Marker-trait associations for barley grain quality traits identified in Karaganda and Kostanay regions (Kazakhstan) using GWAS

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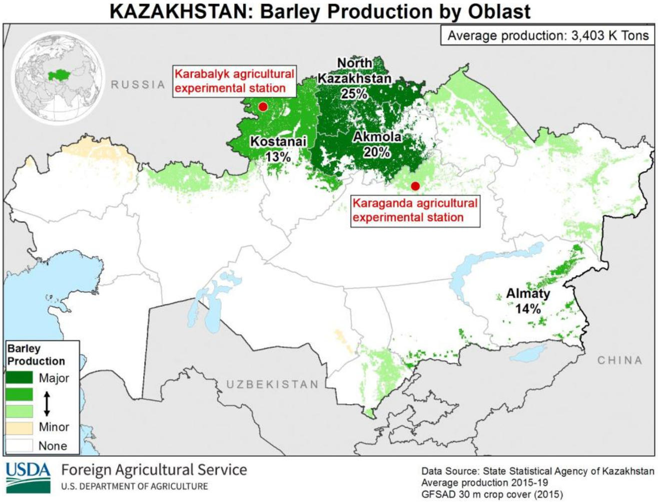
Goal of the study: to identify new SNP-markers associated with major grain quality traits of barley grown in northern and central Kazakhstan



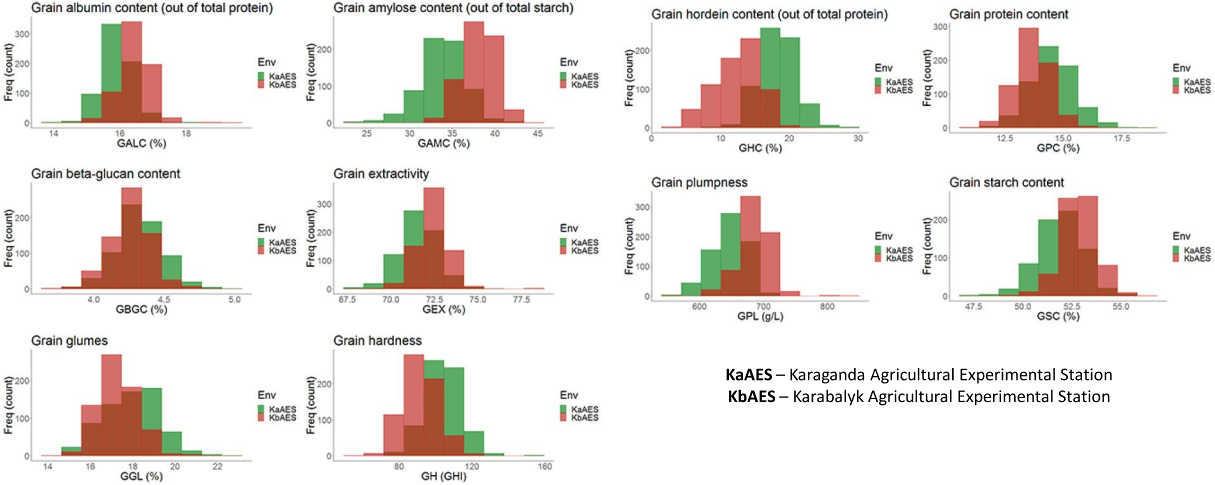
Data Source: State Statistical Agency of Kazakhstan
Average production 2015-19
GFSAD 30 m crop cover (2015)

Figure 1 – Barley-producing regions of Kazakhstan and experimental fields used in the study.

Materials and methods:

- Spring barley collection, including 557 accessions from the USA and 104 accessions from Kazakhstan grown in two regions of Kazakhstan – Karaganda (center) and Kostanay (north) regions in 2010 and 2011 was studied for 10 major grain quality traits (Fig. 1).
- Studied grain quality traits: content of raw protein (GPC, %), β-glucan (GBGC, %), hordein (GHC, %), albumin (GALC, %), amylose (GAMC, %), starch (GSC, %), grain plumpness (GPL, g/L), extractivity (GEX, %), grain hardness (GH, GHI units) and glumes (GGL, %).
- The collection was genotyped using barley iSelect 9K SNP array resulted in 2,344 polymorphic markers.
- TASSEL 5 and R software package were used for statistics and GWAS analyses.

Comparative analysis of barley grain quality traits between two regions



Grain albumin content (out of total protein)

Grain amylose content (out of total starch)

Grain hordein content (out of total protein)

Grain protein content

Grain beta-glucan content

Grain extractivity

Grain plumpness

Grain starch content

Grain glumes

Grain hardness

KaAES – Karaganda Agricultural Experimental Station

KbAES – Karabalyk Agricultural Experimental Station

Figure 2 – Ten grain quality traits in studied barley collection grown in Karaganda (central Kazakhstan) and Karabalyk (northern Kazakhstan) regions.

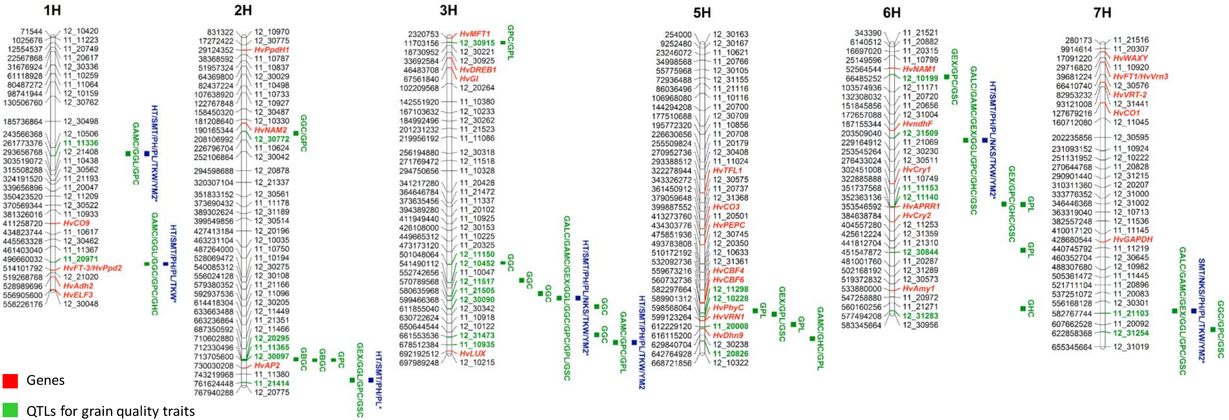
Marker-trait associations identified in the study

Table 1 – the list of MTAs for 9 major barley grain quality traits identified on 6 chromosomes.

#	Grain quality trait	No. of MTAs identified for the trait ($P < 0.001$)	Chromosomes
1	Grain protein content (GPC)	13	1H, 2H, 3H, 6H, 7H
2	Grain plumpness (GPL)	9	3H, 5H, 6H
3	Grain starch content (GSC)	8	2H, 3H, 5H, 6H, 7H
4	Grain amylose content (GAMC)	7	1H, 3H, 5H, 6H, 7H
5	Grain extractivity (GEX)	7	2H, 3H, 5H, 6H, 7H
6	Grain glume (GGL)	6	1H, 2H, 3H, 6H, 7H
7	Grain hordein content (GHC)	5	1H, 5H, 6H
8	Grain albumin content (GALC)	3	3H, 6H, 7H
9	Grain β-glucan content (GBGC)	2	2H
	Total	60	1H, 2H, 3H, 5H, 6H, 7H

Genomic positions of quantitative trait loci identified in the study and possible candidate genes

Sixty MTAs (Table 1) for were combined into twenty-seven quantitative trait loci (QTL) in accordance with their pleiotropic nature (Fig. 3).



🟥 Genes

🟩 QTLs for grain quality traits

🟦 QTLs for adaptation and grain yield components identified earlier

Figure 3 – Physical map of quantitative trait loci (QTL) identified in the study

Conclusions

- Generally, studied collection had demonstrated higher levels of starch content and extractivity and lower protein level in Kostanay region (north), which is preferable for the breeding of brewing barley.

- Sixty marker-trait associations were identified on 6 barley chromosomes (except chromosome 4H). They were unified in 27 QTLs, considering the pleiotropic effect of several markers. Seven of these pleiotropic QTLs were previously described as associated with barley yield-related traits (Genievskaya et al., 2018).

- The phenotypic variation explained by the individual marker varied from 1.69% to 5.32%. Both negative and positive effects were observed for all studied traits; therefore, QTLs identified in the study may be used for the breeding of barley for different purposes and with different quality of the grain.

- QTLs detected in different regions of Kazakhstan have a potential usage for local barley breeding programs.

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