IDT9-099 | A new reason for segregation rate distortion in genetic linkage map

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Segregation rate distortion is the first step to check in any genetic linkage map construction. It shows whether the pattern of segregation for each locus is as expected or distorted. In case of distortion, it is recommended to check the reason for distortion. The reason can be applying wrong marker pattern, low quality gel electrophoresis, different survival of individuals, and remind heterozygosity in the parental lines. One other reason for distortion, especially in polyploid species such as bread wheat, can be amplifying more than one locus by each primer pairs but having the same allele sizes. In this situations, while this primer pairs shows only one band on each parent, the pattern on individuals depend on the type of population and the position of the two loci. If the two loci placed on different chromosomes on an F_2 population, number of heterozygotes will increase (much higher than normal F_2), in RILs the number of heterozygotes will be much more then the remind heterozygosity (higher than normal F_2), and in DH heterozygotes individuals will appear which is not expected (similar to normal F_2). If the loci are on the same chromosome, the number of heterozygotes will increase; this increase depends on the distance; the more distance the more heterozygote. If the two loci reach each other, the distortion will be removed because they are not actually as two loci any more. Finally, this kind of distortion can happen if the similarity between alleles occurs even in one of the parents.

IDT9-100 | Characterization of groundnut resistance to bacterial-wilt caused by *Ralstonia solanacearum* by forward and reverse genetics methods

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Bacterial wilt caused by casual agent *Ralstonia solanacearum* (*Rs*) is *a serious disease* in groundnut and great many other plant species. Forward and reverse genetics strategies were adopted in our study. From the view point of forward genetics, the peanut RILs including 300 F_9 progenies derived from Yueyou 92 × Xinhuixiaoli were tested of disease resistance through inoculation with *R.solanacearum* in the field. Resistance to *R.solanacearum* is a quantitative trait. Three QTLs were mapped on an interval 15 cM using a linkage map with SSR and related SNP markers. An Tir-NBS-LRR resistance gene *AhqBW3* was found closely linked with a BW resistance molecular marker *SNP79* which was mapped in a gene locus next to the R gene. *AhqBW3* was showed downregulation under the challenge of Rs inoculation. From the view point of reverse genetics, a novel NBS-LRR resistance gene *AhRRS5*, an LRR-RLK gene *AhRLK1* and an unkown gene *AhRRS22* were upregulated by *Rs* inoculation which were screened from microarray hybridization. They showed resistance phenotypes in transgenic tobacco overexpressing of these three genes. Among of them, Overexpression of *AhRRS5* significantly enhanced the resistance of heterogeneous tobacco to *R. solanacearum*, with diverse resistance levels in different transgenic lines. Several defense-responsive marker genes in hypersensitive response, including HR, SA, JA, and ET signals, were considerably upregulated in the transgenic lines as compared with the wild type in response to *R. solanacearum*. *NPR1* and *NDR1* were also upregulated in response to the pathogen. These results indicate that *AhRRS5* participates in the defense response to *R. solanacearum* through the crosstalk of multiple signaling pathways and the involvement of *NPR1* and R gene signals for its resistance. These studies may guide the resistance enhancement of peanut and other economic crops to bacterial wilt disease.