

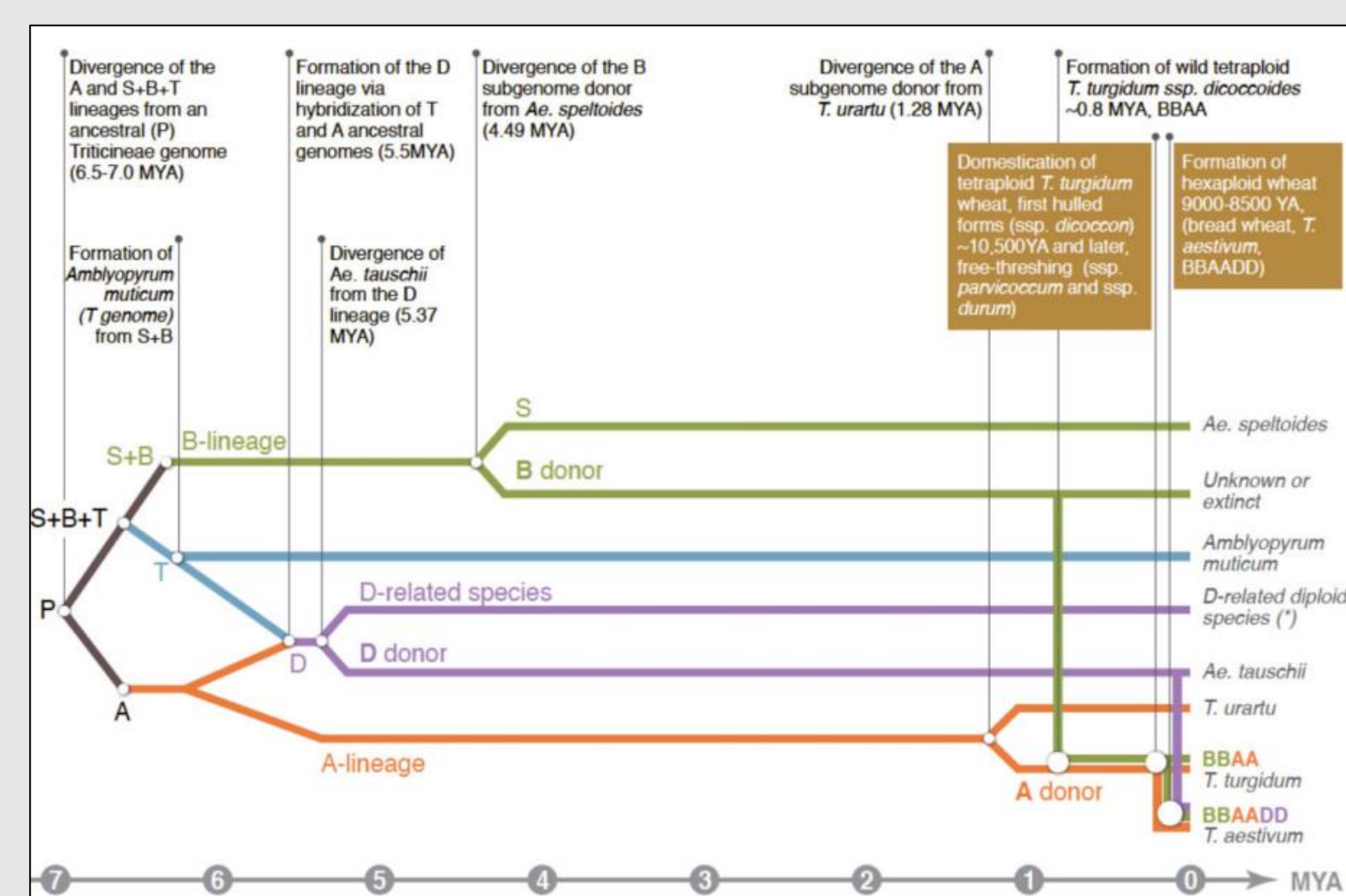
# Development of strategies to improve modern wheat cultivars by adopting genetic diversity from wild relatives



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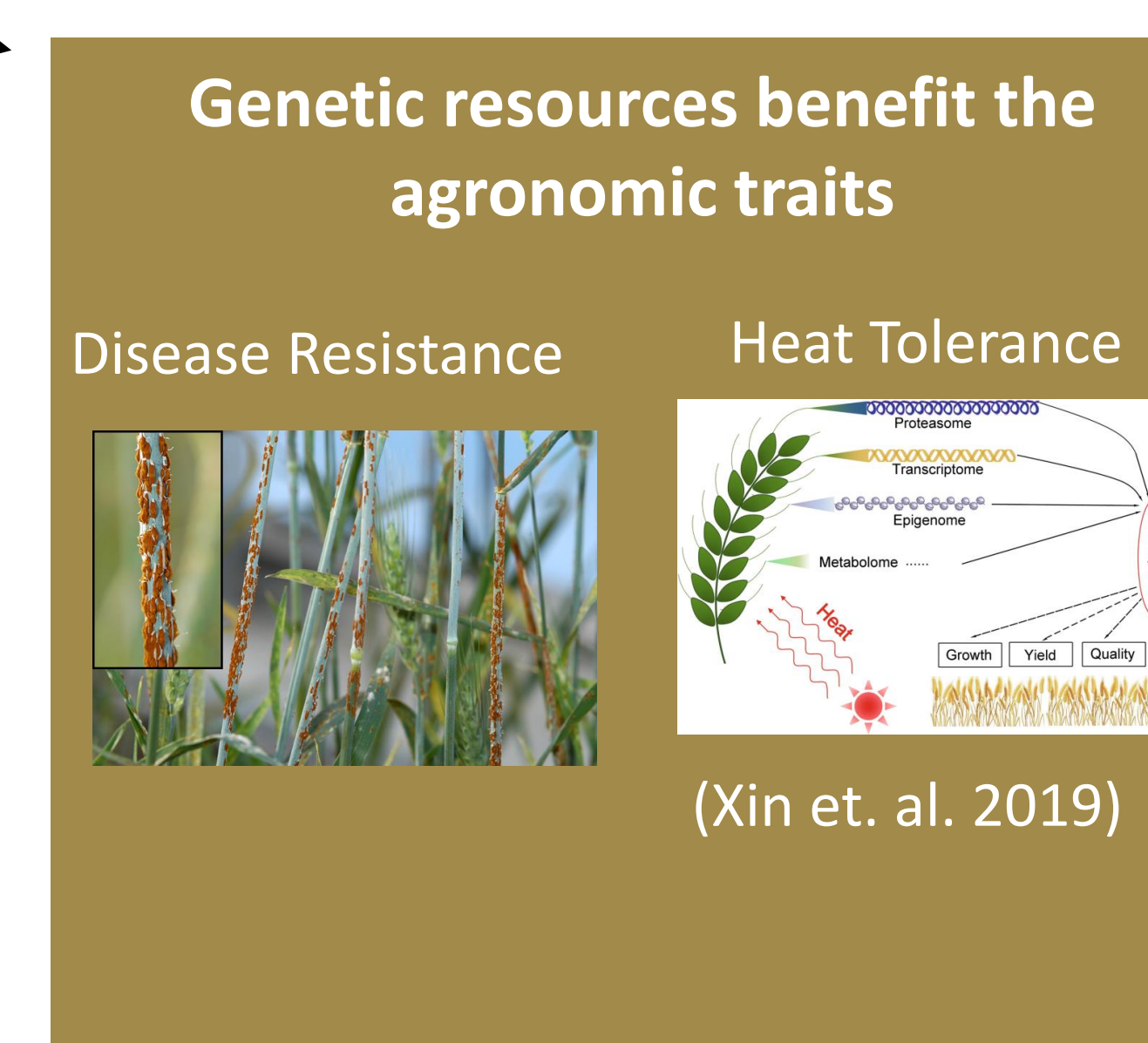
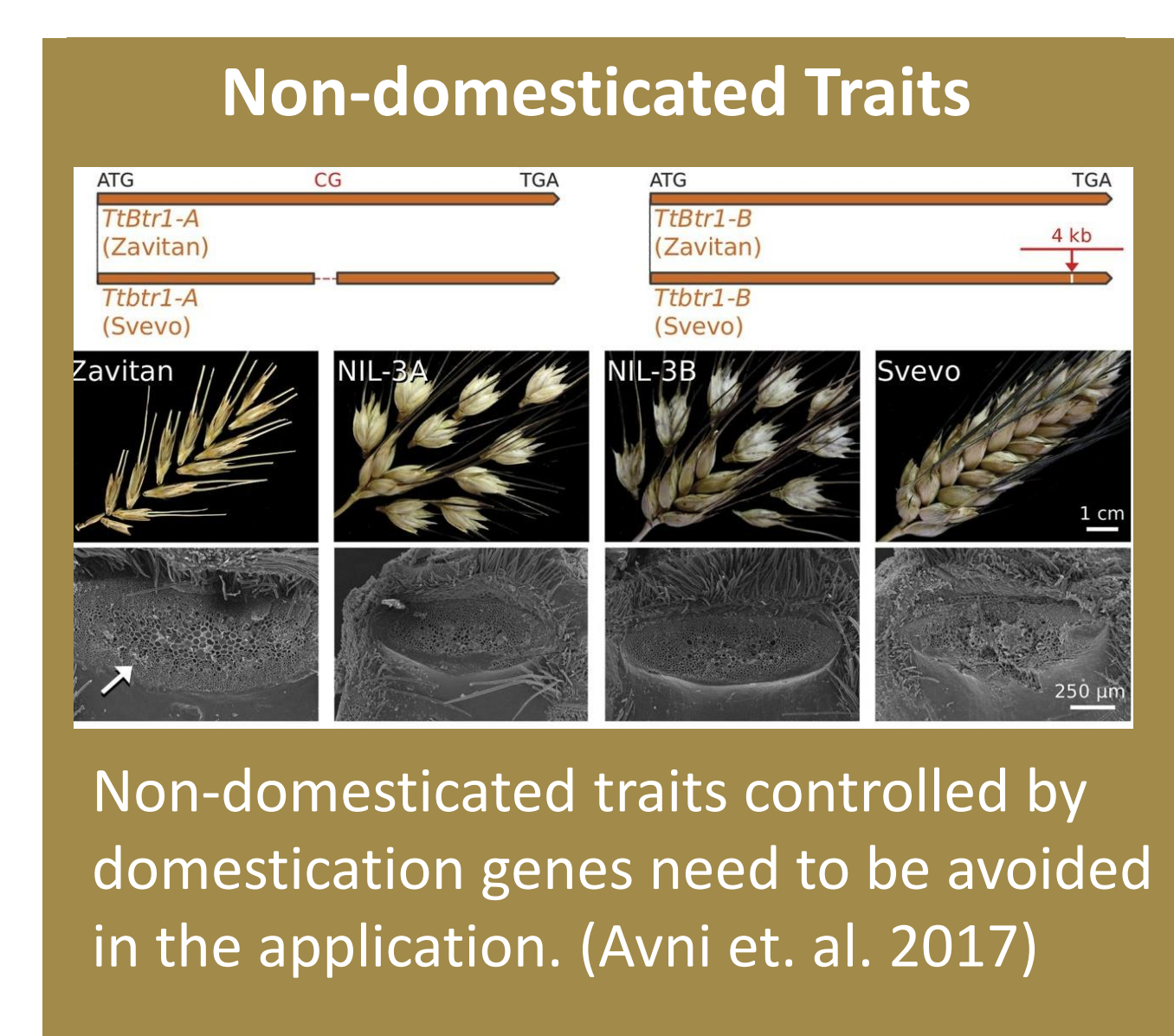
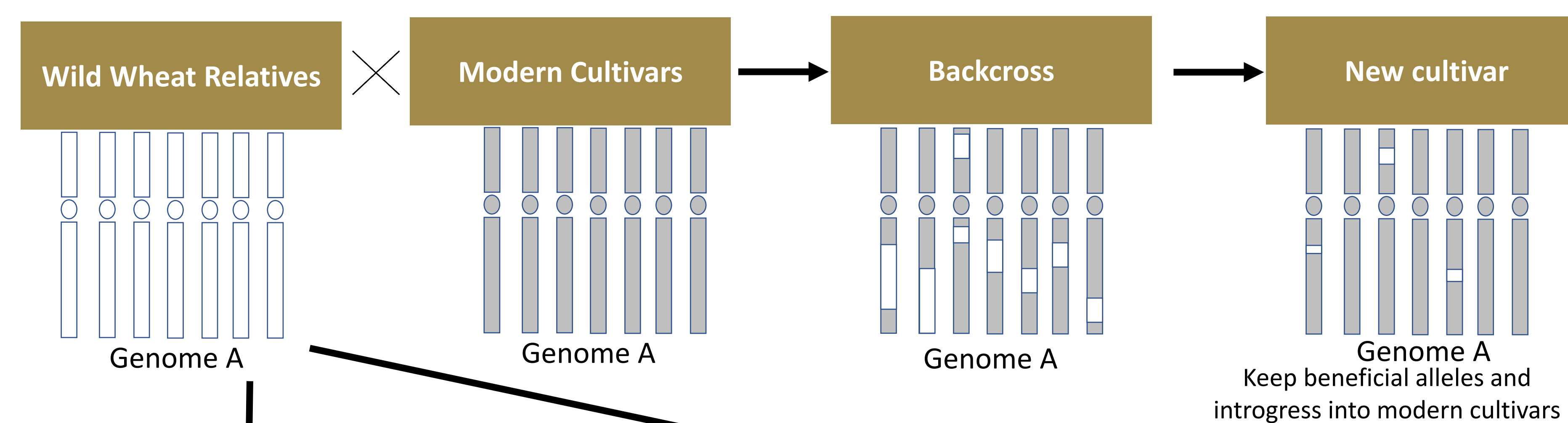
## Introduction

**Figure 1:** A hybridization event between a tetraploid species and a diploid species created hexaploid bread wheat. (Levy and Feldman, 2022).



**Figure 2:** Wild emmer is a tetraploid ancestor of wheat that shows many non-domesticated traits, but also has many beneficial alleles to be applied for the modern cultivar improvement. (Peng et. al. 2011)

## Methods and Results

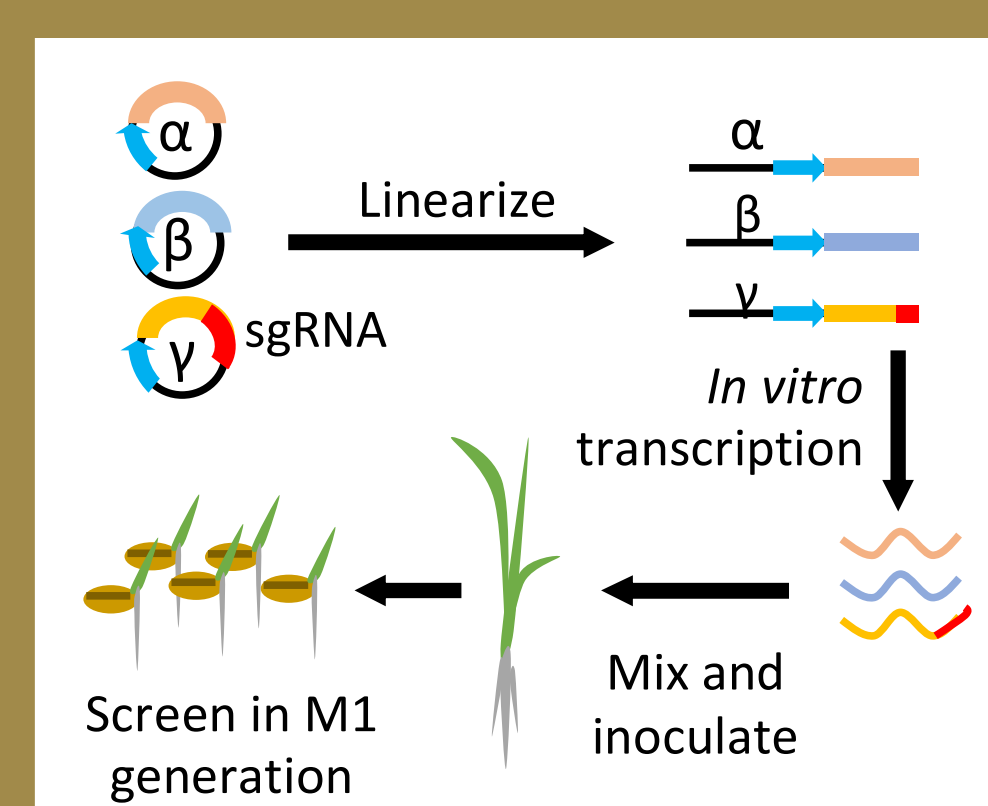


## CRISPR-Cas-based de-novo Domestication

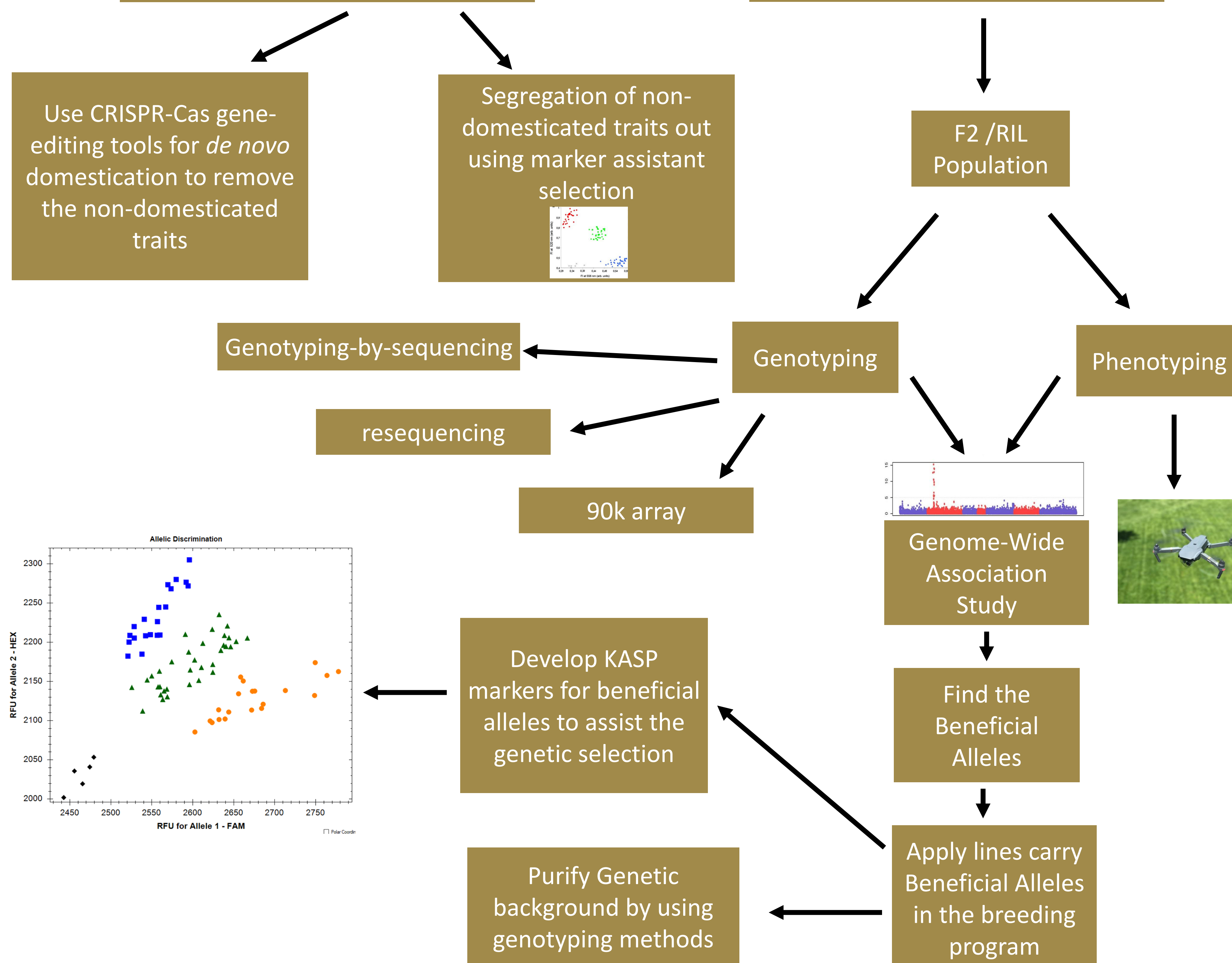
- The  $\alpha$ ,  $\beta$ , and  $\gamma$  chains of the Barley Streak Mosaic Virus (BSMV) were expressed from the the constructs. The guide RNAs were inserted onto the pBSMV $\gamma$ PDS.
- Cas9 expressing plants were inoculated with the BSMV to deliver the guide RNA
- DNA was isolated from the plants 2 weeks after inoculation
- DNA was purified and a PCR was performed in order to prepare the Next Generation Sequencing libraries.
- Next Generation sequencing was used to detect editing events



**Figure 3:** Wheat leaf inoculated with wildtype BSMV and pBSMV $\gamma$ PDS



**Figure 4:** Pipeline of BSMV-based genetic editing in wheat



## Conclusions

- The genetic diversity of wheat wild relatives can be applied for improving agronomic traits in modern wheat cultivar
- The deployment of beneficial alleles from wild relatives can be achieved using different methods including CRISPR-Cas-based *de novo* domestication of wild relatives and removal of wild relative DNA by backcrossing and marker-assisted selection.

## Acknowledgments

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