

## In this issue

### Quorum sensing

Bacterial phenotypes have always been explained on the basis of functional independence of their single-cell organization. Compelling evidence, however, suggest that many diverse functions are the outcome of a concerted effort of a bacterial population, a phenomenon generally referred to as 'quorum-sensing'. Gera and Srivastava (**page 666**) trace the discovery of quorum-sensing through bioluminescence expressed by marine species of *Vibrio*. While this still serves the model system to study the phenomenon based on the genetic, biochemical and functional attributes, the field has diversified tremendously. Bacterial pathogenicity and virulence that has plagued the mankind since time immemorial, also turned out to be a density-dependent response. The diversity of phenotypes ranges from some basic functions such as to survive in an ecological niche, cross communicate with other biotic members and abiotic conditions, population dynamics, growth and gene exchange, to their relationship with plants and animals, both symbiotic and pathogenic. Implicit in this diversity are the common molecular themes that the underlying mechanism explain. This involves the production of an auto-inducer signal, the level of which is assessed by the growing bacterial population such that at a critical threshold the necessary pathway leading to the particular phenotype is expressed. A second line of diversity exists in the type of the signal (acyl-HSL in Gram-negatives and peptide in Gram-positives) and the biochemical nature

of the same. While these details not only change the way the regulation of bacterial functions needs to be looked at but also provides a handle to check the unwanted functions.

### Nano: Societal implications

The rapid pace of discoveries and developments in the fields of nanoscience and nanotechnology is calling for a comprehensive and in-depth understanding of the societal implications of nano-scale science and its deriving technologies in developing countries, an area that so far was largely sidelined by the scientific community. In spite of being an infant at its evolution, some of the known issues related to nanotech and nanomaterials suggest a wide spectrum of potential societal impacts. These need to be further studied, especially in the context of developing countries, where nano commodities, devices and services have the potential to make a significant difference. In the light of the possibility that scientists and researchers have the knowledge and tools to create matter that does not exist in nature, it is a prerequisite to understand and comprehend the potential hazards of nano-scale science and technology. Only if these are understood, policymakers can take informed and responsible choices to limit possible risks of nano-scale science and its deriving technological applications and to rule out future factions and new divides. Nanotechnology's unique and distinct features hold the potential to bridge or even bypass the technological gap between the developed and the developing world, if

designed and implemented to serve the needs of those, who in past were left out of the technological evolution processes. See **page 645**.

### Association studies in bread wheat

Roy *et al.* (**page 683**) describe results of a study, which is one of the few association studies conducted in bread wheat. They show successful utilization of association mapping in studying marker-trait associations for 14 agronomic traits using a set of 519 DNA-based molecular markers (including 221 SSR, 43 SAMPL and 166 AFLP markers) that were used for genotyping a set of 55 elite wheat genotypes. Marker-trait associations were examined on the basis of simple linear and multiple regressions involving regression of trait values on the marker genotypes. A total of 131 SSR, 43 SAMPL and 166 AFLP markers gave significant associations with at least one of the 14 traits with either of the two regression methods used in this study; as many as 51 of these markers, which showed association using both approaches (linear and multiple regression), may prove useful for marker-assisted breeding after necessary validation. Candidate genes were also searched for the above agronomic traits on the basis of proximity of different mapped genes with the SSR markers used in this study. None of the genes identified during this study is directly related with the traits of interest, but may mediate their effect either by other related traits or due to pleiotropic effect of these genes.