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Note

Predicting Chromosomal Locations of Genetically Mapped Loci in Maize Using the Morgan2McClintock Translator

Carolyn J. Lawrence,*,†,[1] Trent E. Seigfried,* Hank W. Bass‡ and Lorinda K. Anderson§

*USDA–ARS, Corn Insect and Crop Genetics Research Unit, Iowa State University, Ames, Iowa 50011, †Department of Agronomy and Department of Genetics, Development and Cell Biology, Iowa State University, Ames, Iowa 50011, ‡Department of Biological Science, Florida State University, Tallahassee, Florida 32306-4370 and §Department of Biology, Colorado State University, Fort Collins, Colorado 80523

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ABSTRACT

The Morgan2McClintock Translator permits prediction of meiotic pachytene chromosome map positions from recombination-based linkage data using recombination nodule frequency distributions. Its outputs permit estimation of DNA content between mapped loci and help to create an integrated overview of the maize nuclear genome structure.

TWO fundamentally different but colinear types of gene maps can be produced, linkage maps and physical maps. Classical linkage (genetic) maps are based on allele-recombination frequencies, whereas physical maps are based on the linear DNA molecules that compose the chromosomes.

In maize, a model genetic and major agricultural species, >1200 high-resolution linkage maps composed of thousands of markers are available, whereas detailed physical maps of DNA sequence and chromosome structure are still in development. The three main types of maize physical maps differ in the level of molecular resolution. They are (1) genome sequence assembly maps at DNA base-pair resolution (see, *e.g.*, Dong *et al.* 2005; Fu *et al.* 2005); (2) fingerprint-contig maps, resolved at the level of overlapping restriction fragments from cloned segments of genomic DNA (see, *e.g.*, Pampanwar *et al.* 2005); and (3) cytological maps constructed by microscopic observation of pachytene chromosome structure (*e.g.*, the Cytogenetic FISH 9 map created by Koumbaris and Bass 2003 and Amarillo and Bass 2004).

Linkage and physical maps have different coordinate systems for positioning loci. The genetic map unit is called a "centiMorgan" (cM) in honor of Thomas Hunt Morgan. One centimorgan is equal to 1% crossing over between two linked loci. Fingerprint-contig and genomic-assembly maps are measured in base pairs, whereas physical maps based on pachytene chromosome structure (also called cytological or cytogenetic maps) position each locus as the fractional distance along the arm from the centromere to the telomere. Recently, maize researchers have begun to call the unit of this sort of map denomination a "centiMcClintock" (cMC) in honor of maize genetics pioneer Barbara McClintock. Here we formally define 1 cMC as 1% of the length of the chromosome arm upon which a given locus resides. For example, if the short arm of chromosome 9 is 8.70 μm in length and the *bronze1* (*bz1*) locus lies 5.66 μm from the centromere on that chromosome arm, *bz1* lies (5.66/8.70 × 100 =) 65% of the distance from the centromere to the chromosome tip or 65 cMC from the centromere. A locus at position 66 would lie exactly 1 cMC from the *bz1* locus. Because maize chromosome arm lengths vary and the centiMcClintock is a relative unit, 1 cMC on, *e.g.*, the short arm of chromosome 9 does not necessarily consist of the same number of micrometers as 1 cMC on any of the 19 other chromosome arms. The cytological conventions are further described and defined at http://www.maizegdb.org/coordinateDef.php.

Recombination rates vary tremendously along individual chromosomes such that the map distance between two loci on a linkage map may not accurately predict the physical distance between them (Anderson *et al.* 2004). This variation has made integrating the two types of maps difficult and also has important implications for genome-assembly efforts and positional-cloning strategies (Sadder and Weber 2002).

[1]*Corresponding author:* 1565 Agronomy Hall, Iowa State University, Ames, IA 50014. E-mail: triffid@iastate.edu

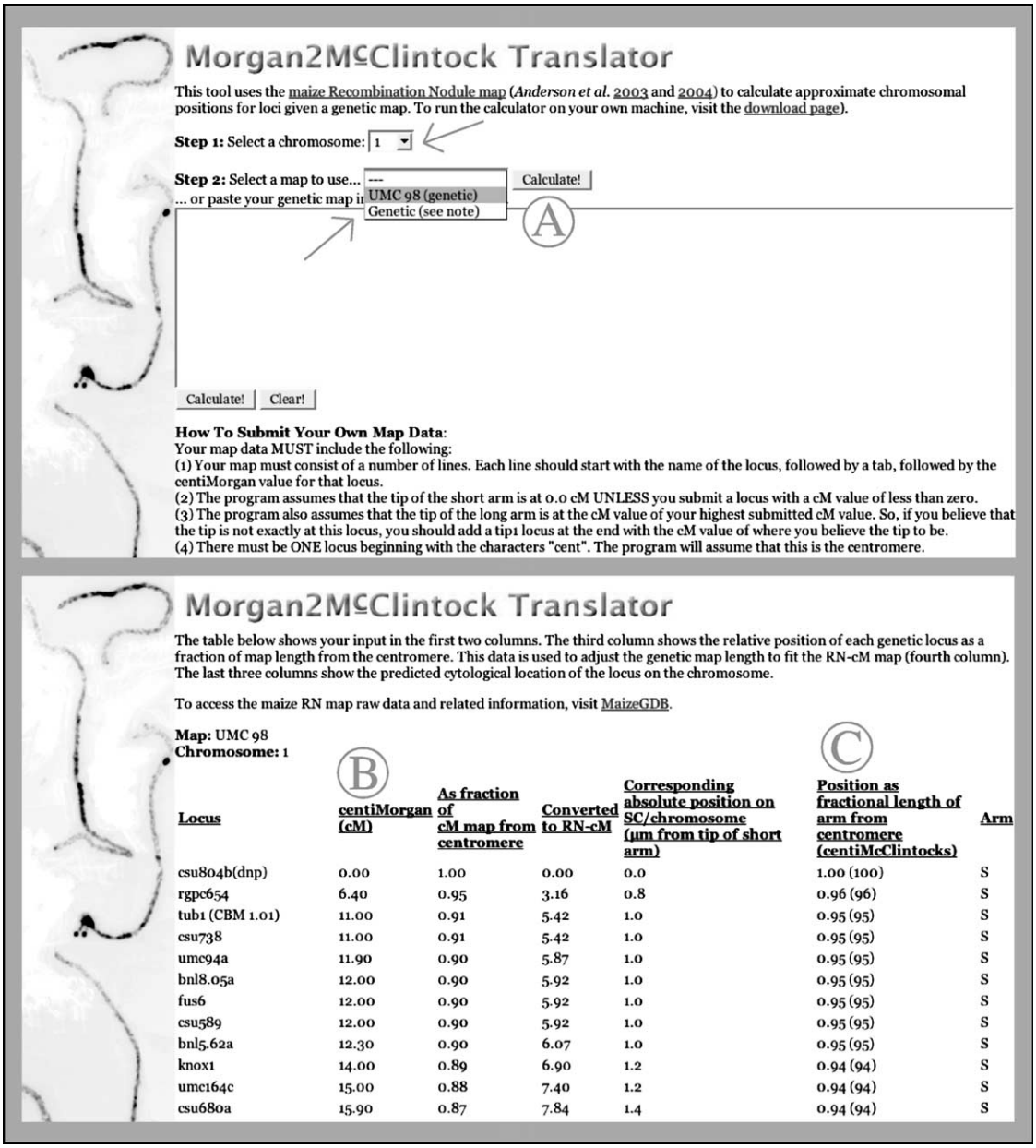

FIGURE 1.—The Morgan2McClintock Translator. Screen capture images taken from http://www.lawrencelab.org/Morgan2McClintock show examples of data input (top) and output (bottom). (A) The user first chooses the maize linkage group as chromosome number (arrow at Step 1) and then the corresponding centimorgan linkage-map data set (arrow at Step 2). The linkage map data can be chosen from among stored data sets available for common maps or pasted directly into a text box for map data not currently stored. Clicking the "Calculate" button submits input data and calculates centiMcClintock values from the RN frequency distribution. The output web page contains a table that summarizes one locus per row and includes columns that describe the input data in centimorgans (B) and the output data in predicted locations along the pachytene chromosome, expressed in microns and in centiMcClintocks (C).

A method for linking genetic maps with chromosome structure has recently been developed. ANDERSON *et al.* (2003) determined the frequency distributions of recombination nodules (RN) along the 10 pachytene chromosomes of maize. Because each RN represents a crossover on the physical structure of the chromosome, these RN maps are unique in that they contain both linkage and cytological information that allows the prediction of the cytological position of any genetically mapped marker (ANDERSON *et al.* 2004). We have developed a tool, the Morgan2McClintock Translator (accessible at http://www.lawrencelab.org/Morgan2McClintock), which automates the cytological-position prediction process for any input linkage data.

Conversion of maize linkage map coordinates into cytological coordinates requires both linkage data and

RN frequencies as input. The Morgan2McClintock Translator includes as data files the maize RN map (Anderson *et al.* 2003) as well as two genetic maps, the University of Missouri at Columbia (UMC) 1998 map (Davis *et al.* 1999) and the 1997 genetic map (Neuffer *et al.* 1995). More than a thousand other genetic maps, which also can be used as input files, are available at MaizeGDB (Lawrence *et al.* 2005 and http://www.maizegdb.org/map.php). The translator itself was coded with PHP, and the equations that it uses to convert linkage maps into cytological maps are those described by Anderson *et al.* (2004). The application can be run online, or it can be downloaded for local use on any machine equipped to serve PHP. Aspects of the input and output displays for the translator for the UMC 98 genetic map are shown in Figure 1 (Davis *et al.* 1999).

The distribution of RNs provides an important connection between genetic maps and chromosomal structure, which has allowed the examination of gene distribution at the chromosomal level in maize (Anderson *et al.* 2006). This integration also permits estimation of DNA and chromosomal distances between genetic loci, a feature that will assist in the sequence assembly of the maize genome. Theoretically, this approach is applicable to other organisms with comparable cytological crossover-distribution data such as tomato (Sherman and Stack 1995) and mouse (Froenicke *et al.* 2002), and we plan to develop a set of similar tools for these organisms that should be useful in comparing genetic and chromosomal aspects of genomes in different species.

Use of the maize Morgan2McClintock Translator will allow researchers to integrate previously disparate views of maize genome structure. For example, the maize cytological maps (http://www.maizegdb.org/cgi-bin/displaycompletemaprecord.cgi?id=40028) are predominantly annotated with chromosomal translocation breakpoints (Coe 1994). For most breakpoints, corresponding germplasm is available from the Maize Genetics Cooperation Stock Center (Scholl *et al.* 2003). Integrating the cytological breakpoint positions with genetic linkage maps would enhance the application of available translocation stocks to genome research, breeding programs, and chromosome engineering efforts. This is one among many ways in which the Morgan2McClintock Translator could be used specifically to add value to maize genetics and structural genomics research and more generally to aid in meiotic chromosome research.

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