Analysis of the regulators involved in the virulence of plant pathogenic bacteria from the species *Dickeya solani*

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Bacteria from the genus Dickeya (formerly *Erwinia chrysanthemi*) are plant pathogens causing severe diseases in many economically important crops. A majority of the strains responsible for potato disease in Europe belong to a newly established *Dickeya solani* species. Although some ecological and epidemiological studies have been carried out, little is known about the regulation of *D. solani* virulence, especially regulation of the expression of pectinolytic enzymes, the main pathogenicity factors. The characterization of *D. solani* strains based on genomic fingerprinting indicated that they are genetically homogenous. A phenotypic characterization of the tested strains indicated differences in their pathogenicity. Mutants of four *D. solani* strains were constructed by inactivating the genes coding either for one of the main negative regulators of *D. dadantii* virulence (kdgR, pecS and pecT) or for the synthesis and perception of signaling molecules (expI and expR). Analysis of these mutants indicated that PecS, PecT and KdgR play a similar role in both species, repressing to different degrees the synthesis of virulence factors. The thermoregulator PecT seems to be a major regulator of *D. solani* virulence. This work also reveals the role of quorum sensing mediated by ExpI and ExpR in *D. solani* virulence on potato.

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Identification of quantitative trait loci (QTLs) for resistance to cowpea weevil in chickpea

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The cowpea weevil (*Callosobruchus maculatus* F.) is one of the most important biotic stresses with qualitative and quantitative effects on chickpea seeds. Resistant (*Cicer reticulatum* Ladiz.) and susceptible chickpea (*C. arietinum* L.) genotypes were crossed and selfed to produce an F2 population consisting of 119 F2 individuals segregating for resistance to the pest. The population was screened for polymorphism with AFLP and SSR markers and evaluated for genetic mapping for resistance with four parameters. The constructed map consisted of 143 markers with a total length of 827 cM. The depth of the current map was 5.78 cM. QTL analysis with Kruskal–Wallis and Interval Mapping approaches revealed two QTL regions on LGI between 0–25 cM and 80–90 cM for resistance to egg laying. Furthermore, another QTL on LGIV between 0 and 5 cM involved in the same resistance. Resistance to larval survival was governed by a major QTL on LGIV between 0 and 5 cM intervals that explained 37% of variation in resistance. The same QTL also involved in seed weight loss parameters. The identified QTLs are useful molecular tools for chickpea breeders to study the resistance and improve new varieties.

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In vitro clonal propagation of two Turkish walnut (*Juglans regia* L.) varieties

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An efficient protocol for in vitro clonal propagation of Kaman 1 and Kaman 5 varieties was achieved using axillary buds. The explants were treated with 70% ethanol for 1 min followed by surface sterilization using one drop per 100 ml of Tween 20 of 0.2% $HgCl_2$ for 5 min and rinsing with sterile distilled water for 3× 5 min. The explants to avoid development of phenolic acids based chlorosis were cultured for 3, 24 and 48 h using 100 mg/l of ascorbic acid, 100 mg/l citric acid, 100 mg/l ascorbic acid plus 100 mg/l citric acid in MS medium. The explants were cultured on MS medium containing 0.5 and 1.0 mg/l of IBA plus 0.5, 1.0 and 1.5 mg/l of BAP for shoot regeneration in 100 mg/l ascorbic acid plus 100 mg/l citric acid treatment for 48 h. The maximum number of 2.00 and 0.67 shoots on Kaman 1 and Kaman 5 walnut varieties per explant were obtained on MS medium containing 0.5 mg/l BAP plus 1.0 mg/l IBA respectively. Well developed sturdy shoots were rooted by conditioning with 4.0 mg/l IBA for 5 min and transferred to sterile soil mixture containing peat:perlite in pots for growth development and acclimatisation.

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Optimized selection of doubled-haploid glutinous rice regenerants in Kazakhstan

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Culture of isolated anthers and microspores, effective method for mass production of haploid rice plants, was used to obtain homozygous lines in one generation of the local sort of rice Violetta. The study targeted dihaploid analogues of glutinous variety of Violetta through screening for low amylose content of the prospective lines to generate the first glutinous rice variety in Kazakhstan. 72 calluses out of 1400 rice anthers were transplanted from N6 to MS