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Research Highlight

ASSESSMENT OF GENETIC VARIATIONS IN CEREAL CYST NEMATODE (*Heterodera avenae*)

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Cereal cyst nematode (*Heterodera avenae*) is a potential threat to wheat crop which belongs to family Heteroderidae. This pathogen is distributed worldwide and significantly reducing the production and quality of crops.

Several management strategies are available against this pathogen e.g., use of resistant varieties, rotational control, chemical control and biological control[1].

Different pesticides can be used for the management of cereal cyst nematode but these pesticides have adverse effects on environment and human health in China because these are not eco-friendly in nature and left residues on the plant. Therefore, there is a need of hour to establish a proper management strategy, the identification of genetic relationships at the species level and intra and interspecific variability is crucial[2]. Molecular information can guide about degree of diversity present among individuals as well as populations of plant-parasitic nematodes[3].

Accordingly, the Inter-simple Sequence Repeats (ISSR) is a PCR procedure that plays a vital role in examination of genetic variation at subspecies level, chiefly to study population structure and differentiation[4].

On the other hand, the Internal Transcribed Spacer (ITS) region of ribosomal DNA (rDNA) is also a vital approach and has been reported to be extremely helpful as a taxonomic marker at species level within nematodes[5].

These facts urged scientists for carrying out a new study in order to examine the genetic variation of *H. avenae* populations in China at two different levels by employing the ISSR technique as well as ITS-rDNA gene sequences. For this purpose, research team examined the DNAs of second-stage Juveniles from 16 populations of *H. avenae* and one population of *Heterodera filipjevi* in by means of 3 ISSR primers[6].

According to the results of ISSR, high genetic diversity was found within tested species on a large geographical scale. However, the analysis of molecular variance (AMOVA) revealed that most of the variations among *H. avenae* come from genotypic variations within region. The ISSR dataset grouped all populations into two clusters according to their geographical origin. On the other hand, base transition of ITS-rDNA sequence was found to show low intraspecific variation in rDNA of tested species.

Last but not the least it is concluded that two different biological entities are present in the *Heterodera avenae*. It is suggested that hybridization, passive dispersal, multiple

introductions and anthropogenic activities can be responsible for these genetic variations of *H. avenae*.

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