

## MG2C 2.1: An Updated Web Service for Drawing Physical Map

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### 2. Keywords

MG2C; Web service; Gene map viewer; Bioinformatics

### 1. Abstract

Genes' physical map is very useful for gene analysis. Although there is some local software to view physical map, few web service is available. In 2015, we developed a web service - MG2C1.0. For last four years, we update the tool to 1.1, 2.0 and 2.1. As for June 2019, the effective use re-cord has reached more than 14,000 times.

The new version has some new features and functions as following: (1) more display styles for users to select; (2) more user-friendly interface web layout; (3) more input data size.

This tool is developed based on Perl language. It is free available use and is upgraded irregularly.

To access the server: [http://mg2c.iask.in/mg2c\\_v2.1/](http://mg2c.iask.in/mg2c_v2.1/).

### 3. Background

Genetic maps over the years have act as important tools in areas of anchoring scaffold sequence to chromosomes, uncovering genetic mechanisms of agronomical traits in plants. The advent of next-generation sequencing has allowed for better genetic maps and physical maps. A physical map can visually display genes on chromosomes based on the position of each gene, which is also a useful tool for exploring genes' function. Simply rendering high-resolution physical map is not easy for users. Map Chart [1] can produce high-resolution and feature-rich maps, and only runs on Windows; There is excel-based software like Map Draw [2], which template with Visual Basic (VB) macro code and modify these code is not easy. Here, we introduce MG2C, an simple web tool in Perl that produce for Scalable Vector Graphics (SVG) physical maps, can be run on any platform by internet browser. The tool has been updated from 1.0 to 2.1. As of June 2019, the effective use record has been more than 14,000 times.

### 4. Implementations

#### 4.1. Input data

MG2C need two input file: file1 is about gene information, which contain five columns, such like gene id, start position of a gene, end position of a gene, chromosome id and gene color; file2 is

about chromosome information, which has two columns, such like chromosome id and chromosome length.

#### 4.2. Usage

MG2C has 31 parameters with default values (Table 1), and you will get its description when your mouse flow onto them.

**Table 1.** Description and default values of parameters for latest version.

Parameters	Default values	Description
chromosome id	font	Times New Man
	size	12px
	color	black
SVG container	width	1000px
	height	900px
single chromosome container	width	270px
	height	400px
	fill	none
	border-width	1px
	border-color	none
chromosome	width	10px
	height	300px
	fill	None
	RX	14px
	RY	14px
	border-width	1px
	border-color	black
gene lines	color	Black
	width	0.5px
	type	1

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gene id	font	Times New Man	Font family of gene id.
	display_type	1	Gene display style, can be set 1 to 5.
	size	11px	Font size of gene id.
	color	black	Font color of gene id.
	margin	15px	Margins between gene id and Chr.
connection between gene ID and gene line	color	black	Color of link between gene id and gene.
	width	0.5px	Width of link between gene id and gene.
scale	units	bp	Units of gene map scale, bp or cM
	width	20px	Width of gene map scale
	position_X	20px	Position X of gene map scale
	N_tick mark	10	N mark lines of each unit.
	decimal place	0	Significant digit.

### 5. Results

The maps from two examples are shown in (Figure 1). The first example (Figure 1A) using MG2C early version to produce 22 *SIZHD* genes' physical map using default parameter values and add some new features by PPT. The second example (Figure 1B) using MG2C latest version to produce 10 *SiLIM* genes' physical map with chromosome fill with black and other parameters are default value.

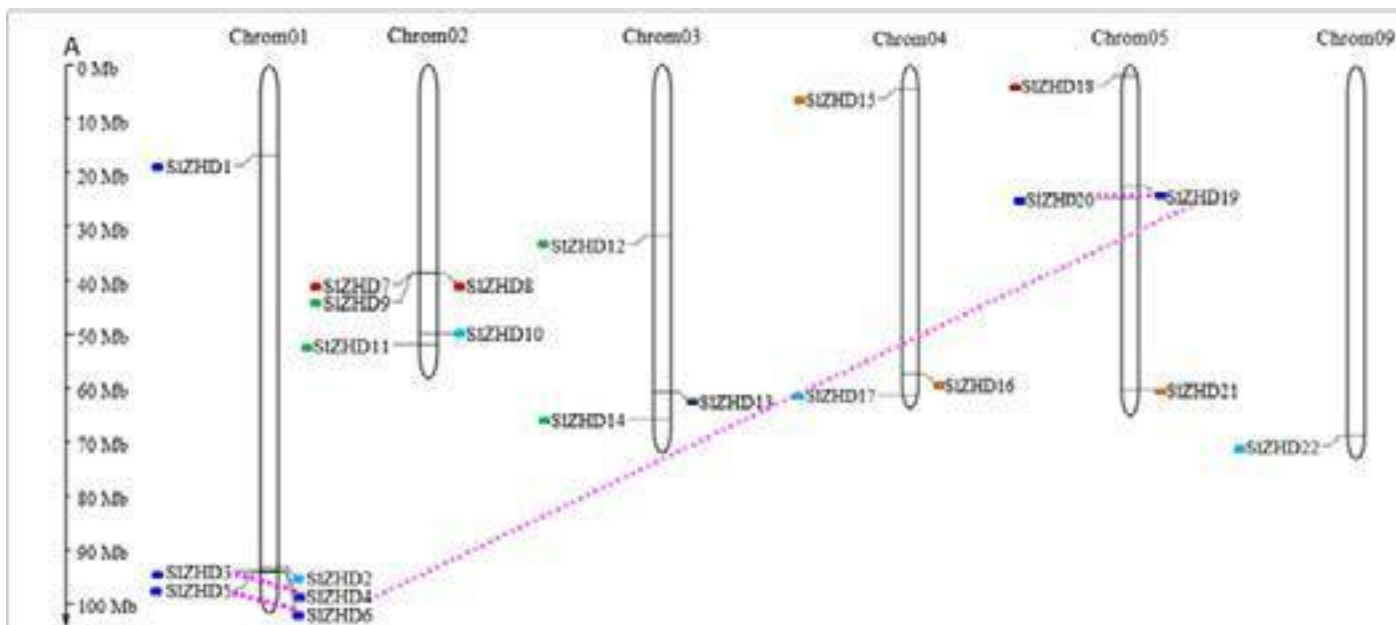


Figure 1(A): Tomato 22 *SIZHD* genes are widely distributed to the six chromosomes [4]

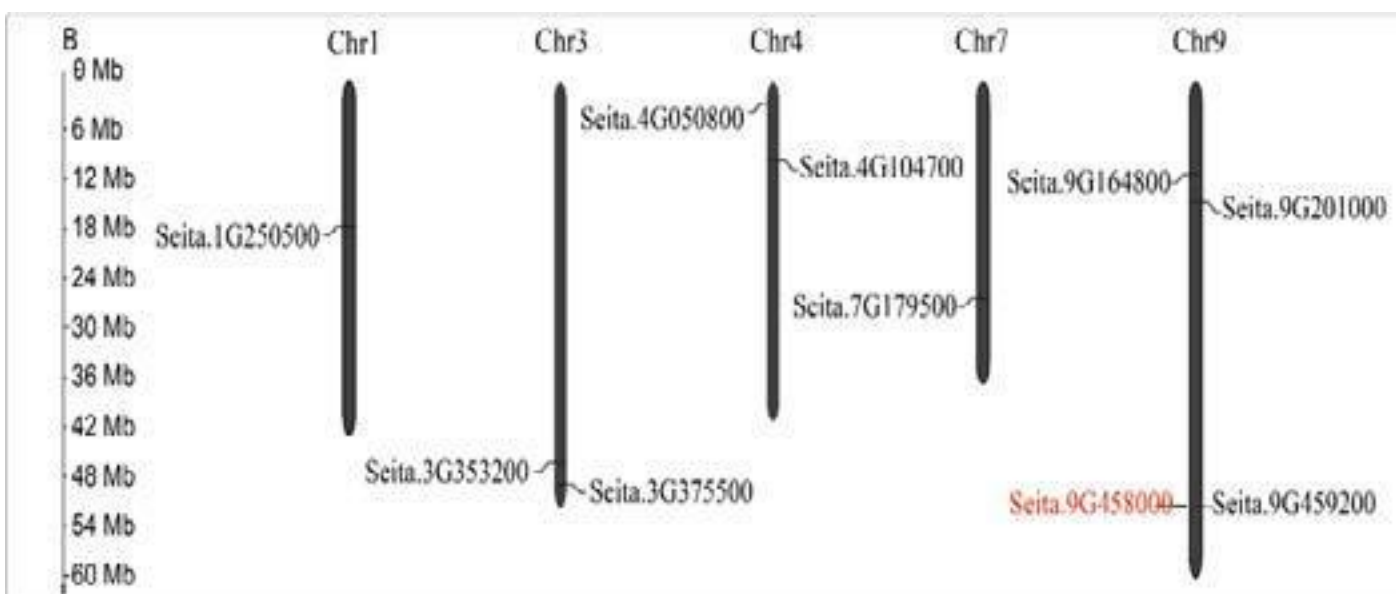


Figure 1(B): *SiLIM* genes' physical map shows the *SiLIM* genes are on Chr1,3,4,7 and 9[5]

## 6. Conclusions

The MG2C is a free simple web tool for drawing physical map by mouse single click. Users can set parameters, input data and gain results in one page. In the case of elements overlapped, users can modify the height of SVG container, single chromosome container and chromosome correctly. In the future, we will continue to update the web tool.

## 7. Funding

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