

Recent and advanced techniques for encapsulation of probiotic bacteria to maintain their biofunctionality



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There has been a tremendous increase of cultured products containing probiotic bacteria in the past two decades. In order to produce probiotic products which, show health benefits, bacterial cells should be present in a viable form at certain numbers during the shelf life of the product. Microencapsulation of bacterial cells is currently gaining attention to increase viability of probiotic bacteria in food systems. There have been several encapsulation techniques that are already used such as spray drying, spray-cooling, fluid-bed agglomeration and coating, freeze and vacuum drying, emulsion-based techniques, coacervation, extrusion-based techniques, adhesion to starch granules and compression coating in terms of encapsulation of the probiotics for their use in the fermented and other functional food products. Recently, alternative techniques; e.g., electrospraying and electrospinning techniques have emerged for efficiently encapsulation of probiotic bacteria. This work reviews a methodological approach for encapsulation techniques including their pros and cons as well as choice of appropriate technology in terms of final yield and level of cell viability.

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From the lab to the field: Combined mutagenesis and accelerated breeding approaches to obtain salt tolerant novel lines in wheat



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Wheat (*Triticum aestivum* L.) is a staple crop with global economic importance for human and animal nutrition. Salinity is becoming one of the major limiting factors for sustainable wheat production in the semi-arid regions of the World. Thus, in this study is combined conventional chemical mutagenesis with somatic embryogenesis and anther cultures for accelerating breeding to get novel salt tolerant wheat mutant lines. For this purpose, various concentrations (from 0 to 5 mM) of NaN₃ was used to induce mutations in both embryogenic calli and seeds obtained with M1 mutagenized populations for anther cultures. Mutagenized and non-mutagenized both embryogenic and androgenic calli were put in selection media and screened for salinity resistance by indirect regeneration in 100 and 150 mM NaCl. Fifty-two salt-tolerant lines were obtained from the NaN₃-mutagenesis. Molecular markers (ISSR, SSR, IRAP, etc.) were used to screen genetic variations between novel salt tolerant mutant lines and enzymatic and non-enzymatic antioxidant approaches (SOD, POD, CAT, APX, GR,

proline, GSSG, GSH, etc.) were used to understand salinity tolerance levels of them. The results suggest that the somatic embryogenesis and the anther cultures in combination with chemical mutagenesis may be a versatile approach for accelerating breeding strategies to create novel genetic variation in populations for both breeding programs and mutation-based forward/reverse genomics studies in wheat.

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Biotechnology approaches in common bean (*Phaseolus vulgaris* L.) breeding



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Common bean (*Phaseolus vulgaris* L.) is an economically, nutritionally, and socially important crop. In this review paper requirement to new cultivars applying biotechnological tools in common bean breeding and existing literature and available data are discussed. Application of different methods for *in vitro* culture, transformation, gene mapping and techniques for genome analysis are described. Further works needed in some investigations are also presented. The relation between traditional bean breeding methods and plant biotechnology techniques are addressed. It is concluded that all these techniques will help creating more genetic diversity, which is the main bean-breeding goal, particularly for the most important agricultural traits. This review manuscript presents an overview on common bean breeding reports to develop common bean cultivars thoroughly the world.

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Analysis of genetic variation among some Turkish oaks using random amplified polymorphic DNA (RAPD) method



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The genus *Quercus* belongs to the family *Fagaceae* which represents broad leaved species in the world. The biggest and the best-known group of this family is the *Quercus* genus with about 500 species in the northern hemisphere.

The genus is taxonomically very problematic in the world, because of extensive hybridization behaviors, weak reproductive barriers and wide geographical distribution. Hence, the systematic relationships in the genus are not completely clear and still debatable, despite various morphological, ecological, molecular and recently cpDNA studies.

Turkey is one of the most important diversity center of the genus *Quercus* according to species number and geographical distribution. The genus *Quercus* is represented by 18 species and 4 infraspecific taxa in three different sections in Turkey.

Most *Quercus* species in Turkey have taxonomic problems like other countries. These problems can be solved by molecular