive investigations into the association of genetic markers with vertebral traits in cattle and horses have been absent from the existing body of research. Drawing upon the aforementioned evidence, it becomes evident that variations in vertebral traits among livestock species (donkeys, sheep, and pigs) can significantly influence changes in body size, carcass length, and weight. Furthermore, it is essential to recognize that vertebral traits are inherently quantitative in nature, controlled by a complex interplay of multiple genes. Thus, the exploration and screening of genes associated with these vertebral traits hold substantial potential for enhancing meat production within the livestock sector, thereby making a notable contribution to the meat industry.

2. Genetic Markers Associated with Number of Vertebrae in Pigs, Donkeys, and Sheep

2.1. Genetic Markers Associated with Number of Vertebrae in Pigs

Pig vertebral classification comprises five distinct segments: cervical, thoracic, lumbar, sacral, and caudal vertebrae. The precise count of cervical, sacral, and caudal vertebrae in pigs is consistent at seven, four, and five, respectively [15]. The key constituents of the vertebral column are the thoracic and lumbar vertebrae, exhibiting considerable variability in their numbers. In Western modern breeds, the thoracic vertebral number spans from 13 to 17, while the lumbar vertebral number ranges from five to seven [13][15]. Wild boars possess 19 thoracic-lumbar vertebrae, whereas Chinese indigenous breeds exhibit a total thoracic and lumbar vertebral count ranging from 19 to 20 [13][15]. Notably, Western commercial breeds such as Large White, Duroc, and Landrace feature a higher number of thoracic-lumbar vertebrae ($n = 21$ to 23) due to rigorous selective breeding [13][15]. In pigs, some causal or tightly linked genes affecting crucial vertebral traits and used in practical production have been reported in previous studies [29][30][31][32]. In practical pig production, the integration of genetic knowledge regarding vertebral traits allows producers to make informed breeding decisions. Selecting breeding stock based on favorable genetic markers can lead to more robust, efficient, and economically viable pig populations. In addition, vertebral malformations can lead to structural deformities, reduced growth rates, and increased susceptibility to injuries. This, in turn, contributes to the sustainability and competitiveness of the swine industry. The summary of genes associated with vertebral traits is provided in **Table 1**.

Table 1. Summary of genes associated with vertebral traits in pigs.

Genes	Associated Traits	Breeds	Country Reference
<i>RSAD2-CMPK2, COL3A1</i>	◊ Bone and skeletal development	Meishan pigs	China [30]
<i>HMGA1, VRTN, BMP2</i>	◊ Effects the number and length of vertebrae and the size of hind leg bones	Duroc × Landrace × Yorkshire crossbred pigs	[31][32]
<i>TIMP2, EML1, SMN1</i>	◊ Rib weights	Pigs	[33]
<i>NR6A1, LTBP2</i>	◊ Number of vertebrae	Xiang pigs	[34]
<i>GREB1L, ABCD4, VRTN, MIB1</i>	◊ Number of ribs	Beijing Black pigs	[27]
<i>ABCD4 Hox family genes (HOXB 1–7, 9, and 13), NTRK2</i>	◊ Vertebral number	Beijing Black pigs	[35]
<i>NR6A1, VRTN PLAG1, BMP2 MC4R</i>	◊ Number of thoracic and lumbar vertebrae	Shanxia Black pigs	[36]

Genes	Associated Traits	Breeds	Country Reference
<i>HOXA10</i>	✧ Development of thoracolumbar vertebrae and rib primordium	Pigs	[37]
<i>BMP2</i>	✧ Growth and bone development ✧ Carcass length	Duroc × (Landrace × Yorkshire) hybrid pigs	[38]
<i>VRTN, LTBP2, BMPR1A, FOS</i>	✧ Number of thoracic vertebrae	White × Minzhu crossbred pigs	[39]
<i>VRTN</i>	✧ Number of vertebrae	Sujiang, Meishan, Bama, Erhualian, and Tibetan pigs	[40]
<i>VRTN</i>	✧ Number of ribs	Suhuai pigs	[13]
<i>VRTN</i>	✧ Number of thoracic vertebrae	Pigs	[41]
<i>VRTN</i>	✧ Number of vertebrae and ribs	Duroc, Landrace, and Large White pigs	Norway [42]
<i>MMP9, VEGF</i>	✧ Pig femur and vertebra	Pigs	USA [43]
<i>NR6A1</i>	✧ Lumbar vertebrae	Large White × Minzhu pigs	China [44]
<i>VRTN, FOS, PROX2, TGFB3</i>	✧ Number of thoracic vertebrae		

2.2. GENETIC MARKERS ASSOCIATED WITH NUMBER OF VERTEBRAE IN DONKEYS

The study by Liu Z et al. [18], which involved a comprehensive survey of 455 donkeys, highlighted the presence of diverse configurations of thoracic and lumbar vertebrae in the Dezhou donkey population [18]. These configurations were identified as T18L5, T18L6, T17L6, T17L5, and T19L5. Notably, T18L5 was the most prevalent, accounting for 75.8% of the population. This finding suggests a certain level of variability in vertebral numbers among Dezhou donkeys. Moreover, research conducted by Liu Z et al. also established a correlation between the body size and weight of donkeys and the number of vertebrae (Figure 1) [18][45]. This correlation could potentially open up avenues for selective breeding and manipulation of vertebral numbers to enhance the structural characteristics of donkeys within the industry. However, it is important to note that the genetic mechanisms governing these traits require further investigation.

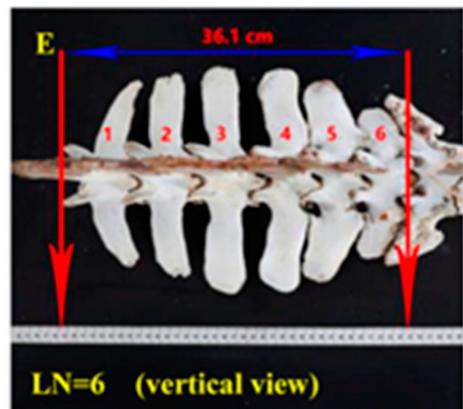
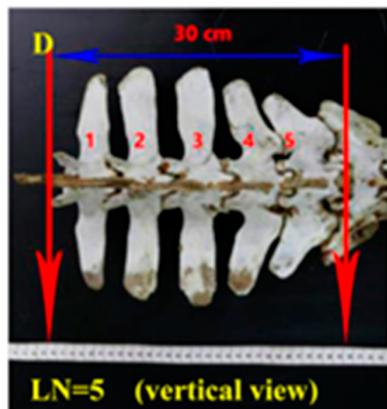
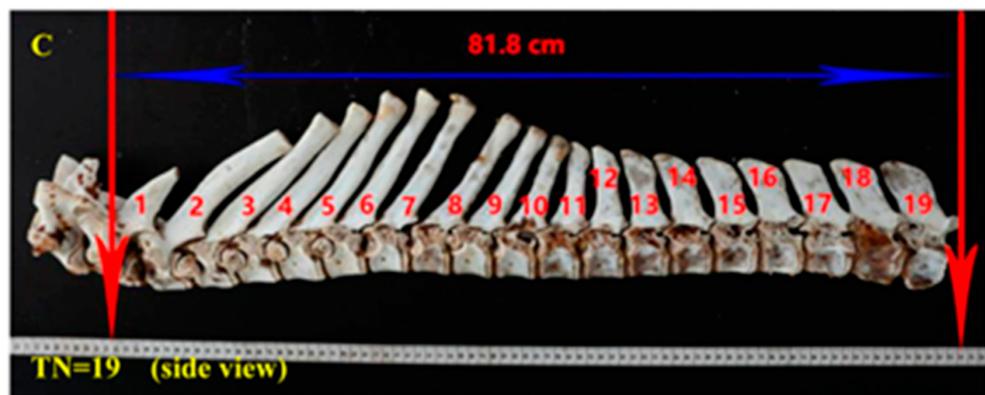
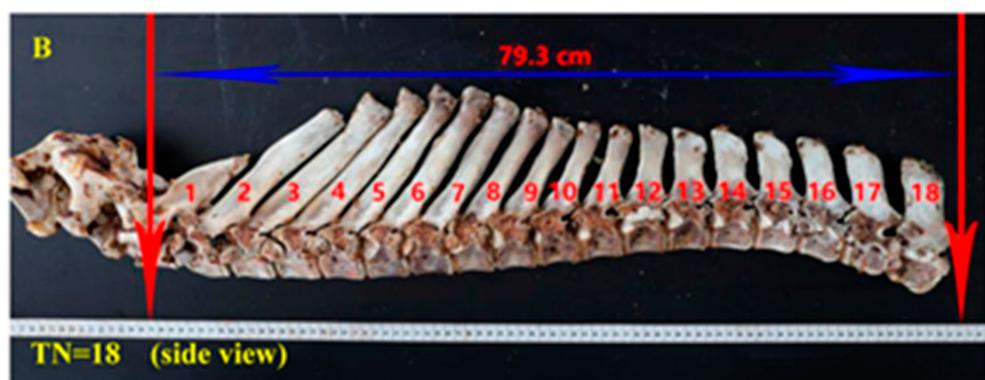
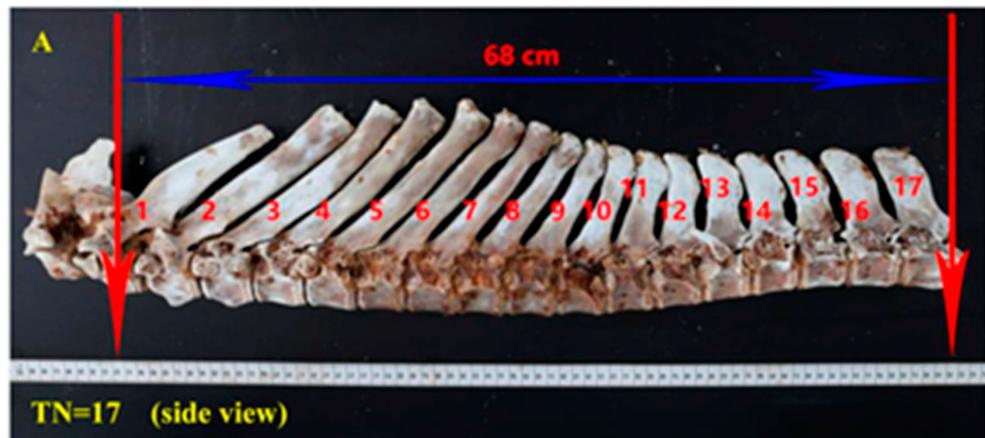


Figure 1. Association of number of vertebrae with body size traits. **(A)** Side overview of 17 thoracic vertebrae; **(B)** Eighteen thoracic vertebrae side overview of seventeen; **(C)** Side overview of 19 thoracic vertebrae; **(D)** Five lumbar vertebrae vertical overview; **(E)** Six lumbar vertebrae vertical overview.

In the context of understanding the genetic basis of vertebral number determination in donkeys, recent studies have made significant contributions [12][18][45][46]. Specifically, the *PRKG2* gene has emerged as a key player associated with both the number and length of thoracic and lumbar vertebrae in donkeys [12]. Specific genetic variants within *PRKG2* were found to be significantly correlated with thoracic and lumbar vertebrae numbers as well as their length. This genetic insight provides valuable information for further research into the molecular mechanisms behind vertebral development.

It is worth noting that *PRKG2*, located on chromosome 3, consists of 18 exons and 17 introns in donkeys, as outlined by Wang C et al. [22]. Interestingly, *PRKG2* has also been implicated in dwarfism in various species, including American Angus cattle [47], humans [48][49], and dogs [50], underscoring its importance in skeletal development across different organisms. Additionally, its involvement in adipocyte and osteoblast differentiation in the human body, as reported by Yi et al., highlights the multifaceted nature of *PRKG2*'s functions [51]. In conclusion, the research on vertebral variations in Dezhou donkeys, coupled with the identification of the *PRKG2* gene and its associated genetic variants, provides a foundation for further exploration into the genetic mechanisms governing vertebral development. The summary of genes associated with vertebral traits in donkeys is provided in **Table 2**.

Table 2. Summary of genes associated with vertebral traits in donkeys.

Genetic Markers	Biological Effect	Breed	Country	Reference
DCAF7	◊ Number of thoracolumbar vertebrae	Dezhou donkeys	China	[11]
	◊ Number of thoracic vertebrae			
PRKG2	◊ The number and the length of lumbar vertebrae			[12]
NR6A1	◊ Number of lumbar vertebrae			[18]
LTBP2	◊ Number of thoracic and lumbar vertebrae			[46]
HOXC8	◊ Number and length of lumbar vertebrae			[28]

Genetic Markers	Biological Effect	Breed	Country	Reference
<i>NLGN1, DCC, FBXO4</i> <i>SLC26A7, TOX, LRP5</i> <i>WNT7A, LOC123286078, LOC123280142, GABBR2, LOC123277146, LOC123277359, BMP7, B3GAT1, EML2</i>	<ul style="list-style-type: none"> ◊ Involved in Wnt and TGF-β signaling pathway regulation, which is linked with embryonic development or bone formation ◊ Number of thoracic vertebrae ◊ Number of lumbar vertebrae 			[10]

Vertebrae in Sheep

In the context of sheep anatomy, sheep typically possess a vertebral arrangement comprising seven cervical vertebrae (C), 13 thoracic vertebrae (T), six lumbar vertebrae (L), and four sacral vertebrae (S), totaling 30 vertebrae. Notably, mutations in the thoracolumbar region, such as T14L6 or T13L7, have been identified as the most prevalent [52]. These mutations are associated with multi-vertebrae sheep, which exhibit enhanced adaptability and meat production performance [52]. The cultivation of such multi-spine sheep carries substantial benefits for the economy, society, and ecology, making it a pivotal endeavor for improving the quality and efficiency of the animal husbandry industry.

In the case of Kazakh sheep, an indigenous breed in Western Xinjiang, China, there exists variability in the number of lumbar vertebrae. While most sheep conform to the standard configuration of 13 thoracic vertebrae and six lumbar vertebrae, denoted as T13L6, Kazakh sheep exhibit variations, specifically in T13L7 and T14L6. These variations correspondingly lead to an increase in carcass length by 2.22 cm and 2.93 cm compared to the typical T13L6 Kazakh sheep. Moreover, there is a corresponding elevation in carcass weight by 1.68 kg and 1.90 kg, respectively [53][54][55]. Significant progress has been achieved in China regarding the screening of genetic markers associated with vertebral traits in sheep [56][57][58][59][60][61][62]. For the sake of clarity, researchers compiled a concise summary of genes related to vertebral count and bone development, presented in **Table 3**.

Table 3. Summary of genes associated with vertebral traits and bone development in sheep.

Genes	Associated Traits	Breeds	Country	Reference
<i>NR6A1</i>	<ul style="list-style-type: none"> ◊ Variation in the number of lumbar spine segments 	Xinjiang Kazakh sheep	China	[56]
<i>SFRP4</i>	<ul style="list-style-type: none"> ◊ It plays a role in bone development and is associated with the presence of multiple lumbar vertebrae 	Duolang sheep		[57]
<i>SYNDIG1L, UNC13C</i>	<ul style="list-style-type: none"> ◊ Influence the number of thoracic vertebrae 	Han sheep and Sunite		[52]

Genes	Associated Traits	Breeds	Country Reference
<i>TBXT</i>	◊ Associated with the determination of caudal vertebrae number and tail length	Sheep	[58]
<i>MGAT4A, KCNH1 CPOX, CPQ</i>	◊ Play a role in determining the number of ribs in vertebrates	Hu sheep	[59]
<i>LTBP2, SYNDIG1L</i>	◊ Associated with the number of both ribs and vertebrae in vertebrates	Large fat-tailed sheep, Altay sheep, Tibetan sheep	[60]
<i>VRTN, HoxA</i>	◊ Linked with vertebral development and associated with the presence of thoracic vertebrae. They also play a role in regulating spinal development and morphology.	Xinjiang Kazakh sheep	[61]
<i>NDRG2</i>	◊ Associated with the development of the spine and provides valuable genetic resources for studying the transcriptome of various vertebral traits	Kazakh sheep	[62]
<i>VRTN</i>	◊ Correlated with thoracic vertebral number, carcass length, and carcass weight in vertebrates	China Kazakh sheep	[55]
<i>NID2, ACAN</i>	◊ Involved in skeletal development and the maintenance of cartilage structure	Afghani sheep	Iran [63]
<i>ALX4, HOXB13, BMP4 EYA2, SULF2</i>	◊ Involved in the embryonic development of tendons, bones, and cartilage as well as the development of limbs, the skeleton, and tail formation	Ethiopian indigenous sheep	Ethiopia [64]

References

1. Whitton, C.; Bogueva, D.; Marinova, D.; Phillips, C.J.C. Are We Approaching Peak Meat Consumption? Analysis of Meat Consumption from 2000 to 2019 in 35 Countries and Its

Relationship to Gross Domestic Product. *Animals* 2021, 11, 3466.

2. Hötzl, M.J.; Vandresen, B. Brazilians' attitudes toward meat consumption and production: Present and future challenges to the sustainability of the meat industry. *Meat Sci.* 2022, 192, 108893.

3. Chai, W.; Qu, H.; Ma, Q.; Zhu, M.; Li, M.; Zhan, Y.; Liu, Z.; Xu, J.; Yao, H.; Li, Z.; et al. RNA-seq analysis identifies differentially expressed genes in different types of donkey skeletal muscles. *Anim. Biotechnol.* 2023, 34, 1786–1795.

4. Ma, Q.; Kou, X.; Yang, Y.; Yue, Y.; Xing, W.; Feng, X.; Liu, G.; Wang, C.; Li, Y. Comparison of Lipids and Volatile Compounds in Dezhou Donkey Meat with High and Low Intramuscular Fat Content. *Foods* 2023, 12, 3269.

5. Chai, W.; Xu, J.; Qu, H.; Ma, Q.; Zhu, M.; Li, M.; Zhan, Y.; Wang, T.; Gao, J.; Yao, H.; et al. Differential proteomic analysis to identify potential biomarkers associated with quality traits of Dezhou donkey meat using a data-independent acquisition (DIA) strategy. *LWT* 2022, 166, 113792.

6. Dagevos, H.; Verbeke, W. Meat consumption and flexitarianism in the Low Countries. *Meat Sci.* 2022, 192, 108894.

7. Realini, C.E.; Ares, G.; Antúnez, L.; Brito, G.; Lizardo, S.; Del Campo, M.; Saunders, C.; Farouk, M.M.; Montossi, F.M. Meat insights: Uruguayan consumers' mental associations and motives underlying consumption changes. *Meat Sci.* 2022, 192, 108901.

8. Wang, T.; Shi, X.; Liu, Z.; Ren, W.; Wang, X.; Huang, B.; Kou, X.; Liang, H.; Wang, C.; Chai, W. A novel A>G polymorphism in the intron 1 of LCORL gene is significantly associated with hide weight and body size in Dezhou donkey. *Animals* 2022, 12, 2581.

9. Gao, G.; Gao, N.; Li, S.; Kuang, W.; Zhu, L.; Jiang, W.; Yu, W.; Guo, J.; Li, Z.; Yang, C.; et al. Genome-wide association study of meat quality traits in a three-way crossbred commercial pig population. *Front. Genet.* 2021, 12, 614087.

10. Yan, S.U.; Li, Y.H.; Zhao, C.H.; Jun, T.E.; Wang, Y.H.; Wang, T.Q.; Shi, X.Y.; Liu, Z.W.; Li, H.J.; Wang, J.J.; et al. Genome-wide association study for numbers of vertebrae in Dezhou donkey population reveals new candidate genes. *J. Integr. Agric.* 2023, 22, 3159–3169.

11. Wang, T.; Wang, X.; Liu, Z.; Shi, X.; Ren, W.; Huang, B.; Liang, H.; Wang, C.; Chai, W. Genotypes and haplotype combination of DCAF7 gene sequence variants are associated with the number of thoracolumbar vertebrae and carcass traits in Dezhou donkey. *J. Appl. Anim. Res.* 2023, 51, 31–39.

12. Wang, T.; Liu, Z.; Wang, X.; Li, Y.; Akhtar, F.; Li, M.; Zhang, Z.; Zhan, Y.; Shi, X.; Ren, W.; et al. Polymorphism Detection of PRKG2 Gene and Its Association with the Number of Thoracolumbar Vertebrae and Carcass Traits in Dezhou Donkey. *BMC Genom. Data* 2023, 24, 2.

13. Jiang, N.; Liu, C.; Lan, T.; Zhang, Q.; Cao, Y.; Pu, G.; Niu, P.; Zhang, Z.; Li, Q.; Zhou, J.; et al. Polymorphism of VRTN Gene g. 20311_20312ins291 Was Associated with the Number of Ribs, Carcass Diagonal Length and Cannon Bone Circumference in Suhuai Pigs. *Animals* 2020, 10, 484.

14. Fogel, J.L.; Lakeland, D.L.; Mah, I.K.; Mariani, F.V. A minimally sufficient model for rib proximal-distal patterning based on genetic analysis and agent-based simulations. *eLife* 2017, 6, e29144.

15. Borchers, N.; Reinsch, N.; Kalm, E. The number of ribs and vertebrae in a Piétrain cross: Variation, heritability and effects on performance traits. *J. Anim. Breed. Genet.* 2004, 121, 392–403.

16. Burgos, C.; Latorre, P.; Altarriba, J.; Carrodeguas, J.; Varona, L.; López Buesa, P. Allelic frequencies of NR6A1 and VRTN, two genes that affect vertebrae number in diverse pig breeds: A study of the effects of the VRTN insertion on phenotypic traits of a Duroc×Landrace–Large White cross. *Meat Sci.* 2015, 100, 150–155.

17. Donaldson, C.L.; Lambe, N.R.; Maltin, C.A.; Knott, S.; Bunger, L. Between-and within-breed variations of spine characteristics in sheep. *J. Anim. Sci.* 2013, 91, 995–1004.

18. Liu, Z.; Gao, Q.; Wang, T.; Chai, W.; Zhan, Y.; Akhtar, F.; Zhang, Z.; Li, Y.; Shi, X.; Wang, C. Multi-Thoracolumbar Variations and NR6A1 Gene Polymorphisms Potentially Associated with Body Size and Carcass Traits of Dezhou Donkey. *Animals* 2022, 12, 1349.

19. Yang, J.; Wen, Y.; Feng, Z.; Ke, M.; Gao, X.; An, D. Correlation analysis for beef performance and multi-vertebra properties of Jinchuan yak. *J. Domest. Anim. Ecol.* 2015, 36, 26–30.

20. Palombo, V.; D’Andrea, M.; Licastro, D.; Dal Monego, S.; Sgorlon, S.; Sandri, M.; Stefanon, B. Single-step genome-wide association study identifies QTL signals for untrimmed and trimmed thigh weight in Italian crossbred pigs for dry-cured ham production. *Animals* 2021, 11, 1612.

21. Yang, W.; Liu, Z.; Zhao, Q.; Du, H.; Yu, J.; Wang, H.; Liu, X.; Liu, H.; Jing, X.; Yang, H.; et al. Population Genetic Structure and Selection Signature Analysis of Beijing Black Pig. *Front. Genet.* 2022, 13, 860669.

22. Wang, C.; Li, H.; Guo, Y.; Huang, J.; Sun, Y.; Min, J.; Wang, J.; Fang, X.; Zhao, Z.; Wang, S.; et al. Donkey genomes provide new insights into domestication and selection for coat color. *Nat. Commun.* 2020, 1, 6014.

23. Chen, W.; Fang, G.F.; Wang, S.D.; Wang, H.; Zeng, Y.-Q. Longissimus lumborum muscle transcriptome analysis of Laiwu and Yorkshire pigs differing in intramuscular fat content. *Genes Genom.* 2017, 39, 759–766.

24. Takasuga, A. PLAG1 and NCAPG-LCRTL in livestock. *Anim. Sci. J.* 2016, 87, 159–167.

25. Liu, J.; Sun, S.; Han, L.; Li, X.; Sun, Z. Association between single nucleotide polymorphism of ActRIIB gene and vertebra number variation in small tail Han sheep. *Acta Vet. Et. Zootech. Sin.* 2010, 41, 951–954.

26. Yue, J.; Guo, H.; Zhou, W.; Liu, X.; Wang, L.; Gao, H.; Hou, X.; Zhang, Y.; Yan, H.; Wei, X. Polymorphism Sites of TGF β 3 Gene and Its Association Analysis with Vertebral Number of Porcine. *Chin. Anim. Husb. Vet. Med.* 2018, 45, 738–744.

27. Niu, N.; Liu, Q.; Hou, X.; Liu, X.; Wang, L.; Zhao, F.; Gao, H.; Shi, L.; Wang, L.; Zhang, L. Genome-wide association study revealed ABCD4 on SSC7 and GREB1L and MIB1 on SSC6 as crucial candidate genes for rib number in Beijing Black pigs. *Anim. Genet.* 2022, 53, 690–695.

28. Shi, X.; Li, Y.; Wang, T.; Ren, W.; Huang, B.; Wang, X.; Liu, Z.; Liang, H.; Kou, X.; Chen, Y.; et al. Association of HOXC8 Genetic Polymorphisms with Multi-Vertebral Number and Carcass Weight in Dezhou Donkey. *Genes* 2022, 13, 2175.

29. Xu, J.; Jiang, A.; Zhang, C.; Zheng, Y.; Zhang, T.; Zhou, L. Potential of eight mutations for marker-assisted breeding in Chinese Lulai black pigs. *Can. J. Anim. Sci.* 2022, 102, 431–439.

30. Liu, C.; Hou, L.; Zhao, Q.; Zhou, W.; Liu, K.; Liu, Q.; Zhou, T.; Xu, B.; Li, P.; Huang, R. The selected genes NR6A1, RSAD2-CMPK2, and COL3A1 contribute to body size variation in Meishan pigs through different patterns. *J. Anim. Sci.* 2023, 101, skad304.

31. Xie, L.; Qin, J.; Yao, T.; Tang, X.; Cui, D.; Chen, L.; Rao, L.; Xiao, S.; Zhang, Z.; Huang, L. Genetic dissection of 26 meat cut, meat quality and carcass traits in four pig populations. *Genet. Sel. Evol.* 2023, 55, 43.

32. Xie, L.; Qin, J.; Rao, L.; Cui, D.; Tang, X.; Chen, L.; Xiao, S.; Zhang, Z.; Huang, L. Genetic dissection and genomic prediction for pork cuts and carcass morphology traits in pig. *J. Anim. Sci. Biotechnol.* 2023, 14, 116.

33. Zhou, F.; Quan, J.; Ruan, D.; Qiu, Y.; Ding, R.; Xu, C.; Ye, Y.; Cai, G.; Liu, L.; Zhang, Z.; et al. Identification of Candidate Genes for Economically Important Carcass Cutting in Commercial Pigs through GWAS. *Animals* 2023, 13, 3243.

34. Wang, X.; Ran, X.; Niu, X.; Huang, S.; Li, S.; Wang, J. Whole-genome sequence analysis reveals selection signatures for important economic traits in Xiang pigs. *Sci. Rep.* 2022, 12, 11823.

35. Niu, N.; Wang, H.; Shi, G.; Liu, X.; Liu, H.; Liu, Q.; Yang, M.; Wang, L.; Zhang, L. Genome scanning reveals novel candidate genes for vertebral and teat number in the Beijing Black Pig. *Anim. Genet.* 2021, 52, 734–738.

36. Li, L.Y.; Xiao, S.J.; Tu, J.M.; Zhang, Z.K.; Zheng, H.; Huang, L.B.; Huang, Z.Y.; Yan, M.; Liu, X.D.; Guo, Y.M. A further survey of the quantitative trait loci affecting swine body size and carcass traits in five related pig populations. *Anim. Genet.* 2021, 52, 621–632.

37. Li, J.; Wang, L.; Yu, D.; Hao, J.; Zhang, L.; Adeola, A.C.; Mao, B.; Gao, Y.; Wu, S.; Zhu, C.; et al. Single-cell RNA sequencing reveals thoracolumbar vertebra heterogeneity and rib-genesis in pigs. *Genom. Proteom. Bioinform.* **2021**, *19*, 423–436.

38. Zhang, H.; Zhuang, Z.; Yang, M.; Ding, R.; Quan, J.; Zhou, S.; Gu, T.; Xu, Z.; Zheng, E.; Cai, G.; et al. Genome-wide detection of genetic loci and candidate genes for body conformation traits in Duroc× Landrace× Yorkshire crossbred pigs. *Front. Genet.* **2021**, *12*, 664343.

39. Liu, Q.; Yue, J.; Niu, N.; Liu, X.; Yan, H.; Zhao, F.; Hou, X.; Gao, H.; Shi, L.; Wang, L.; et al. Genome-wide association analysis identified BMPR1A as a novel candidate gene affecting the number of thoracic vertebrae in a Large White× Minzhu intercross pig population. *Animals* **2020**, *10*, 2186.

40. Zheng, Y.; Cai, C.H.; Wei, C.H.; Wang, X.Y.; Wei, W.A.; Bo, G.A.; Wimmers, K.; Mao, J.D.; Song, C.Y. Two new SINE insertion polymorphisms in pig Vertein (VRTN) gene revealed by comparative genomic alignment. *J. Integr. Agric.* **2020**, *19*, 2514–2522.

41. Duan, Y.; Zhang, H.; Zhang, Z.; Gao, J.; Yang, J.; Wu, Z.; Fan, Y.; Xing, Y.; Li, L.; Xiao, S.; et al. VRTN is required for the development of thoracic vertebrae in mammals. *Int. J. Biol. Sci.* **2018**, *14*, 667.

42. Van Son, M.; Lopes, M.S.; Martell, H.J.; Derkx, M.F.; Gangsei, L.E.; Kongsro, J.; Wass, M.N.; Grindflek, E.H.; Harlizius, B. A QTL for the number of teats shows breed-specific effects on the number of vertebrae in pigs: Bridging the gap between molecular and quantitative genetics. *Front. Genet.* **2019**, *10*, 272.

43. Amundson, L.A.; Hernandez, L.L.; Crenshaw, T.D. Gene expression of matrix metalloproteinase 9 (MMP9), matrix metalloproteinase 13 (MMP13), vascular endothelial growth factor (VEGF), and fibroblast growth factor 23 (FGF23) in femur and vertebra tissues of the hypovitaminosis D kyphotic pig model. *Br. J. Nutr.* **2018**, *120*, 404–414.

44. Zhang, L.C.; Xin, L.I.; Liang, J.; Hua, Y.A.; Zhao, K.B.; Na, L.I.; Lei, P.U.; Shi, H.B.; Zhang, Y.B.; Wang, L.G.; et al. Quantitative trait loci for the number of vertebrae on Sus scrofa chromosomes 1 and 7 independently influence the numbers of thoracic and lumbar vertebrae in pigs. *J. Integr. Agric.* **2015**, *14*, 2027–2033.

45. Liu, Z.; Wang, T.; Shi, X.; Wang, X.; Ren, W.; Huang, B.; Wang, C. Identification of LTBP2 gene polymorphisms and their association with thoracolumbar vertebrae number, body size, and carcass traits in Dezhou donkeys. *Front. Genet.* **2022**, *13*, 969959.

46. Huang, B.; Khan, M.Z.; Chai, W.; Ullah, Q.; Wang, C. Exploring Genetic Markers: Mitochondrial DNA and Genomic Screening for Biodiversity and Production Traits in Donkeys. *Animals* **2023**, *13*, 2725.

47. Koltes, J.E.; Mishra, B.P.; Kumar, D.; Kataria, R.S.; Totir, L.R.; Fernando, R.L.; Cobbold, R.; Steffen, D.; Coppieters, W.; Georges, M.; et al. A nonsense mutation in cGMP-dependent type II protein kinase (PRKG2) causes dwarfism in American Angus cattle. *Proc. Natl. Acad. Sci. USA* 2009, 106, 19250–19255.

48. Soranzo, N.; Rivadeneira, F.; Chinappen-Horsley, U.; Malkina, I.; Richards, J.B.; Hammond, N.; Stolk, L.; Nica, A.; Inouye, M.; Hofman, A.; et al. Meta-analysis of genome-wide scans for human adult stature identifies novel Loci and associations with measures of skeletal frame size. *PLoS Genet.* 2009, 5, e1000445.

49. Tsuchida, A.; Yokoi, N.; Namae, M.; Fuse, M.; Masuyama, T.; Sasaki, M.; Kawazu, S.; Komeda, K. Phenotypic Characterization of the Komeda Miniature Rat Ishikawa, an Animal Model of Dwarfism Caused by a Mutation in Prkg2. *Comp. Med.* 2008, 58, 560–567.

50. Garces, G.R.; Turba, M.E.; Muracchini, M.; Diana, A.; Jagannathan, V.; Gentilini, F.; Leeb, T. PRKG2 Splice Site Variant in Dogo Argentino Dogs with Disproportionate Dwarfism. *Genes* 2021, 12, 1489.

51. Yi, X.; Wu, P.; Liu, J.; He, S.; Gong, Y.; Xiong, J.; Xu, X.; Li, W. Candidate kinases for adipogenesis and osteoblastogenesis from human bone marrow mesenchymal stem cells. *Mol. Omics* 2021, 17, 790–795.

52. Zhong, Y.J.; Yang, Y.; Wang, X.Y.; Di, R.; Chu, M.X.; Liu, Q.Y. Expression analysis and single-nucleotide polymorphisms of SYNDIG1L and UNC13C genes associated with thoracic vertebral numbers in sheep (*Ovis aries*). *Arch. Anim. Breed.* 2021, 64, 131–138.

53. Li, S.; Luo, R.; Lai, D.; Ma, M.; Hao, F.; Qi, X.; Liu, X. Whole-genome resequencing of Ujumqin sheep to investigate the determinants of the multi-vertebral trait. *Genome* 2018, 61, 653–661.

54. Li, C.; Zhang, X.; Cao, Y.; Wei, J.; You, S.; Jiang, Y.; Chen, C. Multivertebrae variation potentially contributes to carcass length and weight of Kazakh sheep. *Small Rumin. Res.* 2017, 150, 8–10.

55. Zhang, Z.; Sun, Y.; Du, W.; He, S.; Liu, M.; Tian, C. Effects of vertebral number variations on carcass traits and genotyping of Vertnin candidate gene in Kazakh sheep. *Asian-Australas. J. Anim. Sci.* 2017, 30, 123.

56. Mi, T.; Liu, K.; Guo, T.; Li, L.; Wang, Y.; Li, C.; Cui, Y.; Dai, J.; Zhang, Y.; Hu, S. Analysis of the eighth intron polymorphism of NR6A1 gene in sheep and its correlation with lumbar spine number. *Anim. Biotechnol.* 2023, 34, 218–224.

57. Li, C.; Liu, K.; Dai, J.; Li, X.; Liu, X.; Ni, W.; Li, H.; Wang, D.; Qiao, J.; Wang, Y.; et al. Whole-genome resequencing to investigate the determinants of the multi-lumbar vertebrae trait in sheep. *Gene* 2022, 809, 146020.

58. Kalds, P.; Luo, Q.; Sun, K.; Zhou, S.; Chen, Y.; Wang, X. Trends towards revealing the genetic architecture of sheep tail patterning: Promising genes and investigatory pathways. *Anim. Genet.*

2021, 52, 799–812.

59. Zhang, D.; Zhang, X.; Li, F.; Liu, T.; Hu, Z.; Gao, N.; Yuan, L.; Li, X.; Zhao, Y.; Zhao, L.; et al. Whole-genome resequencing identified candidate genes associated with the number of ribs in Hu sheep. *Genomics* 2021, 113, 2077–2084.

60. Zhao, F.; Deng, T.; Shi, L.; Wang, W.; Zhang, Q.; Du, L.; Wang, L. Genomic scan for selection signature reveals fat deposition in Chinese indigenous sheep with extreme tail types. *Animals* 2020, 10, 773.

61. Li, C.; Li, M.; Li, X.; Ni, W.; Xu, Y.; Yao, R.; Wei, B.; Zhang, M.; Li, H.; Zhao, Y.; et al. Whole-genome resequencing reveals loci associated with thoracic vertebrae number in sheep. *Front. Genet.* 2019, 10, 674.

62. Zhang, X.; Li, C.; Li, X.; Liu, Z.; Ni, W.; Hazi, W.; Cao, Y.; Yao, Y.; Wang, D.; Hou, X.; et al. Expression profiles of MicroRNAs from multiple lumbar spine in sheep. *Gene* 2018, 678, 105–114.

63. Moradi, M.H.; Mahmodi, R.; Farahani, A.H.; Karimi, M.O. Genome-Wide Evaluation of Copy Gain and Loss Variations in Three Afghan Sheep Breeds. *Sci. Rep.* 2022, 12, 14286.

64. Ahbara, A.; Bahbahani, H.; Almathen, F.; Al Abri, M.; Agoub, M.O.; Abeba, A.; Kebede, A.; Musa, H.H.; Mastrangelo, S.; Pilla, F.; et al. Genome-Wide Variation, Candidate Regions, and Genes Associated With Fat Deposition and Tail Morphology in Ethiopian Indigenous Sheep. *Front. Genet.* 2019, 9, 699.

Retrieved from <https://encyclopedia.pub/entry/history/show/124294>