



# Study on Expression of Melanin-related Proteins in Yak Skins with Different Coat Colors

Xiaoyu Liu<sup>1</sup>, Guowen Wang<sup>1</sup>, Changqi Fu<sup>1</sup>, Shi Shu<sup>1</sup>, Xiuying Shen<sup>1</sup>, Jun Zhang<sup>1</sup>

10.18805/IJAR.BF-1994

## ABSTRACT

**Background:** The multiple coat colors of yaks are mainly determined by melanin synthesized by melanocytes. Comparing the amount and distribution of melanin and melanocytes in the skin of yaks with different coat colours has not yet been described; moreover, studying the expression of melanin-related proteins in the skin of yaks with different coat colors will help to further understand the molecular basis of the regulation of coat color in animals. This study observes the histomorphological structure of white, brown and black yak skin and investigates the expression of melanocyte markers MITF, SOX10, PMEL, TYRP1, DCT, MC1R and KIT, in white, brown and black yak skin.

**Methods:** HE staining and transmission electron microscopy (TEM) were performed for histomorphological observation. Immunofluorescence analyses were performed to assess marker expression.

**Result:** Our results showed that there was no melanin in the skin of white yaks; whereas the melanin formation process was not problematic in brown and black yaks and the formation of brown hair colour could be due to the low number of melanocytes and the fact that melanocytes were mostly early in differentiation.

**Key words:** Coat colors, Melanin, Melanocytes, Melanosomes, Yaks.

## INTRODUCTION

The domestic yak (*Bos grunniens*) is a dominant livestock in the pastoral areas of the Tibetan Plateau in China (Wu *et al.*, 2022). Yak hair is of various colors, including black, brown, blue, white and mixed colors.

Mammalian coat color is determined by the type, quantity and distribution of melanin in the body. Melanin formation includes the development and maturation of melanocytes, morphogenesis of melanosomes (organelles that synthesize melanin) and the anabolism and transport of melanin (Schiaffino, 2010). The following signaling pathways are mainly involved in melanin synthesis:  $\alpha$ -MSH/MC1R/cAMP, PI3K/Akt/GSK3 $\beta$ , Wnt/ $\beta$ -catenin and MAPK signaling pathway (D'Mello *et al.*, 2016; Zou *et al.*, 2021). Melanocortin 1 receptor (MC1R) is a melanocyte surface receptor.  $\alpha$ -MSH/MC1R/cAMP signaling pathway is a core molecular pathway for melanin synthesis. In PI3K/Akt/GSK3 $\beta$  signaling pathway, the binding affinity between Microphthalmia-associated transcription factor (MITF) and M-box was enhanced, thereby upregulating TYR expression and promoting melanin production. Wnt/ $\beta$ -catenin signaling pathway is one of the pathways that regulate the expression of MITF. By increasing the expression of MITF, this pathway stimulates melanin synthesis (Ploper and De Robertis, 2015). The MAPK signaling pathway includes the stem cell factor (SCF/c-Kit) signaling pathway, the endothelin (ET-1/EDNRB) signaling pathway, the NRG1/ErbB signaling pathway and the bone morphogenetic protein (BMPs) signaling pathway. Their final targets are all the MITF gene, thereby regulating the production of melanin. Melanin formation mainly involves three enzymes: Tyrosinase (TYR), tyrosinase-related protein 1 (TYRP1) and tyrosinase-related

<sup>1</sup>Academy of Animal Science and Veterinary Medicine, Qinghai University, Xining 810016, China.

**Corresponding Author:** Xiuying Shen, Academy of Animal Science and Veterinary Medicine, Qinghai University, Xining 810016, China. Email: 18797016200@163.com

**How to cite this article:** Liu, X., Wang, G., Fu, C., Shu, S., Shen, X. and Zhang, J. (2025). Study on Expression of Melanin-related Proteins in Yak Skins with Different Coat Colors. *Indian Journal of Animal Research*. 1-8. doi: 10.18805/IJAR.BF-1994.

**Submitted:** 21-03-2025 **Accepted:** 23-07-2025 **Online:** 12-08-2025

protein 2 (DCT) (Wagatsuma *et al.*, 2023). DCT and TYRP1 serves as markers of early and late melanocyte differentiation, respectively (Manceau *et al.*, 2011). MITF, a regulator of pigmentation, upregulates the expression of these genes by binding to M-box motifs in the promoter regions of TYR, TYRP 1 and DCT (Vachtenheim and Borovanski, 2010). MITF is the earliest melanoblast marker and it is regulated by some molecules involved in neural crest and melanocyte development, such as PA $\times$ 3, SO $\times$ 10 (Kawakami and Fisher, 2017; Thomas and Erickson, 2009). SRY-BO $\times$ 10 (SO $\times$ 10) interacting proteins regulate the establishment of melanocyte lineages as well as promote cell differentiation (Marathe *et al.*, 2017; Willis *et al.*, 2015). The pre-melanosomal protein PMEL is a melanosome-specific antigen that forms a fibrous matrix in early melanosomes to facilitate melanin deposition (Dean and Lee, 2021; Yamaguchi and Hearing, 2009). KIT, like MC1R, is a specific receptor for signaling pathways that regulate melanin synthesis and it is involved in the SCF/c-Kit-mediated melanin synthesis signaling pathway (Liu *et al.*, 2023a).

Cattle coat color is controlled by a number of different genes and their corresponding alleles, including ASIP, TYR, TYRP1, KIT, PMEL, MC1R and MITF (Brenig *et al.*, 2013). Three common functional alleles of *MC1R* (*i.e.*, wild-type  $E^+$ , dominant  $E^D$  and recessive  $e$ ) play a crucial role in determining the primary coat color of cattle (Zhang *et al.*, 2014b). *MC1R* and *PMEL* alleles interact to regulate coat color in Highland cattle (Schmutz and Dreger, 2013). (Zhang *et al.*, 2014a) showed that the brown coat color of domestic yaks in Ganzihe County, Qinghai Province, China, was caused by mutations in *MC1R* or *PMEL* and their all-white phenotype was caused by sequence translocation of *KIT* (Durkin *et al.*, 2012). White hair variation in White Galloway and White Park cattle is associated with *KIT* mutations (Brenig *et al.*, 2013). The white phenotype in a Black Angus calf is caused by *MITF* mutations (Petersen *et al.*, 2023). The *MITF* gene variant is also associated with the white spot phenotype in Brown Swiss cattle (Hofstetter *et al.*, 2019). Yaks have undergone natural selection, human domestication and interspecific hybridization during the evolutionary process. Liu *et al.* (2023b) unraveled the mystery of the white yak's origin, a new mutation caused by the introgression of the color-sided taurine.

The aim of this study was to investigate the morphological differences of yak skin tissues of white, brown and black coat colours and the expression of melanin-related proteins, namely, MITF, SOX10, PMEL, TYRP1, DCT, KIT and MC1R in yak skin tissues of different coat colors.

## MATERIALS AND METHODS

### Animal and sample collection

With the consent of the person in charge, the hip fur tissue of healthy three-year-old white, brown and black yaks was clipped from an abattoir in Xining City, Qinghai Province, China, less than one hour after the yaks had died. The subcutaneous tissue and hairs protruding from the skin surface were removed and a number of small pieces of tissue with the size of 1–5 mm<sup>3</sup> were cut. One part of the treated skin tissues was fixed with 4% paraformaldehyde for HE staining and immunofluorescence staining of tissue sections; the other part was immersed in pre-fixing solution for electron microscopy (2.5% glutaraldehyde) for hair follicle TEM analysis.

### Preparation of paraffin sections

The treated white, brown and black skin tissues were fixed with 4% paraformaldehyde or other fixative at room

temperature for 24–48 hours. Trim-fixed tissues into appropriate size and shape and placed in embedding cassettes, dehydrated and then embedded with paraffin blocks. Cut paraffin blocks at 5 µm and place paraffin ribbon in the water bath at about 40–45°C. Mount sections onto slides and bake at 45–50°C oven overnight.

### HE staining

Soak the baked paraffin section in xylene for 20 minutes and lift once every 10 minutes. Then soaked in 100% ethanol, 100% ethanol, 95% ethanol, 70% ethanol, 50% ethanol, 30% ethanol and ultra-pure water for five minutes each. Dye the paraffin section with hematoxylin for 60s, eosin for 1–2s and let dry. Finally, the section was sealed with sealing liquid, dried, viewed with a microscope and photographed.

### Transmission electron microscopy (TEM)

The treated tissue was cut into small pieces, immersed in pre-electron microscope fixative (2.5% glutaraldehyde) and stored at 4°C for later use. The skin hair follicle tissue was postfixed with 1% osmium tetroxide, dehydrated with acetone series, infiltrated in Epox 812 for a long time and embedded. The ultrathin sections were cut with a diamond knife, stained with uranyl acetate and lead citrate and then examined by JEM-1400-FLASH transmission electron microscopy.

### Immunofluorescence staining

After dewaxing with gradient alcohol, the sections were soaked in sodium citrate for antigen repair, boiled in a microwave on high heat and then heated on low heat for 20 minutes. Subsequently, the slides were washed with PBS and shaken for 5 minutes. After washing, the slides were blocked with 3% H<sub>2</sub>O<sub>2</sub> for 30 minutes and incubated with primary antibody (Table 1) overnight at 4°C. After PBS washing, the corresponding secondary antibody was applied for 1 hour. The nuclei were stained with 4°C, 6-diamidino-2-phenylindole (DAPI). An Inverted epifluorescence microscope (Olympus) performed fluorescence microscopy and photo preservation.

## RESULTS AND DISCUSSION

### Skin morphology of white, brown and black yaks

To examine the localization and amount of melanin in white, brown and black yak skin samples, we performed HE staining of paraffin sections of skin tissues and observed the epidermis and hair follicles. We observed no melanin in the epidermis or hair follicles of white yaks, whereas melanin was present in the epidermis and hair follicles of both brown and black yaks. It could be observed that brown yaks had less melanin in the epidermis than black yaks (Fig 1).

These results suggest differences in the localization and amount of melanin in the skin of yaks with different coat colors. Brown yaks and black yaks can synthesize melanin normally, while white yaks do not. From this, we thought that the white yak skin had very few melanocytes, or the skin had melanoblasts which do not produce melanin granules. Skin tissue slices of white and black yaks from

**Table 1:** Protocols of the antibodies used in this study.

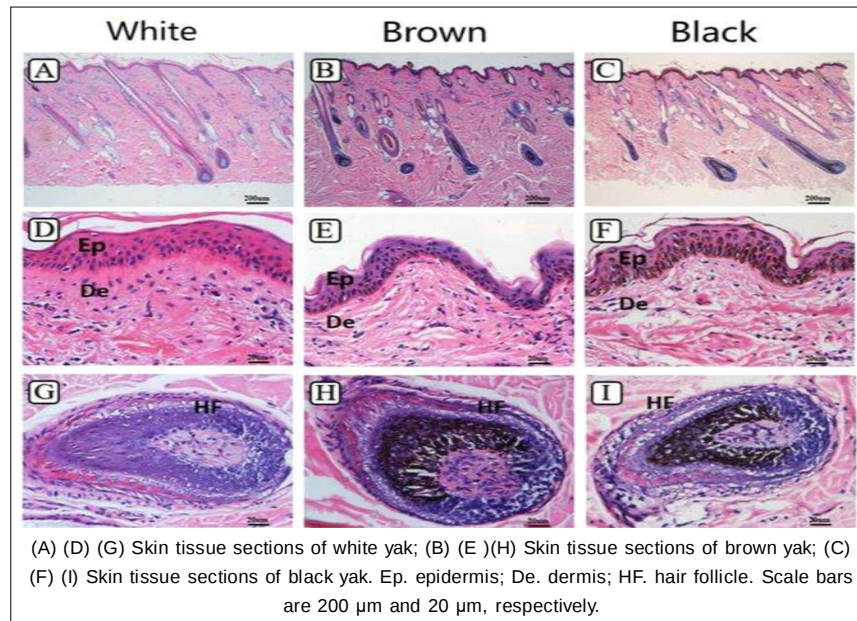
| Antigen | Cat no     | Dilution | Distributor |
|---------|------------|----------|-------------|
| MITF    | ab303530   | 1:200    | Abcam       |
| SOX10   | ab216020   | 1:50     | Abcam       |
| PMEL    | PA5-101023 | 1:200    | Invitrogen  |
| TYRP1   | ab235447   | 1:100    | Abcam       |
| DCT     | 13095-1-AP | 1:50     | Proteintech |
| MC1R    | YT2673     | 1:50     | Immunoway   |
| KIT     | A01335-1   | 1:50     | Boster Bio  |

others showed that only black yaks or cattles were observed melanin deposition near melanocytes in the skin (Amakiri, 1979; Liu *et al.*, 2023b; Oke *et al.*, 2022). This is consistent with our findings.

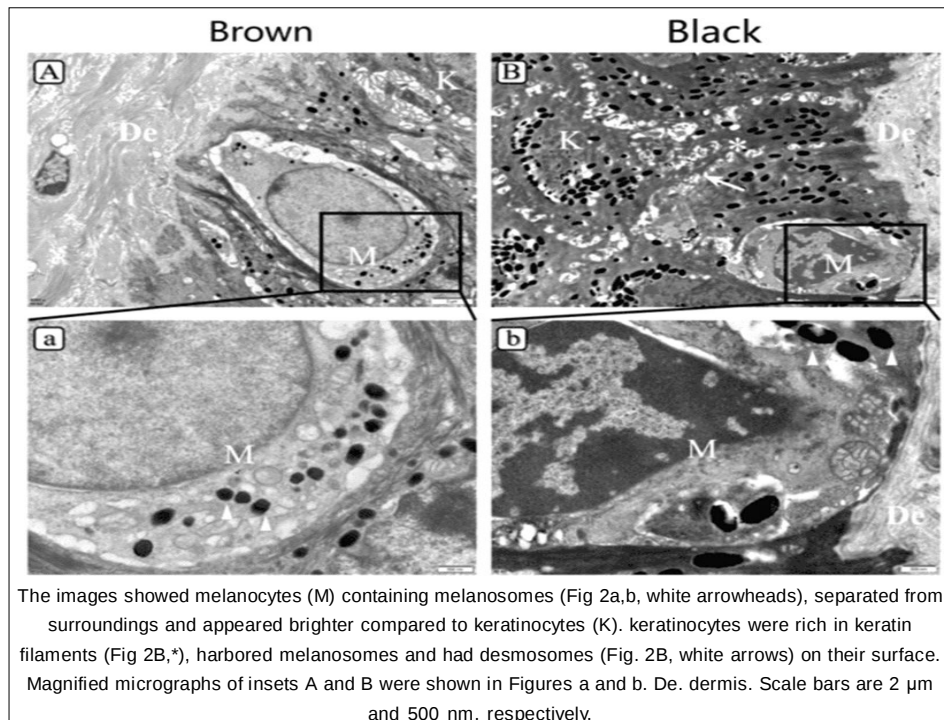
#### TEM of hair follicles of white, brown and black yaks

To clarify the differences in the number of melanocytes and melanosomes in white, brown and black yak skin, we

performed TEM on yak hip skin samples to observe hair follicles. There were no melanocytes and melanosomes in the hair follicles of white yak skin and we only observed keratinocytes (Fig 3A). On the contrary, melanocytes and melanosomes were present in the hair follicles of both brown and black yaks (Fig 2) (Fig 3). We also observed in the microscope that there were fewer melanocytes in brown yak hair follicles, whereas melanocytes were easily visible



**Fig 1:** Morphological structure of yak skin tissues of different coat colors.



**Fig 2:** Melanocytes in TEM of hair follicles of brown yak and black yak.

in black yak hair follicles. In contrast, melanosomes were abundantly and extensively distributed in the hair follicles of black yaks (Fig 3C). In addition, melanosomes in brown and black yaks were distributed in both melanocytes and keratinocytes.

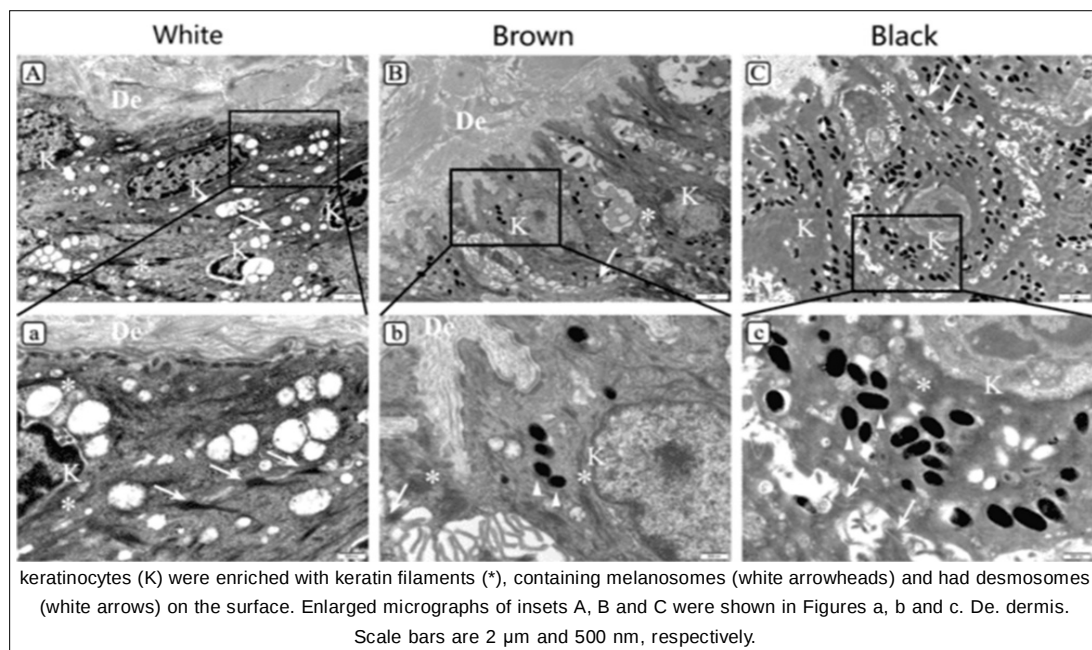
These results were consistent with the morphological findings. This result shows that the reason for coat color formation of white yaks might be that there were almost no melanocytes in the hair follicles, resulting in the inability to produce pigment. At the same time, there was no problem with the process of melanogenesis of brown and black yaks and the reason of brown coat color might be a small number of melanocytes leading to fewer melanin granules, resulting in lighter coat color. Studies have shown that an increase in the expression level of the ASIP protein can hinder the maturation of melanocytes, thereby resulting in the absence of pigment in the skin and hair of white buffalo. This conclusion is also helpful for our results (Liang *et al.*, 2021).

#### Localization expression of melanocyte-specific markers in the epidermis and hair follicles of white, brown and black yaks

In order to detect differences in the localized expression of melanocyte markers in yaks with different coat colors (Michalak-Micka *et al.*, 2022), we performed immunofluorescence analysis on treated white, brown and black yak skin specimens and melanocyte-specific markers included MITF, SOX10, PMEL, TYRP1, DCT, MC1R and KIT (Fig 4). We observed that on the epidermis, MITF was expressed only in brown yaks; on the hair follicle, MITF was expressed in all three coat colors yaks and MITF was expressed on the outer root sheath (ORS) in white yaks,

while it was expressed in both the ORS and dermal papilla (DP) in brown and black yaks (Fig 4A). SOX10 was not expressed on the epidermis of white yaks and it was weakly expressed in the DP of hair follicles (Fig 4 B1, B4); SOX10 was expressed in the epidermis, DP and hair matrix of brown and black yak, while SOX10 was weakly expressed in epidermis of black yak (Fig 4B). PMEL was expressed in the epidermis and ORS of hair follicles of white, brown and black yak and PMEL was relatively weakly expressed in the hair follicles of white yak (Fig 4C). Next, we observed that TYRP1 was not expressed in the epidermis and hair follicles of white yaks and it was expressed in the epidermis and hair matrix of brown and black yaks and for the epidermis, black > brown (Fig 4D). DCT was not significantly different in the epidermis of the three coat colors yaks, with weak expression of DCT in the DP, hair matrix and ORS of hair follicles of brown yaks and very weak expression of DCT in the DP of hair follicles of black yaks (Fig 4E). MC1R was expressed in the epidermis and hair matrix and inner root sheath (IRS) of hair follicles of white, brown and black yaks and relatively weakly in the skin of white yaks (Fig 4F). KIT was expressed in the epidermis and hair follicles of white, brown and black yaks and in the hair matrix, IRS and DP of hair follicles (Fig 4G).

The immunofluorescence results showed significant differences in the location of protein expression in yaks with different coat colors. SOX10 was weakly expressed in the hair follicles of white yaks, but strongly expressed in brown and black yaks. SOX10 is a critical nuclear transcription factor for differentiating neural crest progenitors into melanocytes and it can regulate the expression of MITF transcription factor. We analyzed the immunofluorescence staining of MITF and the expression of MITF in the hair



**Fig 3:** Keratinocytes in TEM of white, brown and black yaks hair follicles.

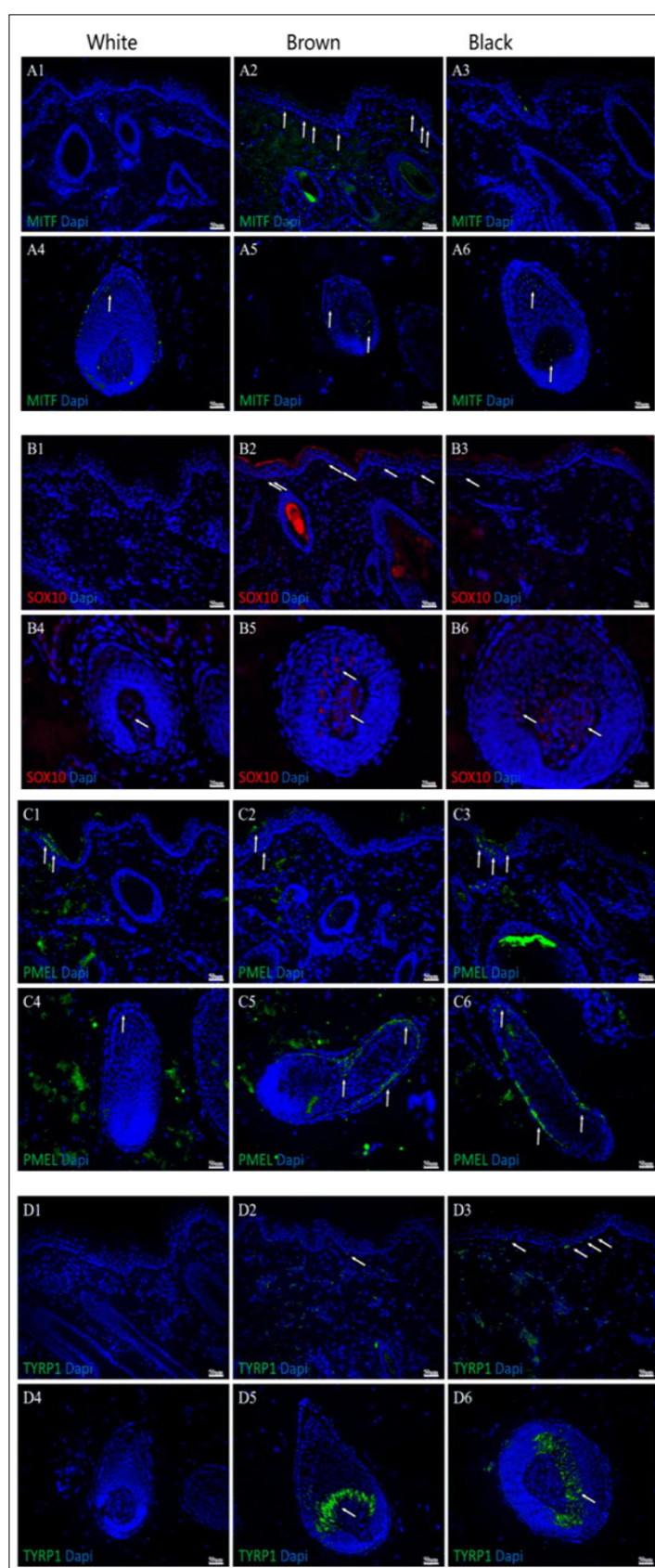


Fig 4: Continue....

Fig 4: Continue....

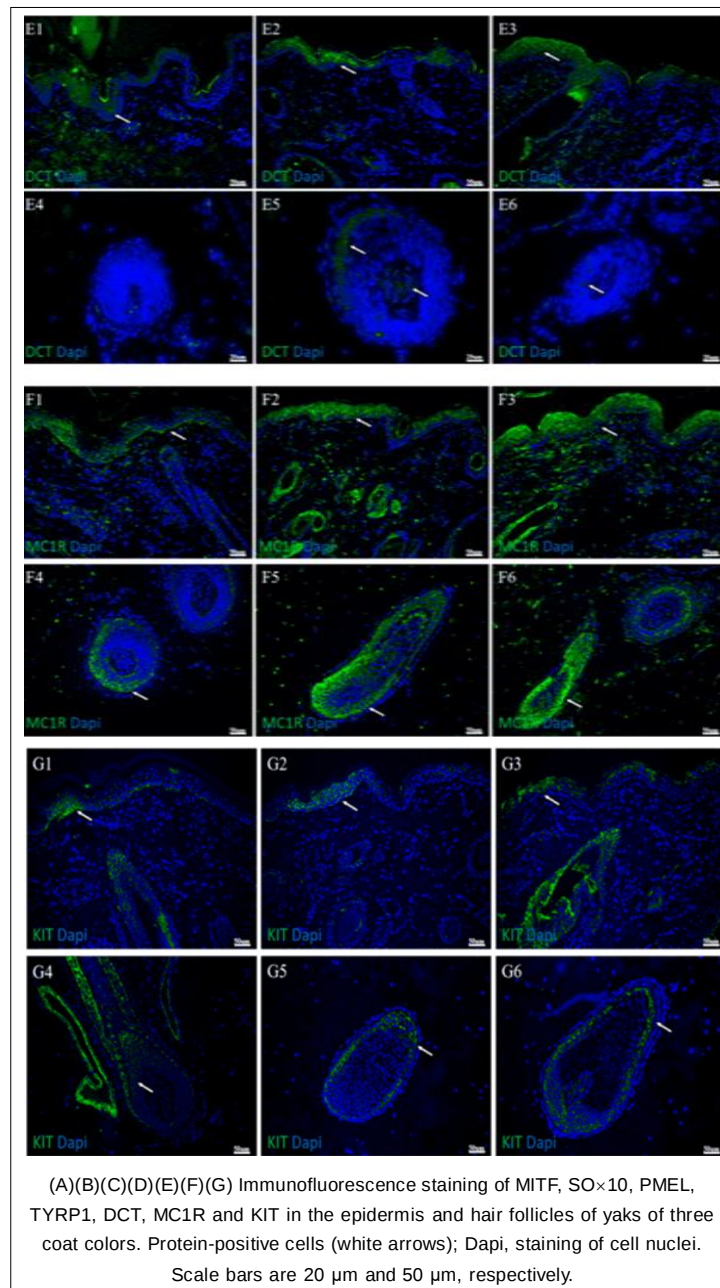


Fig 4: Immunofluorescence expression of specific markers in white, brown and black yak skin tissues.

follicles of white yaks was relatively low. From the above information, we hypothesized that less SO $\times$ 10 transcription factor in white yak skin contributed to fewer melanocytes and reduced the expression of MITF. At the same time, the decreased expression of MITF affected the expression of critical enzymes for melanin formation, which blocked melanin synthesis. In addition, less expression of MC1R in white yak hair follicles resulted in a weakening of the  $\alpha$ -MSH/MC1R/cAMP signaling pathway, a core molecular pathway for melanin synthesis. The expression of PMEL is

regulated by MITF, OA1, MSH, Rab7 and PH value, etc. (Hu *et al.*, 2021). The expression of PMEL was relatively low in white yak hair follicles. PMEL is a component of the fibrillar sheets, without which melanin cannot be deposited. Studies have shown that in light-colored Highland cattle, there is a mutation in the pmel gene (Schmutz and Dreger, 2013). Mutations in the pmel gene can cause the hair color of cattle to become lighter (Wang *et al.*, 2023). In addition, we hardly observed the expression of critical enzymes of melanin synthesis, such as TYRP1 and DCT, in white yak hair follicles.

However, studies have shown that in domestic yak and French breed cattle, TYRP1 has no relation to coat color (Guibert *et al.*, 2004; Zhang *et al.*, 2014a). For fluorescence staining of DCT, DCT was weakly expressed in the hair follicles of black yaks and strongly expressed in brown yaks. DCT has conducted relatively few studies on the coat colors of black and brown yaks. DCT is a marker for melanosomes in stages I-II and we hypothesized that most melanosomes in the hair follicles of black yaks were in stages III-IV, while brown yaks contained melanosomes in all stages, resulting in a slightly lighter coat color. DCT serves as a marker for the early differentiation of melanocytes, TYRP1 serves as a marker for late differentiation of melanocytes. The study on melanin production and related gene expression in the mouth and nose of three native Hanwoo cattles indicated that L-cysteine had a down-regulating effect on the genes Tyr, Tyrp-2 and MC1R. Moreover, L-cysteine significantly reduced the production of true melanin in the mouth and nose of the black Hanwoo cattles, while increasing the production of true melanin in the brown (Amna *et al.*, 2012). We hypothesized that there were more mature melanocytes in black yaks' hair follicles than in brown yaks, which might contribute to the difference in coat color. Down-regulation the expression of MITF and downstream genes TYR and tyrosinase-related proteins inhibits melanogenesis (Zhou *et al.*, 2022). KIT was expressed in all three colors of yaks (Salokhe, 2025; Rank *et al.*, 2025; Upasani *et al.*, 2025).

## CONCLUSION

We reported the morphological differences in the skin tissues of yaks with different coat colors and investigated the protein expression of seven genes, namely, MITF, SOX10, PMEL, TYRP1, DCT, MC1R and KIT, in the epidermis and hair follicles of white, brown and black yaks. Skin melanin formation in white yaks is impaired and the formation of brown hair may be due to the low number of melanocytes as well as the fact that most of the melanocytes are in the early stage of differentiation, which provides an important reference for further molecular mechanisms of coat color regulation.

## ACKNOWLEDGEMENT

This research was supported by Transformation of Scientific and Technological Achievements of Qinghai Provincial Science and Technology Department [2022-NK-167]; 2023 Qinghai Province Kunlun Talent. High-end Innovation and Entrepreneurship Talent Project Training Team; Qinghai Province "Kunlun Talents. High-End Innovative and Entrepreneurial Talents" Plan to Cultivate Leading Talents in 2021; Top Talent project of "Kunlun Talents High - level Innovation and Entrepreneurship Talents" in Qinghai Province(2021); Key Project of the Youth Foundation of Qinghai University [2023-QNY-13]; and Natural Science Foundation Project - Youth [2021-ZJ-968Q].

## Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

## Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish, or preparation of the manuscript.

## REFERENCES

- Amakiri, S.F. (1979). Melanin and dopa-positive cells in the skin of tropical cattle. *Acta Anat (Basel)*. **103**: 434-444.
- Amna, T., Park, K.M., Cho, I.K., Choi, T.J., Lee, S.S., Seo, K.S. and Hwang, I. (2012). Substantial effect of melanin influencing factors on *in vitro* melanogenesis in muzzle melanocytes of differently colored hanwoo. *Asian-Australas J Anim Sci*. **25**: 1029-1037.
- Brenig, B., Beck, J., Floren, C., Bornemann-Kolatzki, K., Wiedemann, I., Hennecke, S., Swalve, H. and Schütz, E. (2013). Molecular genetics of coat colour variations in White Galloway and White Park cattle. *Anim Genet*. **44**: 450-453.
- D'Mello, S.A., Finlay, G.J., Baguley, B.C. and Askarian-Amiri, M.E. (2016). Signaling Pathways in Melanogenesis. *Int J Mol Sci*. **17**.
- Dean, D.N. and Lee, J.C. (2021). Linking Parkinson's Disease and Melanoma: Interplay Between  $\alpha$ -Synuclein and Pmel17 Amyloid Formation. *Mov Disord*. **36**: 1489-1498.
- Durkin, K., Coppieters, W., Drögemüller, C., Ahariz, N., Cambisano, N., Druet, T., Fasquelle, C., Haile, A., Horin, P., Huang, L., Kamatani, Y., Karim, L., Lathrop, M., Moser, S., Oldenbroek, K., Rieder, S., Sartelet, A., Sölkner, J., Ståhlhammar, H., Zelenika, D., Zhang, Z., Leeb, T., Georges, M. and Charlier, C. (2012). Serial translocation by means of circular intermediates underlies colour sidedness in cattle. *Nature*. **482**: 81-84.
- Guibert, S., Girardot, M., Leveziel, H., Julien, R. and Oulmouden, A. (2004). Pheomelanin coat colour dilution in French cattle breeds is not correlated with the TYR, TYRP1 and DCT transcription levels. *Pigment Cell Res*. **17**: 337-345.
- Hofstetter, S., Seefried, F., Häfliger, I.M., Jagannathan, V., Leeb, T. and Drögemüller, C. (2019). A non-coding regulatory variant in the 5' C-region of the MITF gene is associated with white-spotted coat in Brown Swiss cattle. *Anim Genet*. **50**: 27-32.
- Hu, S., Bai, S., Dai, Y., Yang, N., Li, J., Zhang, X., Wang, F., Zhao, B., Bao, G., Chen, Y. and Wu, X. (2021). Deubiquitination of MITF-M Regulates Melanocytes Proliferation and Apoptosis. *Front Mol Biosci*. **8**: 692724.
- Kawakami, A. and Fisher, D.E. (2017). The master role of microphthalmia-associated transcription factor in melanocyte and melanoma biology. *Lab Invest*. **97**: 649-656.

- Liang, D., Zhao, P., Si, J., Fang, L., Pairo-Castineira, E., Hu, X., Xu, Q., Hou, Y., Gong, Y., Liang, Z., Tian, B., Mao, H., Yindee, M., Faruque, M.O., Kongvongxay, S., Khampoumee, S., Liu, G.E., Wu, D.D., Barker, J.S.F., Han, J. and Zhang, Y. (2021). Genomic analysis revealed a convergent evolution of LINE-1 in coat color: A case study in water buffaloes (*Bubalus bubalis*). *Mol Biol Evol.* **38**: 1122-1136.
- Liu, W., Chen, Q. and Xia, Y. (2023a). New Mechanistic Insights of Melasma. *Clin Cosmet Investig Dermatol.* **16**: 429-442.
- Liu, X., Liu, W., Lenstra, J.A., Zheng, Z., Wu, X., Yang, J., Li, B., Yang, Y., Qiu, Q., Liu, H., Li, K., Liang, C., Guo, X., Ma, X., Abbott, R.J., Kang, M., Yan, P. and Liu, J. (2023b). Evolutionary origin of genomic structural variations in domestic yaks. *Nat Commun.* **14**: 5617.
- Manceau, M., Domingues, V.S., Mallarino, R. and Hoekstra, H.E. (2011). The developmental role of Agouti in color pattern evolution. *Science.* **331**: 1062-1065.
- Marathe, H.G., Watkins-Chow, D.E., Weider, M., Hoffmann, A., Mehta, G., Trivedi, A., Aras, S., Basuroy, T., Mehrotra, A., Bennett, D.C., Wegner, M., Pavan, W.J. and de la Serna, I.L. (2017). BRG1 interacts with SOX10 to establish the melanocyte lineage and to promote differentiation. *Nucleic Acids Res.* **45**: 6442-6458.
- Michalak-Micka, K., Büchler, V.L., Zapiórkowska-Blumer, N., Biedermann, T. and Klar, A.S. (2022). Characterization of a melanocyte progenitor population in human interfollicular epidermis. *Cell Rep.* **38**: 110419.
- Oke, O.E., Oso, O.M., Logunleko, M.O., Uyanga, V.A., Akinyemi, F., Okeniyi, F.A., Akosile, O.A., Baloyi, J.J. and Onagbesan, O.M. (2022). Adaptation of the White Fulani cattle to the tropical environment. *J. Therm Biol.* **110**: 103372.
- Petersen, J.L., Sieck, R.L. and Steffen, D.J. (2023). White coat color of a Black Angus calf attributed to an occurrence of the delR217 variant of MITF. *Anim Genet.* **54**: 549-552.
- Ploper, D. and DeRobertis, E.M. (2015). The MITF family of transcription factors: Role in endolysosomal biogenesis, Wnt signaling and oncogenesis. *Pharmacol Res.* **99**: 36-43.
- Schiaffino, M.V. (2010). Signaling pathways in melanosome biogenesis and pathology. *Int J Biochem Cell Biol.* **42**: 1094-1104.
- Schmutz, S.M. and Dreger, D.L. (2013). Interaction of MC1R and PMEL alleles on solid coat colors in Highland cattle. *Anim Genet.* **44**: 9-13.
- Salokhe S. (2025). Exploring challenges faced by farmers in participating in farmers producer organizations: Understanding the key issues impacting FPO success: A review . *Indian Journal of Agricultural Research.* **59**: 843-849. doi: 10.18805/IJARE.A-6294.
- Rank P.H., Patel R.J., Lunagaria M.M., Tiwari M.K. (2025). Enhancing the green gram production by leveraging new dimensions of land and water resources management technologies: A comprehensive review. *Legume Research.* **48**: 909-918. doi: 10.18805/LR-5257.
- Thomas, A.J. and Erickson, C.A. (2009). FOXD3 regulates the lineage switch between neural crest-derived glial cells and pigment cells by repressing MITF through a non-canonical mechanism. *Development.* **136**: 1849-1858.
- Upasani R.R., Barla Sheela (2025). Understanding the mycorrhizal network's ecological symphony: A review. *Agricultural Science Digest.* **45**: 371-379. doi: 10.18805/ag.D-6035.
- Vachtenheim, J. and Borovanski, J. (2010). "Transcription physiology" of pigment formation in melanocytes: Central role of MITF. *Exp Dermatol.* **19**: 617-627.
- Wagatsuma, T., Suzuki, E., Shiotsu, M., Sogo, A., Nishito, Y. and Hashimoto, H., Petris, M.J., Kinoshita, M. and Kambe, T. (2023). Pigmentation and TYRP1 expression are mediated by zinc through the early secretory pathway-resident ZNT proteins. *Commun Biol.* **6**: 403.
- Wang, J., Fan, T., Du, Z., Xu, L., Chen, Y., Zhang, L., Gao, H., Li, J., Ma, Y. and Gao, X. (2023). Genome-wide Association Analysis Identifies the PMEL Gene Affecting Coat Color and Birth Weight in Simmental × Holstein. *Animals (Basel).* **13**.
- Willis, B.C., Johnson, G., Wang, J. and Cohen, C. (2015). SOX10: A useful marker for identifying metastatic melanoma in sentinel lymph nodes. *Appl Immunohistochem Mol Morphol.* **23**: 109-112.
- Wu, M., Zhao, H., Tang, X., Zhao, W., Yi, X., Li, Q. and Sun, X. (2022). Organization and Complexity of the Yak (*Bos Grunniens*) Immunoglobulin Loci. *Front Immunol.* **13**: 876509.
- Yamaguchi, Y. and Hearing, V.J. (2009). Physiological factors that regulate skin pigmentation. *Biofactors.* **35**: 193-199.
- Zhang, M.Q., Xu, X. and Luo, S.J. (2014a). The genetics of brown coat color and white spotting in domestic yaks (*Bos grunniens*). *Anim Genet.* **45**: 652-659.
- Zhang, Y., Li, Q., Ye, S., Faruque, M.O., Yu, Y., Sun, D., Zhang, S. and Wang, Y. (2014b). New variants in the melanocortin 1 receptor gene (MC1R) in Asian cattle. *Anim Genet.* **45**: 609-610.
- Zhou, Y., Zeng, H.L., Wen, X.Y., Jiang, L., Fu, C.H., Hu, Y.B., Lei, X.X., Zhang, L., Yu, X., Yang, S.Y., Huang, L.H., Xiang, H., Huang, J.H., Chen, J., Lei, L. and Zeng, Q.H. (2022). Selaginellin Inhibits Melanogenesis via the MAPK Signaling Pathway. *J Nat Prod.* **85**: 838-845.
- Zou, D.P., Chen, Y.M., Zhang, L.Z., Yuan, X.H., Zhang, Y.J., Inggawati, A., Kieu Nguyet, P.T., Gao, T.W. and Chen, J. (2021). SFRP5 inhibits melanin synthesis of melanocytes in vitiligo by suppressing the Wnt/β-catenin signaling. *Genes Dis.* **8**: 677-688.