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Editorial

Genomics Research in the Last Decade: From Plants to Animals to Microbes

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The past decade has seen enormous progress in the genomics research in the abovementioned area, and the improvement in this area is very important as it directly or indirectly affects the human growth, development and sustainability. The plant genomic research has significant values and impact on agriculture, crop production, drug discovery/medicine and other plant natural products. The responsible genes for delivering important functions of plants, grouped together in biosynthetic gene clusters is hidden away in the dark matter of plant genomes. Current research involving genome sequencing, and now breakthroughs in sequencing technologies, i.e., the use of inexpensive Next-Generation Sequencing (NGS) technology will definitely accelerate the ability to find genes encoding enzymes and pathways for the biosynthesis of new natural products. Increased knowledge of the gene duplication event and plant metabolic gene clusters i.e., their architecture, regulation and assembly will help to understand the specialized metabolic events in plants and in expediting natural product discovery. For example, in soybean and sorghum species, significant depletions of whole-genome duplication-derived specialized metabolic genes were observed, but significant enrichment in local(tandem) duplication-derived specialized metabolic genes were seen. For, gene-clustering works, it has been documented that in rice one-fifth of the metabolic genes situated in clusters, and for *Arabidopsis*, soybean and sorghum one-third of the metabolic genes situated in clusters and clustered genes responsible for varying amount of phenylpropanoid and terpenoid metabolism. A gene-cluster of 10-genes for potential anti-cancer drug noscapine from opium poppy (*Papaver somniferum*) encoding N-methyltransferase, and seven small clusters each of two to three genes encoding enzymes for anti-cancer vinblastine/vincristine biosynthetic pathway from *Catharanthus roseus* have also been documented. Knowing the vast chemical biodiversity of the plant world, and widespread applications of plant derived natural products, researchers should now focus on the poorly understood areas of plants such as genetic background, plant authentication through DNA-barcoding techniques, the agricultural traits, and the medicinal quality of the small medicinal herbs. [In the context of crop plant genome assembly, a recent work from King Abdulla Univ. must deserve mention who generated a genome assembly of the economically and nutritionally important tetraploid crop species quinoa].

Genome research in animals in recent years has progressed rapidly and is contributing to our understanding of chromosome evolution to the human genome. Animal genomic research also contributed significantly over the years in agriculture and human health. As a result of balanced breeding programmes and genomic selection, chickens, cows and pigs are supplying more and more meat, eggs and dairy products to meet the increasing demand of animal protein. Domestic chicken is one of the most important animal on which genomics research advanced rapidly to the sequencing stage. Animal genomics research also plays significant roles in finding the genes responsible for human diseases, as for example the discovery of a mutation in MC4R gene in pig's results in obesity similar to humans. A mutation in the limbin gene responsible for chondrodysplastic dwarfism in Japanese brown cattle also responsible for the similar disease in humans. Enhancement of these contributions along with recent access to complete high-quality genomes of nonhuman primates gorilla genome will also help us understand the human biology (Science p.10.1126, SMRT sequencing and assembly of the gorilla genome). In this context it is worth mentioning, that the entire human genome sequencing, and the human genome project identified more than 20,000 genes in the human genome and this huge digital database of information will help in understanding the links between the genetic code and diseases.

In the last decade revolution in DNA-sequencing technology has changed dramatically microbial genomics research and altered the way infectious diseases are studied. Microbial genomics research is associated with pathogens virulence, drug resistance mechanisms of the organisms, vaccine development and for discovering novel natural products from microorganisms. In addition, in last five years human microbiome and metagenomics related to human health and disease has received a great deal of attention. Till date around 1600 complete bacterial genome, 120 complete archaeal genomes, 40 complete eukaryotic genomes of which around 20 from fungi and for complete 2675 viral species sequences have been determined and many more in progress. Microbial virulence genes are physically segregated in clusters and located within mobile genetic elements and encodes variety of super antigens and toxins. Genome sequences also provides blueprint for essential bacterial and viral components that indicates resistance to certain drugs, some drug resistance traits are encoded by single genes such as rifampicin resistance in *M. tuberculosis*, methicillin resistance in *S. aureus*. Genome based antigen discovery of microbes and viruses can be exploited for vaccine design and thus developed against many like group B streptococcus, and extra intestinal pathogenic *E. coli*. Finally, as microbes produce a wealth of structurally diverse specialized metabolites with a remarkable range of biological activities and a wide variety of applications in medicine and agriculture such as the treatment of infectious diseases and cancer and the prevention of crop damage, they should be examined carefully. As genomics has now revealed that many microbes have far greater potential to produce specialized metabolites than was thought as many specialized metabolite Biosynthetic Gene Clusters (BGCs) remained silent, i.e., not expressed under typical laboratory conditions. Strategies are now developed to identify such silent BGCs in bacteria and fungi to induce the expression of silent BGCs for discovering novel natural products.