Review

Yak- the “almighty livestock” of the rugged Himalayan Mountains

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ABSTRACT

The yak is a remarkable animal because of its distinct physical and structural characteristics that allow it to adapt to the rugged mountains with unfavourable climate. Yaks are regarded as the “almighty livestock” by the herding communities since they are deeply ingrained in the customs, socio-economic processes, and culture. Yaks are well adapted to the harsh climate and hypoxia occurring under high altitude grazing conditions of the Himalayan Mountains. However, it is unclear to which degree different types of hybrids of yaks and cattle, common in the Himalayas, tolerate these conditions and how they perform and behave under these circumstances. Therefore, in this review we are going to discuss some of the mechanisms for their adaptation in the harsh climatic conditions.

Key words: Adaptation, *Bos grunniens*, High altitude, Hypoxia

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INTRODUCTION

Indian yaks are classified into *Arunachali yak, Himachali yak, Ladakhi yak and Sikkimi yak* based upon the geographical area inhabitation and so far, only *Arunachali yak* has been described as a breed in India. Genomics divergence revealing unique populations among Indian Yaks has been identified (Sivalingam *et al*., 2020).The population of yaks in India as per the 19th Livestock census is 0.077 million (19th Livestock Census All India Report 2012). In case of yaks, which are reared under high altitudes, data recording is almost nil or not being followed. Thus, a complete grasp of the genetic underpinnings of yak physiological traits will shed light on how they have adapted to their high-altitude surroundings. Many species have evolved unique physiological traits like superior blood oxygen transport system and high metabolic efficiency, to adapt to the harsh living pressure (Lan *et al*., 2018). These species include Tibetan pigs (Jia *et al*., 2016; Zhang B. *et al*., 2017), Tibetan sheep (Zhang *et al*., 2013); Tibetan chickens (Gou *et al*., 2014), and yaks (Qiu *et al*., 2012; Qi *et al*., 2019).Yaks have got adapted to very high-altitude regions where the oxygen content is very low and the genes responsible for the adaptation to hypoxic conditions has already been reported (Qiu *et al*., 2012).

Adaptation mechanisms of Yaks

Yaks are well adapted to the harsh climate and hypoxia occurring under high altitude grazing conditions of the Himalayan Mountains. However, it is unclear to which degree different types of hybrids of yaks and cattle, common in the Himalaya, tolerate these conditions and how they perform and behave under these circumstances. Species living at high altitudes are exposed to strict selection pressures and physiological challenges owing to harsh environmental conditions, such as thin air, cold temperatures, ultraviolet exposure, and low pressure (Miao *et al*., 2015). At present, published studies have identified EPAS1, EGLN1, and PPARA genes that play important roles in high-altitude adaptation (Haasl and Payseur, 2016; Heinrich *et al*., 2019). Also, genomic variants and the functional pathways related to adaptation in Indian yak populations have been identified through whole genome resequencing (Kumar *et al*., 2023). Exploring the molecular mechanisms underlying hypoxia adaptation has long garnered attention. Yak (*Bos grunniens*), a native mammal on the Qinghai-Tibet Plateau and its adjacent regions, provides meat and other necessities for Tibetans. Compared with lowland cattle, yaks have a larger alveolar area per unit area, thinner alveolar

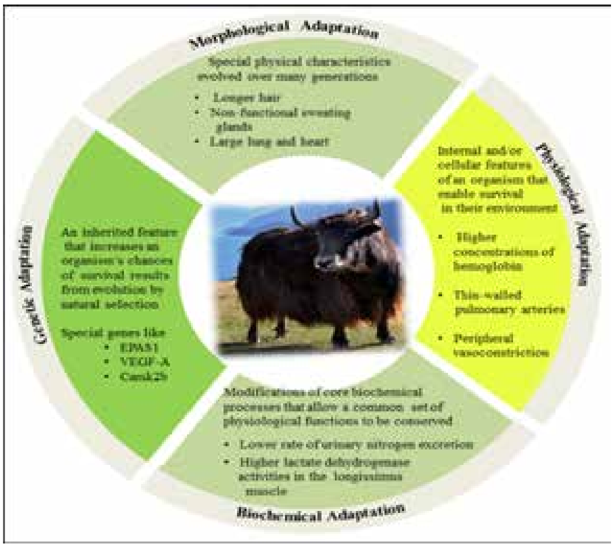

Fig 1: *Schematic representation of the yak adaptation to high-altitude environmental stress in comparison to a closely related species (Ayalew et al., 2021).*

spacing, thinner gas-blood barrier (Wei and Yu, 2008), and stronger expression of some genes related to oxygen supply as well as defence system under hypoxia pressure (Wang *et al*., 2016). Therefore, a thorough understanding of the genetic basis of the physiological characteristics of yak will provide insight into their adaptation to the high-altitude environment.

By comparing yaks and cattle, 4975 mRNAs, 252 circRNAs and 75 miRNAs were identified differentially expressed. The pathways enriched in the mRNAs, circRNAs and miRNAs identified from the comparison of yaks and cattle were mainly associated with metabolism, including 'glycosaminoglycan degradation', 'pentose and glucuronate inter-conversions' and 'flavone and flavonol biosynthesis' (Ge *et al*., 2021). As stated earlier, Yaks have numerous anatomical and physiological traits that equip them for life at high altitude, including large lungs and heart (Wiener *et al*., 2003), lack of hypoxic pulmonary vasoconstriction (Dolt *et al*., 2007), increased foraging ability (Shao *et al*., 2010), strong environmental sense and high energy metabolism (Wiener *et al*., 2003; Wang *et al*., 2011). Genomic comparisons between closely related species provide insights into the genetic basis of mammalian divergence and adaptation (Kosiol *et al*., 2008). The PSGs (Pregnancy-specific glycol-proteins) detected in yak were enriched for genes involved in the hypoxia response and energy metabolism. Of 81 genes examined in the response to hypoxia functional category (GO 0001666), 3 (3.7%) showed evidence of positive selection in yak (compared to none in cattle), which is significantly higher than the background level of positive selection across the genome ($P < 0.05$) (Qiu *et al*., 2012).

Need for studying the high altitude adaptation mechanisms in Yak

High-altitude habitats are characterized by extremely harsh climates consisting of low temperature and low oxygen pressure (Ayalew *et al*., 2021). A motivation for studying high-altitude adaptation across species is the potential for novel insights into a common molecular basis of adaptation, thus a focus on non-model organisms for the analysis of selection signatures can be observed over recent years (Haasl and Payseur, 2016). Domesticated ruminants, which live at all altitudes where human populations are found, can contribute to this cross-species approach and can help to confirm known or identify new mechanisms of adaptation to hypoxia. In addition to genome-wide adaptive changes at the DNA sequence level; gene expression as an intermediate phenotype connecting DNA sequences and physiological traits is highly informative in revealing molecular pathways/networks involved in genetic adaptation. The native high-altitude yak has evolved multiple unique adaptations, including morphological, physiological, biochemical, and genetic changes due to long-term selection. To gain a more holistic understanding of high-altitude adaptations, these types of studies need expansion, and efforts should be made to integrate work on DNA sequence polymorphism with analyses of transcriptional variation as well as the proteins involved.

CONCLUSION

Indeed, cold and hypoxia act synergistically on an organism's performance at high altitudes, yet the vast majority of studies have focused solely on adaptation to hypoxia. Hence, joint investigations of these co-occurring environmental stressors should be the priority for future research. Furthermore, the current climate change scenario characterized by rising temperature undoubtedly alters the natural habitats of yaks by creating new environmental conditions to which these animals were never before exposed. Therefore, further studies to determine how these shifts in climate contribute to changes in the yak production and the livelihoods of highlanders are indispensable. The information gained from this type of studies will not only enhance our understanding of the molecular mechanisms involved in hypoxic adaptation in the yaks but may also contribute to improvements in the understanding and prevention of hypoxia-related diseases.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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