

## 8 Challenges and Future Directions in Saker Falcon Research

### 8.1 Data integration limitations and biases

Integrating field observations with genomic data presents significant challenges, including inconsistencies in data collection methods, spatial and temporal mismatches, and varying data quality. These limitations can introduce biases that affect the reliability of ecological-genomic analyses. For example, differences in monitoring intensity or technology adoption across regions may lead to uneven data coverage, while the integration of heterogeneous datasets requires robust frameworks to ensure comparability and minimize error propagation. Addressing these challenges will require standardized protocols, improved data sharing infrastructures, and interdisciplinary collaboration to harmonize methodologies and reduce integration biases.

### 8.2 Emerging genomic technologies in wildlife conservation

Rapid advances in genomic technologies—such as next-generation sequencing, environmental DNA (eDNA) analysis, and portable sequencing platforms—are transforming wildlife conservation. These tools enable high-resolution population genetic studies, real-time monitoring of genetic diversity, and the detection of adaptive genetic variation even in non-model species. However, the adoption of these technologies also brings challenges, including the need for specialized expertise, high costs, and the management of large, complex datasets. Future directions should focus on making genomic tools more accessible, developing user-friendly analytical pipelines, and integrating genomic insights into practical conservation management.

### 8.3 Long-term monitoring and climate change adaptation

Long-term ecological monitoring remains essential for understanding population trends and adaptive responses to climate change. However, sustaining such efforts is challenged by funding limitations, logistical constraints, and the need for consistent methodologies over time. Climate change introduces additional complexity, as shifting environmental baselines may alter species distributions, phenology, and adaptive pressures. Future research should prioritize the development of adaptive monitoring frameworks that can respond to changing conditions, leverage remote sensing and automated data collection, and incorporate predictive modeling to inform proactive conservation strategies.

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## Conflict of Interest Disclosure

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## References

- Abdellaoui A., Yengo L., Verweij K., and Visscher P., 2023, 15 years of GWAS discovery: Realizing the promise, *American Journal of Human Genetics*, 110(2): 179-194.  
<https://doi.org/10.1016/j.ajhg.2022.12.011>
- Alqudah A.M., Sallam A., Baenziger P.S., and Börner A., 2020, GWAS: fast-forwarding gene identification and characterization in temperate cereals: lessons from barley—a review, *J. Adv. Res.*, 22: 119-135.  
<https://doi.org/10.1016/j.jare.2019.10.013>
- Ashwath M., Lavale S., Santhoshkumar A., Mohapatra S., Bhardwaj A., Dash U., Shiran K., Samantara K., and Wani S., 2023, Genome-wide association studies: an intuitive solution for SNP identification and gene mapping in trees, *Funct. Integr. Genomics*, 23(4): 297.  
<https://doi.org/10.1007/s10142-023-01224-8>
- Bashir L., Mehmood A., Manzoor S., Thendral U., Yadav J., Saha S., Yadav M., Meena D., and Padder U., 2024, A comprehensive review on GWAS: basic concepts and role in agriculture, *Int. J. Agric. Ext. Soc. Dev.*, 7(10): 302-314.  
<https://doi.org/10.33545/26180723.2024.v7.i10e.1231>
- Baxter I., 2020, We aren't good at picking candidate genes, and it's slowing us down, *Curr. Opin. Plant Biol.*, 54: 57-60.  
<https://doi.org/10.1016/j.pbi.2020.01.006>
- Cano-Gomez E., and Trynka G., 2020, From GWAS to function: using functional genomics to identify the mechanisms underlying complex diseases, *Front. Genet.*, 11: 424.  
<https://doi.org/10.3389/fgene.2020.00424>
- Chang-Brahim I., Koppensteiner L., Beltrame L., Bodner G., Saranti A., Salzinger J., Fanta-Jende P., Sulzbachner C., Bruckmüller F., Trognitz F., Samad-Zamini M., Zechner E., Holzinger A., and Molin E., 2024, Reviewing the essential roles of remote phenotyping, GWAS and explainable AI in practical marker-assisted selection for drought-tolerant winter wheat breeding, *Front. Plant Sci.*, 15: 1319938.  
<https://doi.org/10.3389/fpls.2024.1319938>