Indian Yak Genomics

Source: TH

For the first time, **Indian scientists** have successfully assembled a **chromosome-level genome** of the **Indian yak (Bos grunniens)**, an essential high-altitude bovine species.

- **Indian Yak Genomics:** The project used **long-read sequencing technology** and advanced **bioinformatics**, enabling precise mapping of **genes to specific chromosomes.**
    - Long-read sequencing is a **DNA sequencing** method that reads **long stretches of DNA, thousands to millions of base pairs**, unlike **short-read sequencing**, which reads shorter fragments (typically **100–300 base pairs**).
    - **Bioinformatics** combines **biology, computer science, and math** to analyze and interpret large biological datasets, such as **DNA, RNA,** and **protein sequences**.
    - Moreover, this genomics study will help in **allele mining,** enhancing scientific research and **local livestock management.**
        - Allele mining **identifies genetic variations** linked to desirable traits like **disease resistance, drought tolerance, or high yield** within or across species.
- **Indian Yak:** In India, yaks are found **above 7,000 feet** in **Ladakh, Sikkim, Arunachal Pradesh, and Himachal Pradesh.**
- **Food Animal:** In **2022**, **Food Safety and Standard Authority of India (FSSAI)** approved the Himalayan Yak as a **'food animal'**, allowing its use in **food production or consumption** to help arrest its declining population.

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