

## MetaBrew:

### A comprehensive database of malting quality traits in brewing barley

S. WEISE, U. SCHOLZ, M.S. RÖDER, I.E. MATTHIES\*

Leibniz Institute of Plant Genetics and Crop Plant Research, Corrensstr. 3, 06466 Gatersleben, Germany

\*Corresponding author, matthies@ipk-gatersleben.de

#### Abstract

MetaBrew is a manually curated and comprehensive repository of high quality analysis data concerning kernel, malting and brewing quality of barley cultivars. This includes meta information about the genotypic and phenotypic background (pedigree, row number, seasonal habit, environment, experiment sources). Exploration and export of the information is supported by a web application. MetaBrew is available at <http://metabrew.ipk-gatersleben.de>.

**Key words:** barley – malting quality – phenotypic traits

#### Introduction

Although barley is mainly used for feed, the production of malt for products such as beer and whisky is of high economical importance (Fox et al. 2003). Due to the complexity of traits involved in the malting and brewing process, the selection of suitable cultivars and breeding strains to improve the quality is difficult, time consuming and expensive while most of these parameters show a high variation in their performance. Therefore, it is beneficial to have a broad phenotypic data basis in order to evaluate quality levels by statistical methods.

Here, we present a database to screen for phenotypic data interesting for any breeding and malting programme. We are using this data stock to perform association studies in order to select diagnostic markers in candidate genes important for malting quality. Due to the requests of breeders and researcher colleagues we would like to make this data repository publicly available and offer possibilities for searching, filtering and extracting data.

#### Database description

For persistent storage of the MetaBrew data the relational database management system Oracle is used, whereas the MetaBrew application is based on the Oracle Application Express (APEX) technology. This application is split into two parts. The first one is intended to collect and to curate data and is restricted only for internal access. The second part is a read-only web application thus allowing browsing, searching and exporting of data.

#### Content

MetaBrew comprises phenotypic data of 96 malting and brewing parameters obtained from 162 barley cultivars. The data collection comprises older and modern European varieties from the past 20 years (1985–2005) grown at different locations in Germany. Raw data was recorded either from the statistical year books of the German Brewing Society or from official trials by the German Seed Board. This data was hand-curated and organised. Therefore, the data was recorded in MS-Excel templates and imported using Java-based procedures. Consistency checks were performed during the import. Links to the original experiments and information such as the locations data has been collected at, soil conditions or types of testing are available. Furthermore, additional background information about pedigree, row number etc. was obtained either by

personal communication with barley breeders or from official information from seed boards. MetaBrew contains single entries (one cultivar at one location in one year) and average entries (one cultivar in one year at several locations). Average values were labelled and, if available, stored together with the number of single entries used to calculate the average. To ensure a high data quality, all entries were cross-checked manually. Controlled vocabulary (e.g. trait names) was used to ensure consistency and to allow single data comparisons from different sources. Up to now, approximately 60,000 phenotypic data points are available. The data stock will be actualised and extended once every year.

### **Web application**

The web interface of the MetaBrew database is accessible at <http://metabrew.ipk-gatersleben.de>. It allows detailed browsing and searching of data, user feedback and data export. There are navigation tabs for traits, sources of data, cultivars, observations and statistics, which open sub tabs each with several items. Data can be grouped by cultivar, trait, year, row number or seasonal habit, respectively. Statistical information such as standard deviation or variance is given per trait and cultivar. All data can be exported to MS Excel compatible files. Selective data can be visualised graphically using scatter plots or box plots, respectively. Fig. 1 shows a compilation of screenshots of the MetaBrew web application.

### **Application of the MetaBrew database**

MetaBrew is intended to assist brewers and maltsters to select the optimal strain or cultivar for future breeding programmes or for malting, respectively. Many detailed information about the performance of specific traits for different cultivars are given. This helps to predict promising crossing parents for breeding new barley cultivars. Also, cultivars with good malting properties can be selected according to this data in order to produce high quality beer.

By combining genotypic and phenotypic information, it is possible to perform association studies in a large extent. Association studies will show the impact of genetic changes in certain candidate genes on malting parameters, which may be interesting not only for breeders but also for the brewing industry. We are using MetaBrew for association studies on a large subset of information contained in this database. First results are described in (Matthies et al. 2009).

### **Conclusion**

In barley, general and specific information about malting and brewing properties of single cultivars in a compact and structured way was lacking. In this paper we presented the first version of the MetaBrew database, a repository of comprehensive, high quality data about phenotypic traits with impact on malting and brewing quality. The structure allows data extraction according to the individual question of interest of the user. MetaBrew is an ongoing project and currently consists of a large collection of manually curated data. Information content will be extended and actualised every year.

### **Acknowledgements**

We would like to thank Susanne Kirsten for excellent technical assistance concerning data input.

### **References**

Fox, G., Panozzo, J., Li, C., Lance, R., Inkerman, P. and Henry, R. 2003. Molecular basis of barley quality. *Australian Journal of Agricultural Research* 54(11&12):1081–1101.

Matthies, I., Weise, S. and Röder, M., 2009: Association of haplotype diversity in the  $\alpha$ -amylase gene amy1 with malting quality parameters in barley. Molecular Breeding, 23(1):139-152.

**Fig. 1** Compilation of screenshots of the MetaBrew web interface showing (a) extracts from the database about cultivars and traits, (b) correlation between two traits for a set of cultivars and (c) average data of a trait.

**MetaBrew**

Home Traits Sources Cultivars **Observations** Statistics

Observation data **Average data** Average data by cultivar Average data by row number Average data by seasonal habit

Home > Observations > Average data

Average data

Trait	Cultivar	Average	Minimum	Maximum	Standard deviation	Variance
Kernel yield [dt/ha]	Venus	74.83	64.2	83.7	9.87	97.4
Kernel yield [dt/ha]	Borwina	64.87	61.2	67.4	3.25	10.57
Kernel yield [dt/ha]	Corona	74.15	61.7	85.6	7.68	59.05
Kernel yield [dt/ha]	Jana	76.18	69.4	84.7	6.5	42.29
Kernel yield [dt/ha]	Libelle	64.3	57.9	70	5.62	31.61
Kernel yield [dt/ha]	Astrid	72.77	66.8	79.3	4.2	17.61
Kernel yield [dt/ha]	Jasmin	73.66	68	79.5	3.39	11.49
Kernel yield [dt/ha]	Cabrio	79.03	75.8	84.9	5.09	25.9
Kernel yield [dt/ha]	Gamelan	77.8	73.4	82.8	4.73	22.36
Kernel yield [dt/ha]	Catania	77.47	70.9	83.7	6.41	41.04
Kernel yield [dt/ha]	Plus	74.4	67	82.7	7.89	62.23
Kernel yield [dt/ha]	Sissy	63.84	58.9	67.1	3.1	9.61
Kernel yield [dt/ha]	Korinna	64.45	61.6	67.3	4.03	16.25
Kernel yield [dt/ha]	Alexis	61.14	54.2	67.3	4.2	17.68
Kernel yield [dt/ha]	Hanna	75.34	67.2	83.1	4.66	21.68

Download

<Previous row(s) 1201 - 1215 of 5635 Next >

WEISE

# Barley Genetics Newsletter (2009) 39:1-4

MetaBrew

Logout |

b)

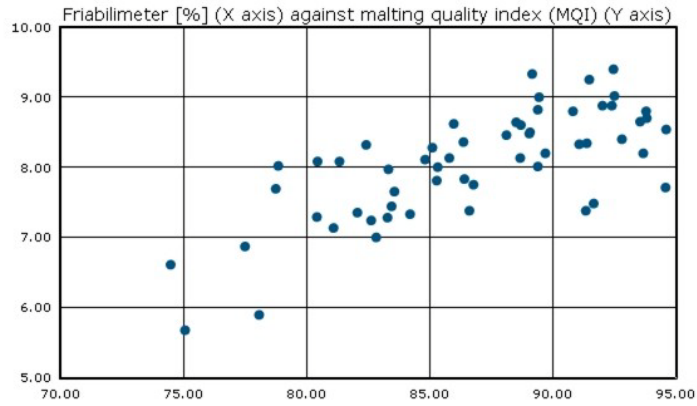
Home Traits Sources Cultivars Observations **Statistics**

Scatterplot Averages per trait Correlation

Home > Statistics

Scatterplot

Friabilimeter [%] malting quality index (MQI) 2-rowed spring barley Plot



MetaBrew

Logout |

c)

Home Traits Sources Cultivars Observations **Statistics**

Scatterplot Averages per trait Correlation

Home > Statistics > Averages per trait

Averages per trait

Viscosity [mPas] 2-rowed spring barley Plot

