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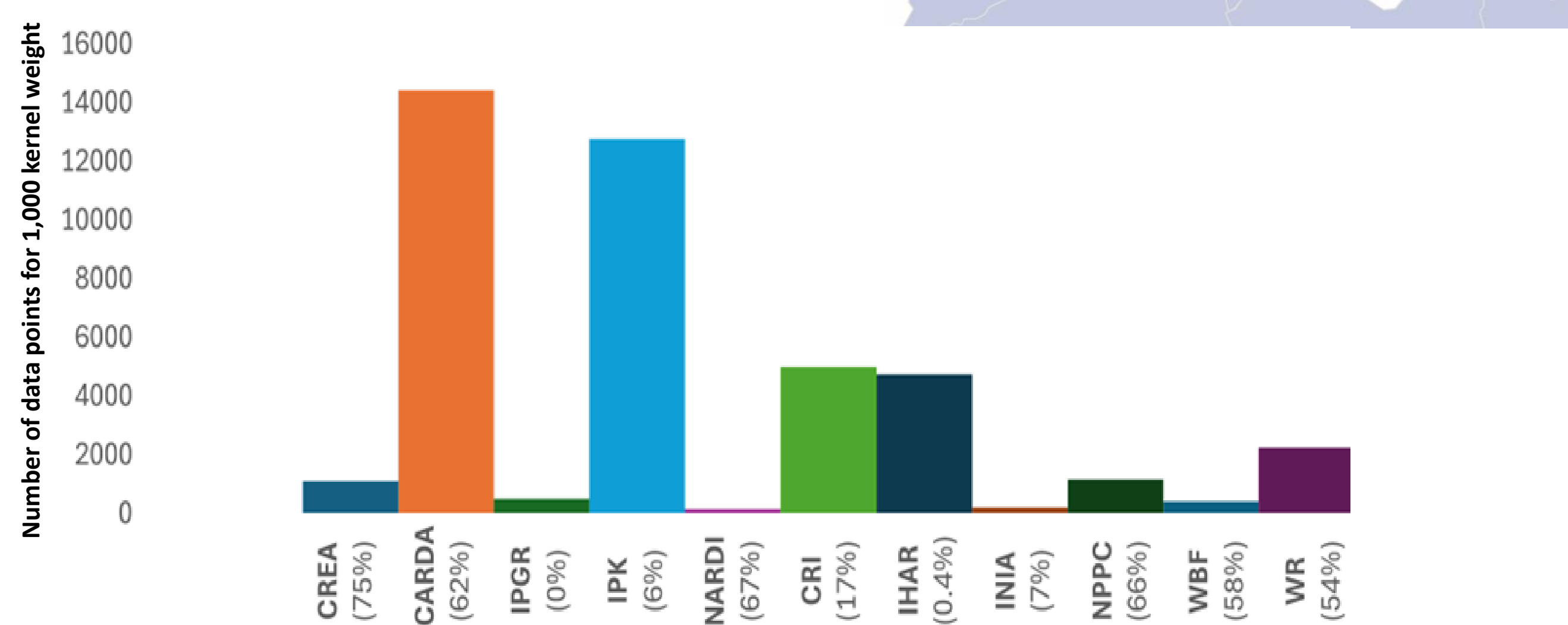
## Summary

Durum wheat is a cornerstone of Mediterranean agriculture and cuisine, yet its resilience and productivity face increasing challenges from climate change and shifting production environments. Stabilizing yields under those conditions requires identifying and deploying new, resilient and diverse genetic resources. This work presents two comprehensive approaches to mobilizing genetic resources under two projects called AGENT and BOLD. Within the AGENT initiative, historical phenotypic data from 43,293 wheat accessions were curated issued from a global network between 9 European and ICARDA genebanks. Precision subsets from each genebank served as training population for genomic selection, enabling the prediction of genomic breeding values (GEBVs) and supporting more informed selection by breeders. The BOLD initiative emphasized participatory assessment and targeted use of diversity. 46 elites lines derived from crosses with crop wild relatives (CWR) were evaluated in multi-environment trials in Morocco and other partner countries. Interestingly, These CWR-derived lines outperformed commercial checks across most sites, showing 11-48% yield gains alongside improved disease resistance to some rusts, rot root and Hessian fly, and several quality traits. Participatory trials with Moroccan farmers identified preferred lines for varietal release and commercialization based on agronomic performance and farmer priorities.

## From sparse phenotyping to genome-wide prediction accuracy

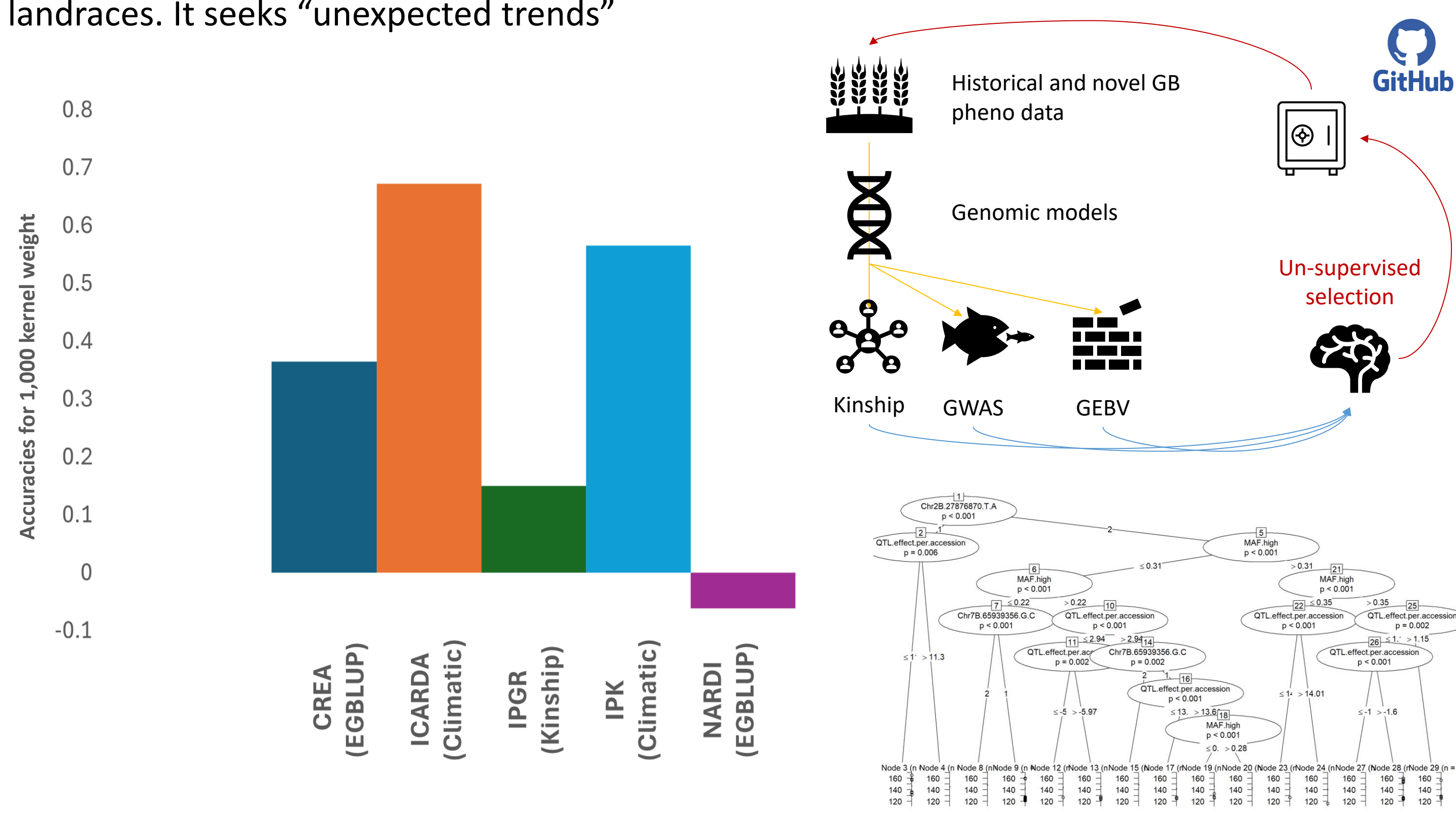
To achieve high genetic gain, breeders need access to genetic variance. The AGENT project addresses this by transforming wheat and barley genebanks into bio-digital resource centers.

$$\Delta G = \frac{i \cdot r \cdot \sigma_A}{L}$$

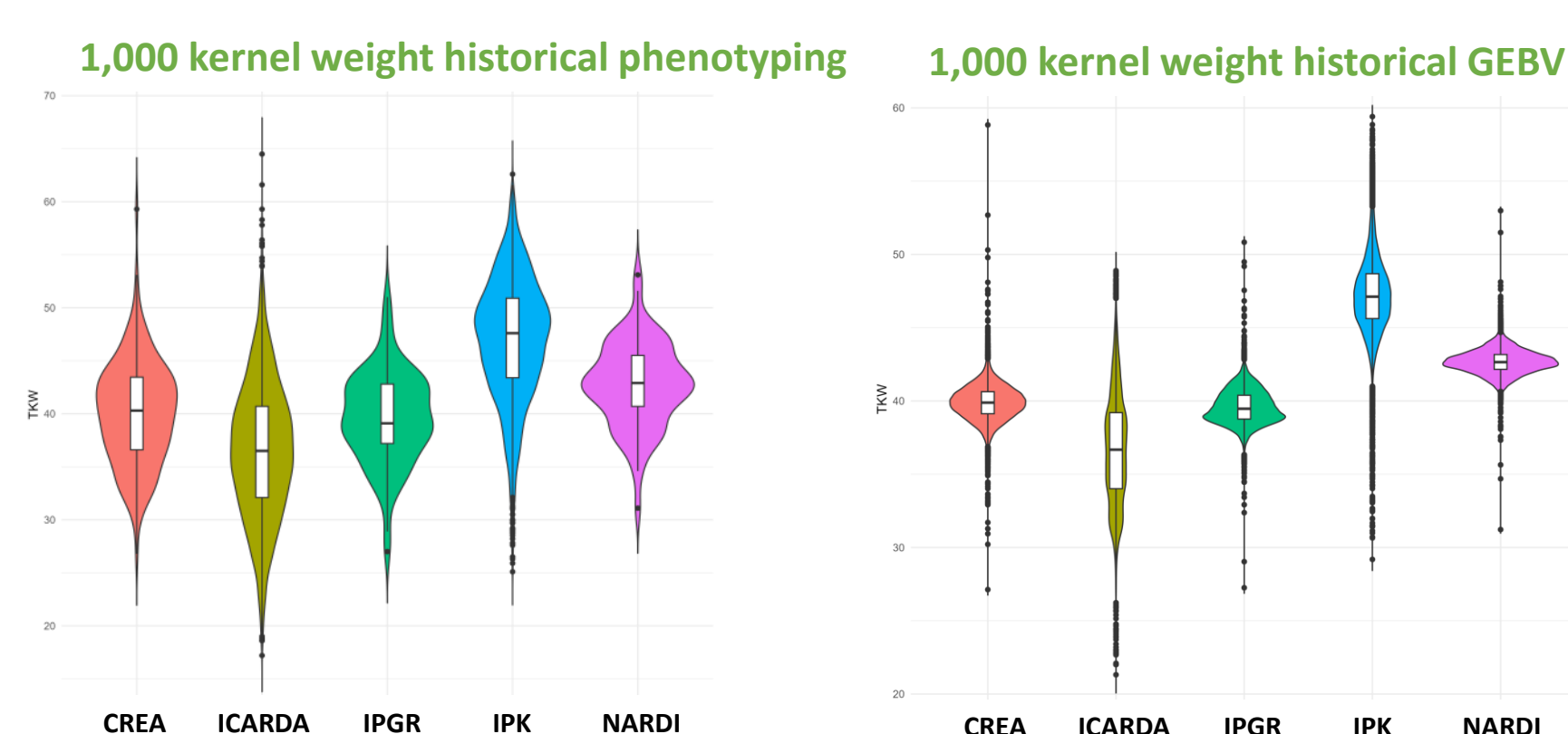


- Historical data of 1,000 kernel weight derived from a total of 117,738 wheat accessions from 11 genebanks was analyzed.
- Number of data points of ICARDA genebank was the higher.
- IPGR and IHAR had the lowest number of missing data, while CREA had the highest number.

Under the AGENT project with IPK we have developed a full pipeline “AGENT-G” to run genomic models using historical and newly generated phenotypic data to estimate the value of the GB accessions based on major (GWAS) and minor (GEBV) alleles. Further, we have now linked that with 5 models of machine learning to improve the selection of “useful” landraces. It seeks “unexpected trends”



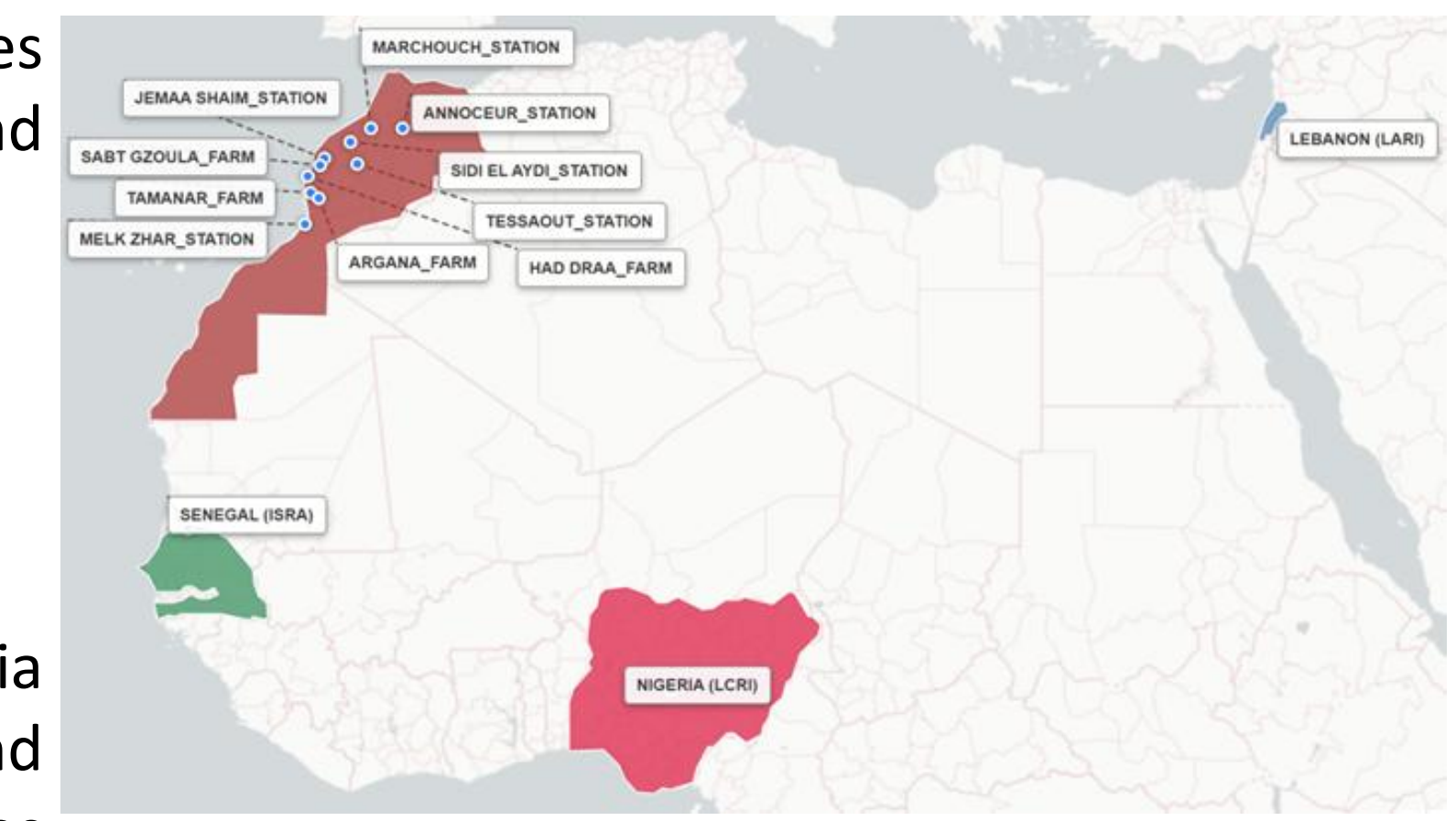
- The “AGENT-G” script pipeline available on Git Hub was used to run GWAS and GS. [https://github.com/AGENTproject/WP4/tree/main/Analysis\\_Pipeline](https://github.com/AGENTproject/WP4/tree/main/Analysis_Pipeline)
- Used models were: EGBLUP, Climatic, kinship, kinship + Climatic, kinship + Fixing, kinship + Fixing + Climatic, Fixing, Fixing + Climatic.
- The GS pipeline automatically selects the best model.
- The greatest advantage is that each best model can be used for each trait / location / genebank combination.



- Using predictions, TKW values for each genebank/location were assigned.
- The predicted distribution also maintains its overall distribution.

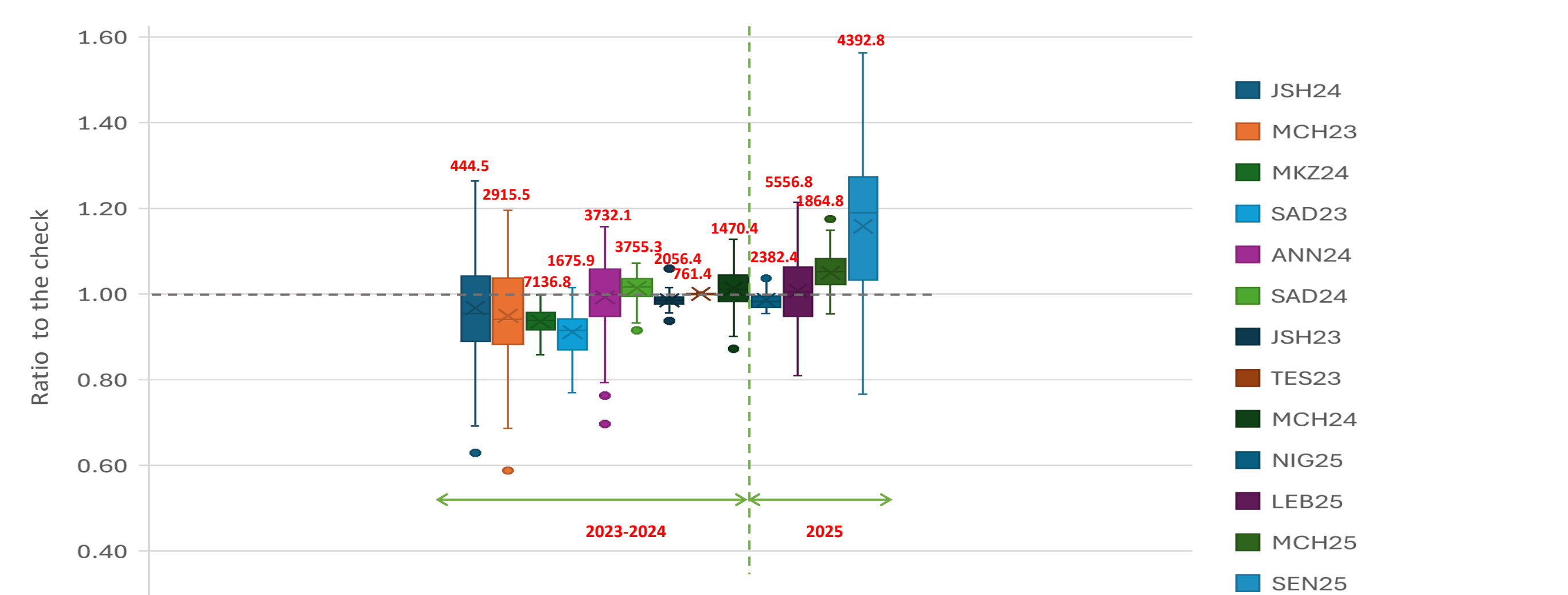
## Performances of CWR-derived elites in multi-location trials for two seasons

96 CWR derived lines were first tested across locations in Morocco, then the best entries for yield performance, disease resistance and nutritional quality are selected.

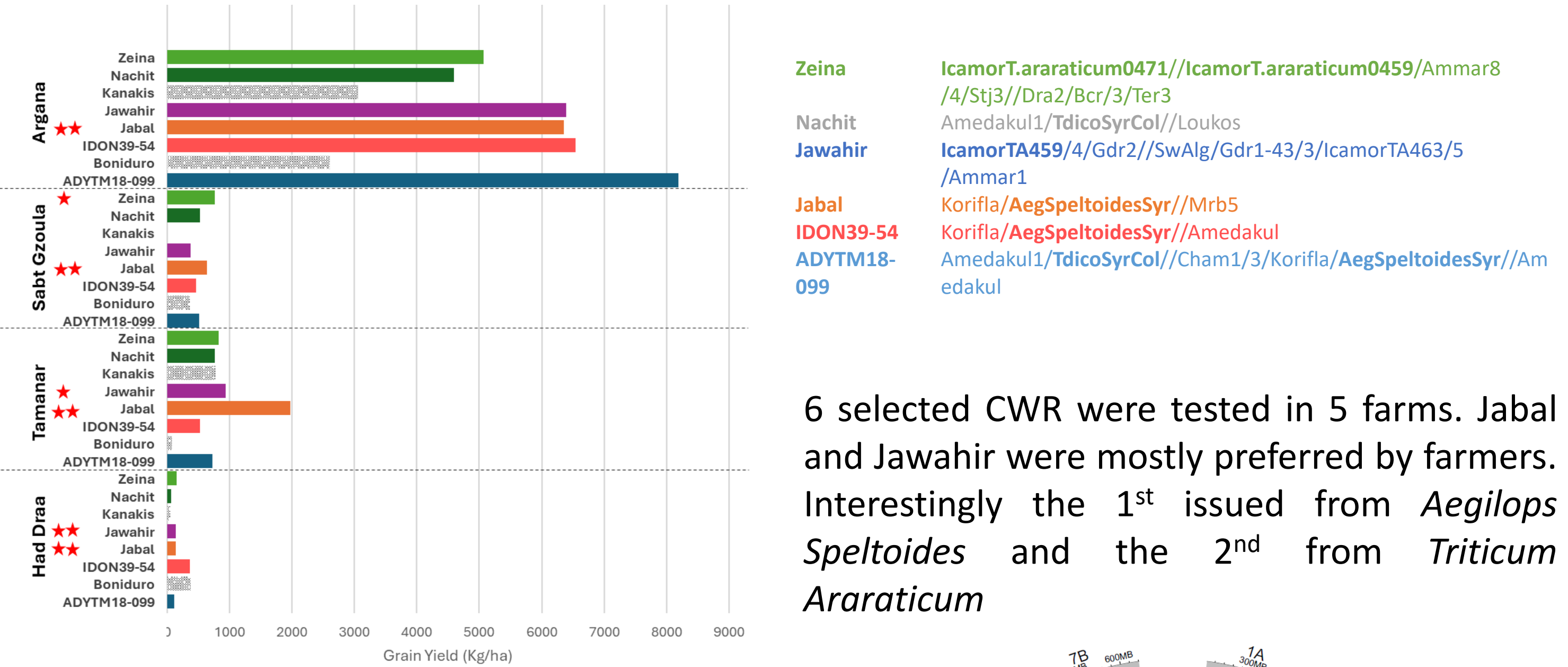


5 partners in Senegal (ISRA), Ethiopia (EIAR), Nigeria (LCRI), Lebanon (LARI) and Tunisia (INRA) test 46 best selected entries during 2 seasons 2024-2026 based on MPPs.

Each partner distribute the best selected CWR derived lines to 5 farmers

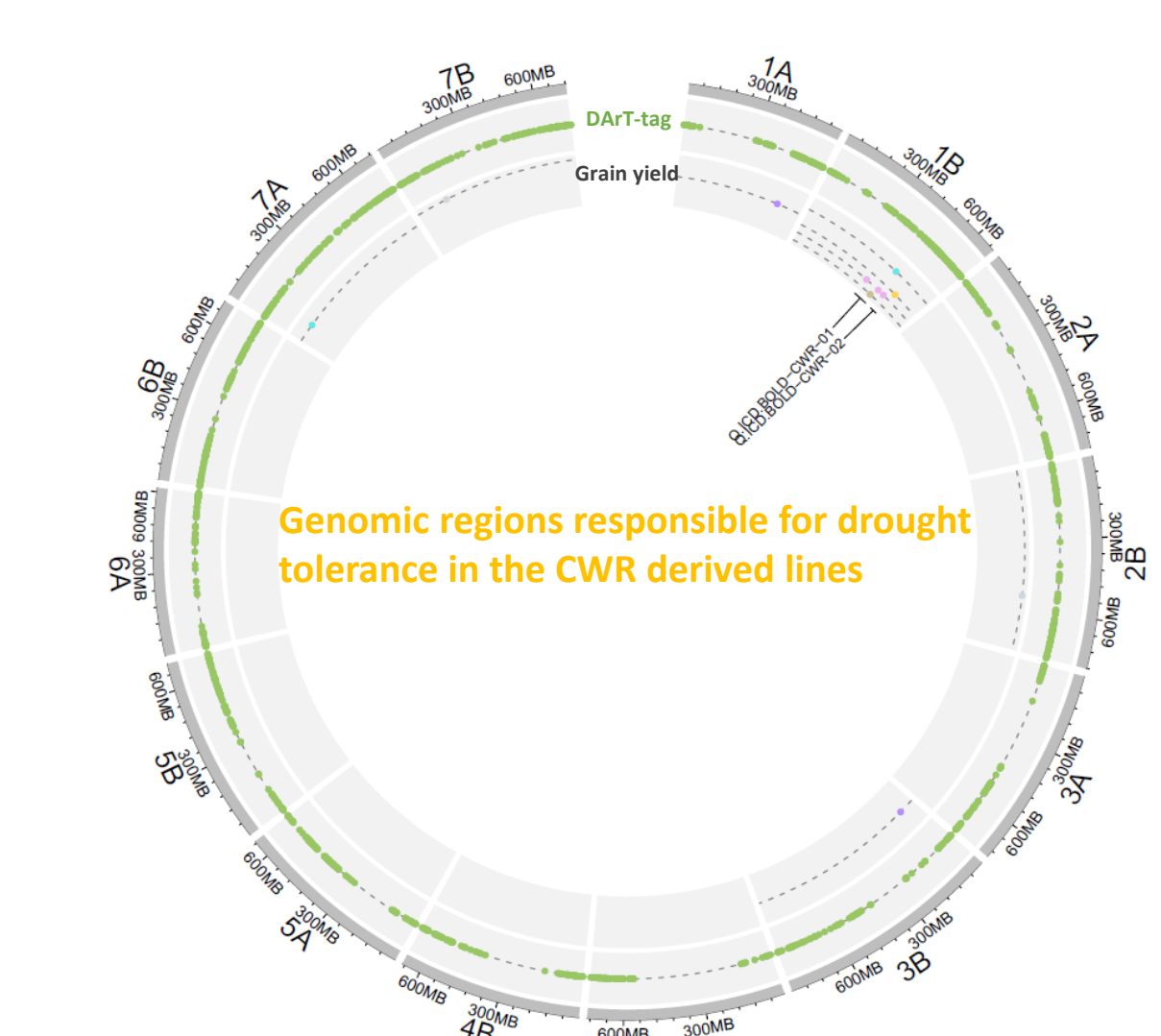


- In the majority of sites, the 96 CWR derived lines performed similarly or better than the commercial checks for grain yield.
- The selected 46 entries selected based on MPPs tested across partners, showed outperforming grain yield compared to the commercial checks.



6 selected CWR were tested in 5 farms. Jabal and Jawahir were mostly preferred by farmers. Interestingly the 1<sup>st</sup> issued from *Aegilops Speltoides* and the 2<sup>nd</sup> from *Triticum Araraticum*

GWAS using 2218 DaT-seq markers revealed two genomic regions significantly linked to drought resistance.



## Acknowledgement

This work was realized as part of the two projects: 1. 'Activated Genebank Network (AGENT)', that was supported by the European Union's Horizon 2020 research and innovation program under grant agreement No 862613. This project aims to transform genebanks from passive seed libraries into advanced bio-informatics resource centers. For further information, visit the project website: <https://www.agent-project.eu/>. 2. 'Biodiversity for Opportunities, Livelihoods and Development' (BOLD), under the phase I (DIIVA-PR) and the phase II (BOLD-DIVA-PR II) of BOLD project supported by the Government of Norway. BOLD is managed by the Global Crop Diversity Trust and implemented in partnership with national and international genebanks and plant breeding institutes around the world. The project aims to strengthen food and nutrition security worldwide by supporting the conservation and use of crop diversity. For further information, visit the project website: <https://bold.croptrust.org/>

