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GENOME AS A TOOL OF GENETIC ENGINEERING

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***Abstract*—** The study was conducted from different modern research data to review the innovation latest technology in the genomics and its application in Agriculture, biomedicine, and plant derived medicine. Application of genome in genetic engineering and molecular biotechnology have been exhibited well. Genetically Modified Organism (GMO), Agrobacterium mediated recombination and genetic engineering using molecular biotechnology in plant, medicine and biomedicine have been highlighted from technology based different research data. Moreover, molecular biotechnology in biopharmaceuticals, pharmacogenomics, new medical therapies, genetic testing, transgenic fruit, vegetable and flower production, using Agrobacterium mediated gene, DNA cloning have been presented well showing innovation data.

***Keywords*—** Genomics, Agriculture, Biomedicine, Medicine, Genetic Engineering.

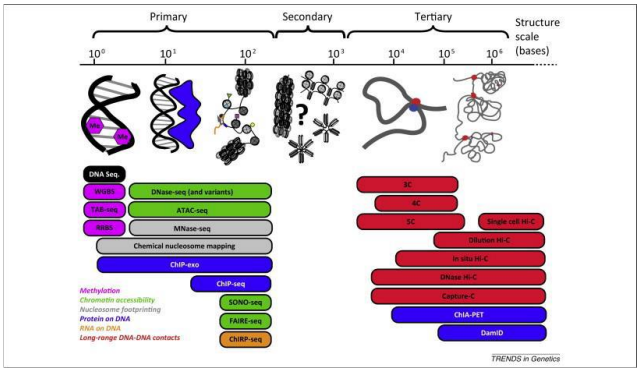
I. INTRODUCTION

A genome (DNA or RNA) is an organisms complete set of DNA, including all of its genes. Each genome contains all of the information needed to build and maintain that organism. In human, a copy of the entire genome more than 3 billion DNA base pairs is contained in all cells that have a nucleus. New DNA may be inserted in the host genome by first isolating and copying the genetic material of interest using molecular cloning methods to generate a DNA sequence, or by synthesizing the DNA, and then inserting this construct into the host organism. Genes may be removed, or knocked out, using a nuclease. Gene targeting is a different technique that uses homologous recombination to change an endogenous gene, and can be used to delete a gene, remove exons, add a gene, or introduce point mutations.

II. GENETICALLY MODIFIED ORGANISM (GMO)

Genetically modified organism (GMO) is considered as an organism that is generated through genetic engineering. The first GMOs were bacteria in 1973, GM mice were generated in 1974. Insulin-producing bacteria were commercialized in 1982 and genetically modified food has been sold since 1994. Glofish, the first GMO designed as a pet, was sold in the United States December in 2003. Genetic engineering biotechnology has been applied in numerous fields including agriculture, industrial biotechnology, and medicine. Enzymes used in laundry detergent and medicines such as insulin and human growth hormone are now manufactured in GM cells, experimental GM cell lines and GM animals such as mice or zebra fish are being used for research purposes, and genetically modified crops have been commercialized objective of the study was to review the various superlative techniques of genome application in plant, fruit, and vegetable, biomedicine and medicine from different research data. The high-throughput- next generation sequences technologies are currently the hottest topic in the field of human and animals genomics researches, which can produce over 100 times more data compared to the most sophisticated capillary sequencers based on the sanger method. With the outgoing developments of high throughput Sequencing machines and advancement of modern informatics tools at unprecedented pace, the target goal of sequencing individual genomes of living organism at a cost of $1,000 each is seemed to be realistically feasible in the near future. In the relatively short time frame since 2005, the HT-NGS technologies are revolutionizing the human and animal genome researches by analysis of chromatin immunoprecipitation coupled to DNA microarray or sequencing, whole genome genotyping, genome wide structural variation, de novo assembling and re-assembling of genome, mutation detection and carrier screening, detection of inherited disorders and complex human diseases, DNA library preparation, paired ends and genomic and personal genomics. In the review, we addressed the important features of HT-NGS like, first generation DNA sequencers, birth of HT-NGS, second generation HT-NGS platforms, third generation HT-NGS platforms. Systematic biochemical and genetic experimentation in simpler model organisms has contributed to the rapid increase in the proportion of

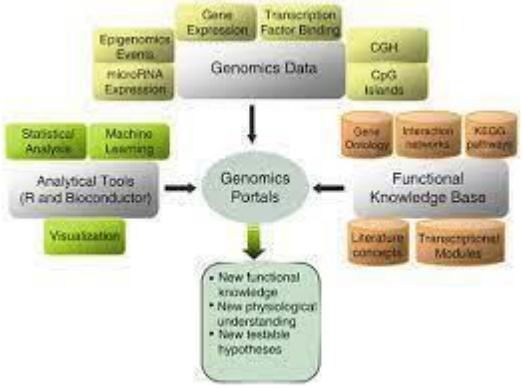
characterized genes. For example, about 80% of yeast genes have some annotated function. Beyond simpler model systems such as yeast, however, cost and time requirements may preclude many systematic analyses, for example, resources-intensive phenotype assays in adult animals. Fortunately, efforts in simpler model organisms have illustrated that gene functions can be inferred on the basis of data types that are easier to collect systematically. Protein sequences features, expression patterns, and protein-protein interactions, for example, can provided powerful clues to function. This raises the prospect of directing resource-intensive experimentation toward the genes most likely to yield positive results. In yeast, this concept is well established, and the tradeoffs between performance measures, the efficacy of combinations of different data types in making different types of predictions, and the applicability of diverse inference algorithms are topics of active research. One of the important realizations of the genomics era is that whole-genome, or polyploidy, is far more prevalent in the evolutionary history of plants then Genomic analysis over the past 15 years have demonstrate that all flowering plants are polyploidy, and multiply so. That is, the phylogenetic history of angiosperms abounds with WGD events, the most recent of which are superimposed on earlier duplications that took place early in angiosperms evolution, and before that on duplications that occurred at the root of the seed plants. Our understanding of the cyclical nature of polyploidy was first suggested by analyses of expressed sequence tags in many different plant species. These analysis revealed peaks of sequences similarity among genes within genome representing multiple gene duplications, whose collective existence and features suggest they to a common origin.



The development of DNA sequencing technology has been a great and memorial journey filled with many historical events. In the last decade, nearly all of DNA sequence production has restrictively been executed with capillary based, semi-automated applications of the Sanger biochemistry and its variations. Over the year, the field of DNA sequencing has been revived and prospered due to various scientific breakthroughs. These technologies advancements eventually lead to the encouragement for developing novel experimental designs for this field due to various reasons. Ultimately, next-generation sequencing technologies were released in 2005. They are known as "high throughput sequencing technologies that parallelize the sequencing process, producing millions of sequence at once at a much lower per-base cost than conventional sanger sequencing".

III. APPLICATIONS OF GENOME EDITING TECHNOLOGY IN THE TARGETED THERPY OF HUMAN DISEASES

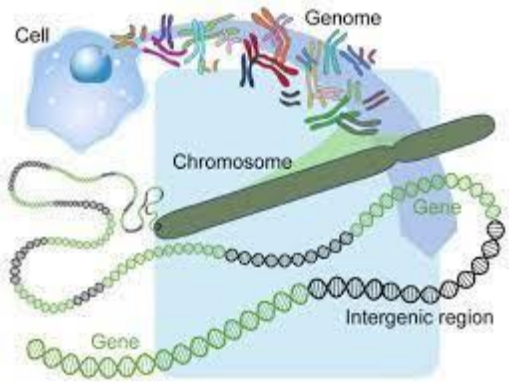
Based on engineered or bacterial nucleases, the development of genome editing technologies has opened up the possibility of directly targeting and modifying genomic sequences in almost all eukaryotic cells. Genome editing has extended our ability to elucidate the contribution of genetics to diseases by promoting the creation of more accurate cellular and animal models of path of pathological processes and has begun to show extraordinary potential in a variety of fields, ranging from basic research to applied biotechnology and biomedical research. Recent progress in developing programmable nucleases, such as zinc-finger nucleases, transcription activator-like effector nucleases and clustered regularly interspaced short palindromic repeat (CRISPR), has greatly expedited the progress of gene editing from concept to clinical practice. Here, we review recent advances of the three major genome editing technologies and discuss the applications of their derivative reagents as gene editing tools in various human diseases and potential future therapies, focusing on eukaryotic cells and animal models.



IV. HIV/AIDS

HIV/AIDS has long been at the forefront of the development of gene- and cell-based therapies. Although conventional gene therapy approaches typically involve the addition of anti -HIV genes to cells using semi randomly integrating viral vectors, newer genome editing technologies based on engineered nucleases are now allowing more precise genetic manipulations. The possible outcomes of genome editing include gene disruption, which has been most notably applied to the CCR5 coreceptor gene, or the introduction of small mutations or larger whole gene cassette insertions at a targeted locus. Insect genome editing was first reported

1991 in Drosophila melanogaster but the technology used was not portable to other species. Not until the recent development of facile, engineered DNA endonuclease systems has gene editing become widely available to insect scientists. Most applications in insects to data have been technical in nature but this is rapidly changing. Functional genomics and genetics-based insect control efforts will be major beneficiaries of the application of contemporary gene editing technologies.



V. CONCLUSION

Gemone-editing, which involves the precise manipulation of cellular DNA sequences to alter cell fates and organism traits, has the potential to both improve our understanding of human genetics and cure genetic diseases. Here I discussed the scientific, technical and ethical aspects of using CRISPR regularly interspaced short palindromic technology for therapeutic applications in human. New technologies have recently emerged that enable targeted editing of genomes in diverse systems.

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