

MASRUSPLANTS v3.0: an updated web resource of DNA markers for marker-assisted selection of rust resistance genes in cereal crops

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Motivation and aim: Cereal crops, which are the most important agricultural resource in Russia, thrive in a variety of environmental and climatic conditions. Throughout its life cycle, cereal crops encounter numerous stressors that negatively impact yield and compromise grain quality. Among biotic threats, rust fungi (*Puccinia* spp.) are among the most aggressive pathogens of cereal crops — bread wheat (*Triticum aestivum* L.), durum wheat (*T. turgidum* L. var. *durum*), barley (*Hordeum vulgare* L.), triticale ($\times$ *Triticosecale* Wittm. ex A. Camus), oats (*Avena sativa* L.), rye (*Secale cereale* L.) and other globally cultivated crops. Under favorable environmental conditions, these pathogens can multiply rapidly, causing significant economic losses. Genetic resistance represents the most efficacious and sustainable agricultural strategy for mitigating the impact of rust pathogens. Implementation of this approach necessitates the integration of molecular breeding techniques, including marker-assisted selection and genomic editing, to engineer novel cereal crops cultivars exhibiting pyramided resistance mechanisms.

Materials and methods: Accurate molecular identification of resistance genes is a critical and accelerated process in modern breeding programs, serving as an integral component of crop improvement strategies. To systematize genomic resources for molecular breeding, we present an expanded version of the MASRUSPLANTS database (v3.0), which now integrates curated data on DNA markers associated with molecularly confirmed rust resistance genes. The updated platform, accessible at <https://masrusplants.ru>, provides an online database to advance precision breeding initiatives and optimize the introduction of resistance genes into cereal crops.

Results: The main goal of the MASRUSPLANTS v3.0 database aims to ensure wide availability of the marker-assistant selection (MAS) technology for scientific and agro-industrial communities, which will accelerate the development of resistant varieties based on genomic predictors. The MASRUSPLANTS v3.0 database systematically compiles detailed genomic data on molecular markers and their associated resistance genes, including *Sr* (stem rust resistance), *Lr* (leaf rust resistance), and *Yr* (stripe rust resistance) genes. Each marker entry is annotated with comprehensive metadata, encompassing marker classification, chromosomal localization, primer sequences, standardized PCR amplification protocols, and bibliographic references. One of the key introductions is the expansion of data on each resistance gene presented in the database.

The information on genes is now divided into several groups:

- I. General characteristics;
- II. Origin and source;
- III. Chromosomal localization;
- IV. Molecular genetic markers;
- V. Resistance characteristics;
- VI. Application in breeding;
- VII. Databases and key studies.

Additionally, some groups include subgroups. For example, group V (Resistance characteristics) is further categorized into Resistance type, Efficiency, Phenotype, and Limitations. Furthermore, all DNA markers cataloged within the database have undergone experimental validation at the Laboratory of Plant Molecular Genetics and Cytogenetics, Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences (IC&G SB RAS), and the empirical testing has been confirmed by original electropherograms.

Conclusions: The database architecture is organized into four primary ontological entities: molecular protocols, chromosomal maps, marker loci, and cultivated varieties/breeding lines. Functional linkages between these entities are designed to facilitate efficient navigation and integration of data pertaining to molecular markers and their corresponding disease resistance genes.

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