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Perspective

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Diallel Crosses for Yield Traits in Bread Wheat

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Introduction

In several wheat production can be increased either by bringing more area under cultivation or vertically by increasing per unit yield. It is not possible horizontally to increase area under wheat due to other competing crops and shortage of irrigation water. Therefore, the only alternative left is to increase yield, which is possible by introducing genetically superior new high yielding cultivars that are adapted to a wider range of environments. Due to greater diversification, wheat provides many opportunities for the development of new and improved genotypes through crossing and recombination of favorable genes. Wheat breeders, all over the world, have been utilizing the existing genetic resources to modify the wheat varieties in order to meet the requirement of an ever increasing population. Strains that possess a wide range of variability in economically important yield contributing traits have been utilized by the breeders to develop new varieties. Dialled mating designs have been used primarily to estimate genetic variances when parents are either random individuals or inbred lines from a random mating population in linkage equilibrium. They have also been used to estimate combining ability and heterotic potential of fixed lines or varieties in crosses or for basic studies on the genetic structure of populations. Several methodologies for the analysis and interpretation of dialled crosses have been suggested.

Evolution of New Genes

Additionally, heritability plays a predictive role in breeding programs and expresses the reliability of phenotype as a guide to its breeding value. It is understood that the breeding values of individuals are derived from appropriate analyses. It is the breeding value, which determines how much of the phenotype would pass onto the next generation. There is a direct relationship between heritability and response to selection, which is referred to as genetic progress. Plant parasitism has evolved independently on at least four separate occasions in the phylum Nematoda. The application of next-generation sequencing to plant-parasitic nematodes has allowed a wide range of genome or transcriptome-level comparisons and these have identified genome adaptations that enable parasitism of plants. Current genome data suggest that horizontal gene transfer, gene family expansions, evolution of new genes that mediate interactions with the host and parasitism-specific gene regulation are important adaptations that allow nematodes to parasitize plants. Sequencing of a larger number of nematode genomes, including plant parasites that show different modes of parasitism or that have evolved in currently unsampled clades and using free-living taxa as comparators would allow more detailed analysis and a better understanding of the organization of key genes within the genomes. This would facilitate a more complete understanding of the way in which parasitism has shaped the genomes of plant-parasitic nematodes. Natural acquisition of novel genes from other organisms by horizontal or lateral gene transfer is well established for microorganisms. There is now growing evidence that horizontal gene transfer also plays important roles in the evolution of eukaryotes. Genome-sequencing and projects of plant and animal associated nematodes such as Brugia, Meloidogyne, Bursaphelenchus and Pristionchus indicate horizontal gene transfer as a key adaptation towards parasitism and pathogenicity. However, little is known about the functional activity and evolutionary longevity of genes acquired by horizontal gene transfer and the mechanisms favoring such processes.

Inter-species and Inter-genic Analysis

We examine the transfer of cellulase genes to the free-living and beetle-associated nematode Pristionchus pacificus for which detailed phylogenetic knowledge is available to address predictions by evolutionary theory for successful gene transfer. We used transcriptomics in seven Pristionchus species and three other related diplogastrid nematodes with a well-defined phylogenetic framework to study the evolution of ancestral cellulose genes acquired by horizontal gene transfer. We performed intra-species, inter-species and inter-genic analysis by comparing the transcriptomes of these ten species and tested for cellulase activity in each species. Species with cellulase genes in their transcriptome always exhibited cellulase activity indicating functional integration into the host's genome and biology. The phylogenetic profile of cellulase genes was congruent with the species phylogeny demonstrating gene longevity. Cellulase genes show notable turnover with elevated birth and death rates. Comparison by sequencing of three selected cellulase genes in 24 natural isolates of Pristionchus pacificus suggests these high evolutionary dynamics to be associated with copy number variations and positive selection. We could demonstrate functional integration of acquired cellulase genes into the nematode's biology as predicted by theory. Thus, functional assimilation, remarkable gene turnover and selection might represent key features of horizontal gene transfer events in nematodes.

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