

2002

Storage of molecular marker data in databases for efficient use in plant breeding programs

Matthias Frisch
Universität Hohenheim

Kendall R. Lamkey
Iowa State University, krlamkey@iastate.edu

Albrecht E. Melchinger
Universität Hohenheim

Follow this and additional works at: http://lib.dr.iastate.edu/agron_pubs

 Part of the [Agricultural Science Commons](#), [Agriculture Commons](#), [Agronomy and Crop Sciences Commons](#), [Genetics Commons](#), and the [Plant Breeding and Genetics Commons](#)

The complete bibliographic information for this item can be found at http://lib.dr.iastate.edu/agron_pubs/39. For information on how to cite this item, please visit <http://lib.dr.iastate.edu/howtocite.html>.

This Article is brought to you for free and open access by the Agronomy at Iowa State University Digital Repository. It has been accepted for inclusion in Agronomy Publications by an authorized administrator of Iowa State University Digital Repository. For more information, please contact digirep@iastate.edu.

Storage of molecular marker data in databases for efficient use in plant breeding programs

Abstract

With the increased use of molecular markers in plant breeding programs, appropriate storage of these data becomes an important issue. The concept for storage of molecular marker data in databases proposed in this paper is simple and generic so that it can be implemented on a personal computer and integrated in large-scale database systems. Application of the proposed data structure simplifies standardized statistical analyses and reanalyses of experimental data as well as data exchange and reuse of programmed analysis routines.

Disciplines

Agricultural Science | Agriculture | Agronomy and Crop Sciences | Genetics | Plant Breeding and Genetics

Comments

This article is from *Zeitschrift für Agrarinformatik* 10 (2002): 23–27.

Rights

Works produced by employees of the U.S. Government as part of their official duties are not copyrighted within the U.S. The content of this document is not copyrighted.

STORAGE OF MOLECULAR MARKER DATA IN DATABASES FOR EFFICIENT USE IN PLANT BREEDING PROGRAMS

MATTHIAS FRISCH, KENDALL R. LAMKEY, AND ALBRECHT E. MELCHINGER*

ABSTRACT. With the increased use of molecular markers in plant breeding programs, appropriate storage of these data becomes an important issue. The concept for storage of molecular marker data in databases proposed in this paper is simple and generic so that it can be implemented on a personal computer and integrated in large-scale database systems. Application of the proposed data structure simplifies standardized statistical analyses and reanalyses of experimental data as well as data exchange and reuse of programmed analysis routines.

Classical plant breeding uses phenotypic information about a plant or its relatives to improve the genotype of future generations. The phenotype of a plant is assessed by measuring, e.g., yield or resistance and superior phenotypes are assumed to be the result of superior genotypes. Breeding progress is made by mating superior genotypes to generate the next generation. This concept was extended during the last 15 years by including results from DNA analyses, so called molecular markers, in the decision process of plant breeding. Meanwhile, molecular markers have become an important tool in plant breeding (Lee 1995; Melchinger 1990; Young 1999). Areas of application include studies about genetic diversity, inheritance of quantitative characters, marker-assisted selection, and genetic fingerprints for forensic investigations as well as plant variety protection. The data underlying these various applications have the same general structure.

Molecular marker data are analyzed either with statistical software, for example Piepho and Koch (2000) used SAS (R) (SAS-Institute 1988), or data are analyzed with programs written especially for this task such as Arlequin (Schneider et al. 1997), GDA (Lewis and Zaykin 1999), G-MENDEL (Holloway and Knapp 1993), or PLABQTL (Utz and Melchinger 1996). Often experimental data are stored either as input files of such programs or with spreadsheet software. Because neither of these options are designed for data storage the following problems often arise: (1) The same data are repeatedly stored in different locations, this may provoke data inconsistency if only one copy of the dataset is changed and requires an unnecessarily large amount of storage capacity; (2) only the experimenter can reproduce the coding and structure of the stored data, which complicates reanalysis of the data; (3) considerable time is required to convert data stored in a certain format into another format that can be input in larger databases or another software; and (4) combining data from several experiments for a joint analysis is difficult. To our

M. Frisch and A.E. Melchinger: Institute of Plant Breeding, Seed Science, and Population Genetics, University of Hohenheim, 70593 Stuttgart, Germany. K.R. Lamkey: USDA-ARS, Department of Agronomy, Iowa State University, Ames, Iowa 50011-1010, USA. *Corresponding Author (melchinger@uni-hohenheim.de).

Zeitschrift für Agrarinformatik (2002) 10:23–27.

knowledge, there exists no concept for efficient storage of molecular marker data, which focuses on applications in a plant breeding program .

Our objective was to develop a data structure for storage of molecular marker data in databases, which overcomes the shortcomings of data management in spreadsheets or input files of analysis software. The proposed data structure avoids redundant storage of experimental data and provides a standardized storage format, which facilitates retrieval, reanalysis, and exchange of the data.

DATABASE STRUCTURE

The basic entity of data storage is the observation of presence or absence of an allele at a marker locus for a DNA sample in a study. In the present context, we used allele to describe one of several possible outcomes of an experiment, which generates distinguishable results when applied to different DNA samples. The term marker was used to describe the combination of all methods used to generate these results. In a more abstract terminology: Marker was used as a synonym for ‘polymorphism generating experiment’ and allele as synonym for ‘result of a polymorphism generating experiment’. In order to trace the origin of a DNA sample to the individual from which it was generated, a unique identifier is assigned to each sample. A study comprises the application of a set of experiments to a set of DNA samples.

Molecular marker data are obtained by scoring the banding pattern on an electrophoresis gel (Fig. 1) or by a DNA sequencer. Each band on a gel or each peak detected by the sequencer results from DNA of a certain fragment length. The presence or absence of bands, certain banding patterns, or peaks for a certain DNA sample are assessed, and the presence or absence of the corresponding alleles is determined. A marker can have one or several alleles, for example a single sequence repeat (SSR) marker generates fragments of varying length, each of which is regarded as an allele. In contrast, an amplified fragment length polymorphism (AFLP) marker generates only one single band, which is either scored qualitatively or quantitatively (Piepho and Koch 2000) by measuring the intensity of the band with a DNA sequencer. An allele can also consist of a certain banding pattern, e.g., for a restriction fragment length polymorphism (RFLP) marker.

Considering the observation of an allele in a genotype in a study, there are three possibilities: (1) The allele was observed, (2) the allele was not observed, or (3) the result of the experiment is unknown. The information stored in the database represents which of these three events occurred for each combination of DNA sample and allele. In the case of qualitative scoring of AFLPs, also the intensity of the band is stored. For a study with i individuals and k markers of which each has a_k alleles, $n = i \sum_k a_k$ database entries are required. (Obviously only those alleles occurring at least once in the study are relevant.)

In studies, where at least one allele of each marker was observed for each DNA sample, the complete information can be stored by generating a database entry with only observed and missing alleles. Each combination of DNA sample and allele, for which no database entry is present, indicated that the respective allele was not observed. In such a study with m missing values, the maximum of $n = 2ik + m$ database entries are required. This storage mode requires considerably less database entries than storing also unobserved alleles (the amount of saving depends on the average number of alleles per marker), it usually can be applied with high quality data sets.

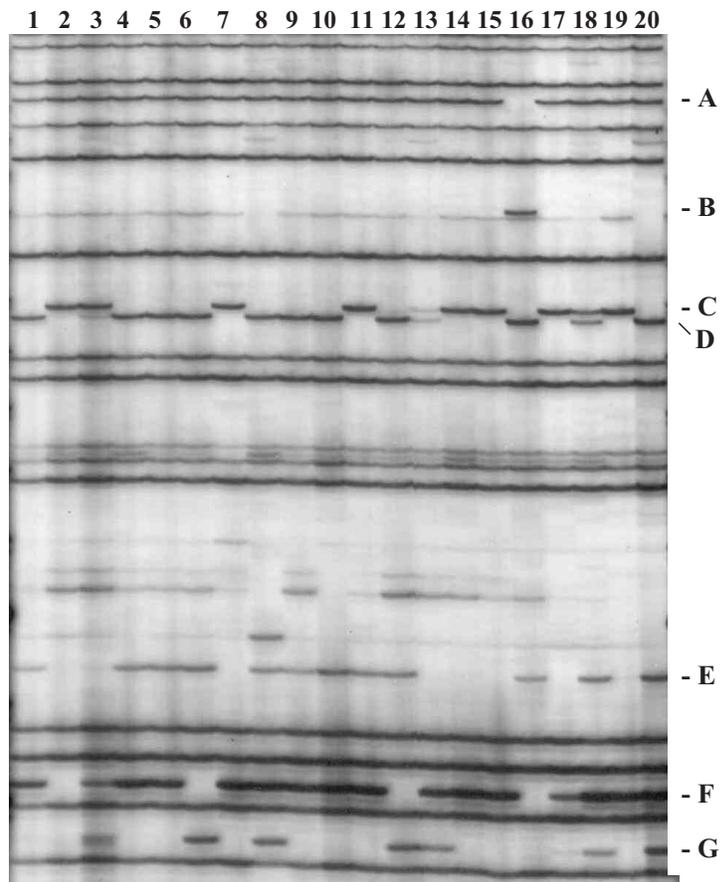


FIGURE 1. Analysis of genetic diversity in corn salad (*Valerianella locusta L.*) using AFLP markers with the primer combination Eco-AGT x Mse-CG. The numbers 1 to 20 denote the DNA samples from 20 inbred lines, A to G are polymorphic markers (Jasmina Muminovic, unpublished data).

The core of the database structure is a table named 'observed marker data', which holds the information about the results of the experiments. For each database entry one row in this table is generated, consisting of columns for study, identifier, allele, and state.

An example for entries in the 'observed marker data' table is shown in Table 1. The first data block shows results from an RFLP study with maize inbred lines named 'tigs'. (The name of the studies can be chosen freely.) In this study only observed alleles (state = 1) and missing alleles (state = 9) were entered into the database. For example, line CML117 was heterozygous at marker BNL5.62, carrying alleles 10.975 and 394, while line CML118 carries allele 11.884 homozygous. At line CML118, the observation for the allele 9.979 at the marker UMC164 is missing. The second block of data shows results from an AFLP study with wheat inbred lines. The data shows markers M004 to M010, resulting from applying the

TABLE 1. Example for entries in the ‘observed marker data’ table, showing results from a RFLP study with maize inbred lines, an AFLP study with wheat lines, and a SSR study with maize populations.

Study	Identifier	Allele	State
...
tigs	CML117	BNL5.62/10.975	1
tigs	CML117	BNL5.62/3.949	1
tigs	CML117	UMC164/11.479	1
tigs	CML117	UMC164/37.445	1
tigs	CML118	BNL5.62/3.295	1
tigs	CML118	UMC164/9.979	9
tigs	CML120	BNL5.62/11.884	1
...
wheat01	D01	P6061M49-M004	0
wheat01	D01	P6061M49-M005	0
wheat01	D01	P6061M49-M006	1
wheat01	D01	P6061M49-M007	1
wheat01	D01	P6061M49-M008	0
wheat01	D01	P6061M49-M009	0
wheat01	D01	P6061M49-M010	0
wheat01	D01	P6061M49-M011	0
wheat01	D01	P6061M49-M012	1
...
cimmyt03	POP22-1	phi08-360	1
cimmyt03	POP22-1	phi08-366	1
cimmyt03	POP22-17	phi08-366	1
cimmyt03	POP22-18	phi08-366	1
cimmyt03	POP22-19	phi08-360	1
cimmyt03	POP22-3	phi08-370	1
cimmyt03	POP22-21	phi08-363	1
cimmyt03	POP22-5	phi08-366	1
cimmyt03	POP22-22	phi08-363	1
cimmyt03	POP22-22	phi08-372	1
...

primer P6061M49 to the inbred line D01. In this study, the complete information for each combination of line and marker was entered into the database (state = 0 for absent alleles in addition to the 1’s and 9’s). (With qualitative scoring the 1’s for observed alleles would be replaced with a number coding for the scored intensity of the band.) In the third data block, results from a SSR study with a maize population are shown. For example, the first individual of Population 22 (coded by POP22-1) is heterozygous at marker phi08, it carries the alleles 360 and 366.

Additional tables contain information about (1) the assignment of the analyzed individuals to taxonomic units (table ‘list of identifiers’), (2) alleles and markers

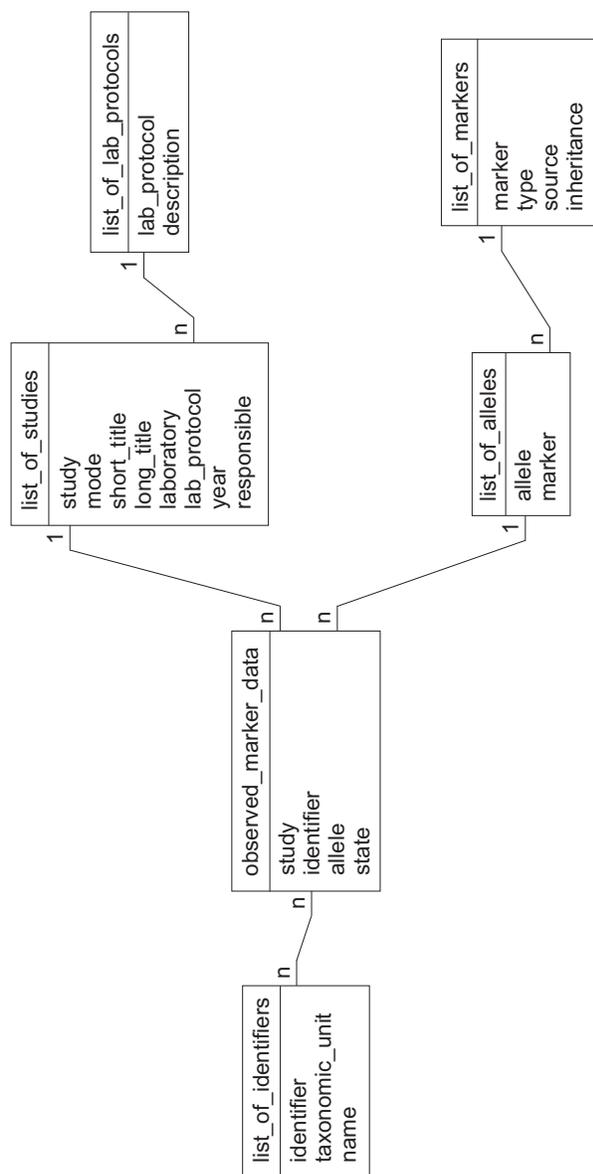


FIGURE 2. A diagrammatic representation of the structure of the database described. Each rectangle symbolizes a table in the database, the first line of text in the rectangle refers to the name of the table and the subsequent lines of text refer to the column headings. The lines symbolize the logical structure between the contents of the tables by joining rows with identical content. At the ends of each line the symbols 1 or n describe the relationship: A 1 next to a table indicates that the respective entry occurs only once in this table, while an n means that it may occur an arbitrary number of times in a table.

(tables 'list of markers' and 'list of alleles'), and (3) studies and used lab protocols ('list of studies' and 'list of lab protocols'). A diagram with all tables, the corresponding column definitions, and the relations between the tables is shown in Fig. 2.

The table 'list of studies' describes the studies for which data are stored in the database, it contains information about the mode of entering the data (either complete or only observed and missing alleles), a title for the study, the year when it was carried out, the lab where it was carried out, the name of the responsible person(s), and the name of the lab protocol used. Information about lab protocols are stored in a table named 'list of lab protocols'. The lab protocol should be comprehensive and describe each step in such a detail that it could be reproduced by others. Because each lab protocol can be applied to several studies, the table 'list of lab protocols' is related 1 : n with the table 'list of studies' via an identifier for each lab protocol. The table 'list of studies' is related 1 : n with the table 'observed marker data' via the name of the study (each study consists of many entries in table 'observed marker data').

The table 'list of identifiers' contains information about the taxonomic units to which an identifier belongs and a corresponding name. At least one entry for each identifier is required, which is generated during the data entry. In addition to this primary identification, an identifier can be assigned to an arbitrary number of further taxonomic units. Consequently the tables 'list of identifiers' and 'observed marker data' are related $n : n$ via the description of the identifier. The following example illustrates this concept (Table 2): Consider that during data entry an identifier was assigned to the taxonomic unit 'maize-individual' with the name 'POP22-1', this plant can subsequently be assigned to the taxonomic unit 'maize-population' with the name 'POP22' and to the taxonomic unit 'maize-heterotic-pool' with the name 'A'.

Information about markers is stored in the 'list of markers', it holds for example information about the type, source, and inheritance. A list of all alleles that were observed by applying a certain marker is stored in the table 'list of alleles'. The table 'list of markers' is related 1 : n with the table 'list of alleles' (each marker can have several alleles), and the table 'list of alleles' is related 1 : n with the table 'observed marker data' (each allele can be observed at several DNA samples).

DISCUSSION

Implementation of the above database structure on a personal computer proved to be in the scope of experimenters who are responsible for the respective statistical data analysis. We provide a sample implementation, which uses the database software SQL-Server (TM) as back end for data storage and the statistical software SAS (R) as front end for data import, data processing, and printing reports along with a detailed description and the complete source code. The sample implementation comprises routines to create tables and indexes, import data from a wide range of raw formats, export data to a format that can be used for data exchange, and update data in order to bring studies using different nomenclature into line. Furthermore, routines to print reports, retrieve data such that they can be analyzed with SAS, and download datasets from an internet server (which uses the proposed data model) are included.

TABLE 2. Example for entries in the ‘list of identifiers’ table, showing individuals used in a RFLP study with maize inbred lines, an AFLP study with wheat lines, and a SSR study with maize populations.

Identifier	Taxonomic unit	Name
CML117	maize-line	CML117
CML117	maize-line	CML117
CML118	maize-line	CML118
CML120	maize-line	CML120
...
CML117	maize-heterotic-pool	A
CML118	maize-heterotic-pool	A
CML118	maize-heterotic-pool	B
...
D01	wheat-line	D01
...
POP22-1	maize-individual	POP22-1
POP22-17	maize-individual	POP22-17
POP22-18	maize-individual	POP22-18
POP23-1	maize-individual	POP23-1
...
POP22-1	maize-population	POP22
POP22-17	maize-population	POP22
POP22-18	maize-population	POP22
POP23-1	maize-population	POP23
...
POP22-1	maize-heterotic-pool	A
POP22-17	maize-heterotic-pool	A
POP22-18	maize-heterotic-pool	A
POP23-1	maize-heterotic-pool	B
...

Application of the relational database model together with a medium degree of normalization of the underlying tables allows the integration of data from these small personal databases into large-scale production databases. While the internal format of a large-scale implementation of the proposed data structure requires further structural components (e.g., linking the tables with automatically generated numerical primary keys or using triggers to assure referential integrity more conveniently), the presented tables can be used as templates for views used for data retrieval and data input by plant breeders. This ensures a common interface for data exchange, standardized analyses, and joint analyses of data from different sources.

The flexibility of the proposed data structure as a working tool for the experimenter and the possibility of integration in larger solutions is one of its main advantages. In contrast, the integration of data stored in spreadsheet format or in

input format for analysis software in large-scale database systems is difficult, time consuming, and prone to errors.

Oftentimes, molecular marker data are generated from individuals or populations for which other data are also stored in databases. Examples are pedigree databases or yield trial databases. The taxonomic unit for which these data were collected may vary and differ from the taxonomic unit used for DNA extraction and marker analyses. By assigning an identifier in the marker database to the taxonomic unit for which external data is stored, marker data and external data can be joined and queried together. If there are existing databases for marker or allele information, the ‘list of alleles’ table and the ‘list of markers table’ can be replaced by the existing tables (or in the case of a different organization with corresponding views).

The possibility to link the marker data to other existing data sources enables the experimenter to perform a wide range of data analyses. Performing such analyses with separately stored data would require extensive data editing, which is time consuming and a source of errors.

We applied the proposed data model to store the data of several fingerprinting projects: (1) An RFLP study comparing the genetic diversity in progenitor and derived lines of the reciprocal recurrent selection program with Iowa Stiff Stalk Synthetic and Iowa Corn Borer Synthetic No. 1 maize populations (Hagdorn et al. 2002); (2) a SSR study about genetic diversity in tropical maize populations and the relation between genetic diversity and heterosis (Warburton et al. 2002, Reif et al. 2002); (3) a study assessing the quality of SSR data from maize inbreds originating from different sources of maintenance breeding (Heckenberger et al. 2002); and (4) a comparison of different marker systems in wheat cultivars (Bohn et al. 1999).

Using the proposed data structure created large synergy effects: (1) The need for editing data files, which is considerably error-prone, was eliminated. (2) Using the database together with a standard statistical software system assured a high quality of statistical analysis. (3) Due to the standardized data structure, it was possible to reuse statistical analysis routines programmed for one project in other projects with related subjects. (4) The data base assured the quick availability of data from earlier studies for reanalysis.

Acknowledgments. We thank Drs. Martin Bohn, Joanne Labate, and Marylin Warburton for comments and suggestions on the database structure and the sample implementation. We also thank the anonymous reviewers for comments which helped to improve this paper.

Note. Mention of trade names or commercial products in this article is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture.

REFERENCES

- [1] Bohn, M., H. F. Utz, A. E. Melchinger (1999): Genetic diversity among winter wheat cultivars determined on the basis of RFLPs, AFLPs, and SSRs and their use for predicting progeny variance. *Crop Science* 39: 228-237.
- [2] Hagdorn, S., K.R. Lamkey, M. Frisch, P.E.O. Guimaraes, A.E. Melchinger (2002): Molecular Genetic Diversity among Progenitors and Derived Elite Lines of BSSS and BSCB1 Maize Populations. *Crop Science*. In press.
- [3] Heckenberger, M., A. E. Melchinger, J. S. Ziegler, L. K. Joe, J. D. Hauser, M. Bohn (2002): Variation of DNA fingerprints among accessions within maize inbred lines and implications

- for identification of essentially derived varieties. I. Genetic and technical sources of variation in SSR data. *Molecular Breeding*. In press.
- [4] Holloway, J. L., S. J. Knapp (1993): G-MENDEL 3.0 software for the analysis of genetic markers and maps. Oregon State University, Corvallis, Oregon.
 - [5] Lee, M. (1995): DNA markers in plant breeding programs. *Advances in Agronomy* 55: 265-344.
 - [6] Lewis, P. O., D. Zaykin (1999): Genetic Data Analysis: Computer program for the analysis of allelic data. Dept. of Statistics, North Carolina State University, Raleigh, North Carolina.
 - [7] Melchinger, A. E. (1990): Use of molecular markers in breeding for oligogenic disease resistance. *Plant Breeding* 104: 1-19.
 - [8] Piepho, H.-P., K. Koch (2000): Codominant analysis of banding data from a dominant marker system by normal mixtures. *Genetics* 155: 1459-1468.
 - [9] Reif, J. C., A.E. Melchinger, X.C. Xia, M.L. Warburton, D.A. Hoisington, S.K. Vasal, G. Srinivasan, M. Bohn, M. Frisch (2002): Genetic diversity within and between seven tropical maize populations investigated with SSR markers and relation to the heterosis of their crosses. In review.
 - [10] SAS-Institute (1988): SAS/STAT User's guide, Release 6 Edition. SAS-Institute Inc., Cary, North Carolina.
 - [11] Schneider S., J.-M. Kueffer, D. Roessli, L. Excoffier (1997): Arlequin: A software for population genetic data analysis. Genetics and Biometry Laboratory, University of Geneva, Geneva, Switzerland.
 - [12] Utz, H. F., A. E. Melchinger (1996): PLABQTL: a program for composite interval mapping of quantitative trait loci. *J. Quant. Trait Loci* 2 (1).
 - [13] Warburton, M. , X. Xia, J. Crossa, J. Franco, A. E. Melchinger, M. Frisch, M. Bohn, D. Hoisington (2002): Large scale fingerprinting methods for the analysis of genetic diversity of CIMMYT maize germplasm. *Crop Science*. In press.
 - [14] Young, N. D. (1999): A cautiously optimistic vision for marker-assisted breeding. *Molecular Breeding* 5, 505-510.