ISSN: 2322-0066

Research and Reviews: Journal of Biology

Advances in Genetic Engineering

Sneha Lakshmi R.P

Department of Pharmaceutical Analysis, Omega College of Pharmacy, Osmania University, Hyderabad, India.

ShortCommentary

Received: 15/05/2015
Accepted: 18/05/2015

*For Correspondence
Department of Pharmaceutical Analysis, Omega College of Pharmacy, Osmania University, Hyderabad, India.

Keywords: Genetic engineering, DNA/RNA, Pleiotropy

Introduction

Genetic engineering, the artificial manipulation, modification, and recombination of DNA or other nucleic acid molecules in order to modify an organism or population of organisms.The term genetic engineering initially meant for a wide range of techniques for the modification addition , deletion, multiplication or manipulation of organisms through the processes of heredity and reproduction. As such, the term embraced both artificial selection and all the interventions of biomedical techniques, among them artificial insemination, in vitro fertilization (e.g., “test-tube” babies), sperm banks, cloning, and genemanipulation. [1-9]

But the term now denotes the narrower field of recombinant DNA technology, or gene cloning in which DNA molecules from two or more sources are combined either within cells or in vitro and are then inserted into host organisms in which they are able to propagate. Gene cloning is used to produce new genetic combinations that are of value to science, medicine, agriculture, or industry. [10-14]

In this post-genome era of advanced high-throughput DNA/RNA sequencing technologies, information may no longer be a bottleneck to understand and tackle complicated genetic diseases such as cancer. Gene interactions can potentially contribute to the improvement of disease classification accuracy.Previously the concept of genetics was applied to a limited number of diseases with obvious phenotypes where simple people use to observe and relate. It was never easy to establish a clear cut of heritability range between genetic variation and a risk of suffering from a complex disorder due to many reasons including but not limited to; gene variations, non-linear interactions between genetic variance and phenotype severity, complex gene-gene interactions and many others. [15-19].

lassic gene targeting relies on the homologous recombination when DNA fragment is introduced in the genome. All eukaryote cells repair DSBsthrough DNA repair mechanisms, including error-prone nonhomologous end joining (NHEJ) andhomology-directed repair [20-23].

In human complex diseases, the phenomenon that a genetic variant or gene can affect multiple diseases (or phenotypes) is referred as “Pleiotropy” [24]. Pleiotropy is usually considered as the most important source for genetic correlation between traits [25-29] in which the genetic engineering play an important role.

In the case of Fetal growth, is determined by various factors. That includes nutrients, minerals and other necessary element, nutrient concentration gradient between maternal and fetal blood, placental blood flow for the growth of fatal. Their mutation and expression are related to the perinatal growth phenotype [30-33].

Technology of genetic modifying is an alternative way to improve both the quality and the quantity of agricultural products. Genetically Modified Organism (GMO) as the product of new technology requires an excellent management strategies especially for the biosafety of the products before being released and commercialized. It can act against different environmental affecting factor towords agriculture, such asGlobal climate change is believed to be one of the factors that cause the decreasing of agricultural products.

In the EU, the governing of activities involving genetic engineering began in 1990 with the adoption of Directive 90/219/EEC on the contained use of genetically modified microorganisms [34] and Directive 90/220/EEC on the deliberate release into the environment of genetically modified organisms [35]

This knowledge will be “game changer” for the future of the biotechnology industry. The open source community around iGEM has a worldwide impact. Nevertheless, the South American participation (5.3%) along these 10 years is small when compared to the North American (38.6%), the European (28.3%) and the Asian (27.8%). Africa has only participated twice while Asia has presented a fast growth in the number of teams at the competition. [36]

Biotechnology approaches have the potential to enhance crop production under different stress conditions. On the one hand, abiotic stresses are complex in nature; on the other hand, there are several challenges that have restricted the realization of the full potential of using biotechnology approaches in crop breeding, nevertheless, with current and fast emerging technologies such as RNAi. Eventually, the adoption of biotech crops to mitigate abiotic stresses, that are expected to increase in frequency and intensity in coming years, will depend on public perceptions and public acceptance, as well as on cultural and institutional processes in developing countries. [37]

This paper describes the assessment of the antibacterial effect of leathers obtained by different tanning methods that had been impregnated with silver nanoparticle emulsions or silver silica nanocomposites with the aim of verifying the potential use of these methodologies in footwear production. This would make it possible to prevent or minimise the presence of microorganisms that cause foot odour or are involved in the development or worsening of various foot diseases. For this purpose, silver nanoparticles were synthesised using three reducing agents: sodium borohydride, gelatine/glucose and glycolic Aloe vera extract. The type of reducing agent used determined the kinetics of the reduction reaction. [38]

Metabolites formed from enzymatic biotransformation of compounds possess structures similar to that of the parent compound. Identification of the tentative structure of metabolites, using liquid chromatography and mass spectrometry, helps to design and synthesize new molecules or materials similar to that of the parent compound. Subjecting the synthesized new compounds for various in vitro and in vivo assays will help to enhance the pharmacological properties of the compounds. Thus, the synthesized metabolites can be a compound or material, whose properties might be similar to that of the parent drug, and can serve as an ideal back up compound for parent drug in clinical trials. [39]

Genetically, DCM is heterogeneous. Mutations in presenilins have been detected in all clinically affected subjects with heart failure from three DCM families, as well as four severe sporadic DCM patients who were performed heart transplantation due to heart failure [40]

REFERENCES

1. Akbar Nikkhah. Production Curve Management of Starch Nutrition in Ruminants: A Global Biotechnique J Bioprocess Biotech. 2015; 5:e123.
2. Vasiliki E.Kalodimou Stem Cells Cloning Prons& Cons ClonTransgen 2014; 3: 127.
3. Mingdong Liu and Jiayou Zhang. Construction of Functional GFP-Neo Fusion Protein by Selection from a Peptide Library ClonTransgen 2014; 3: 131.
4. Mohammad Al-Haggar. Genetics of α1 Anti-Trypsin (AAT) Deficiency Gene Technology 2014, 4:e113.

5. Adriana Carol EleonoraGraziano and VeneraCardile. Genetic Test and Gene Therapy for Krabbe Disease: An Update Gene Technology 2013, 4: 118.
6. Csuka D et al. Hereditary Angioedema Due to C1-Inhibitor Deficiency-From a Genetic Point of View Hereditary Genet.
7. Dogra D et al. Population Genetics for Autosomal STR Loci in Sikh Population of Central India Hereditary Genet.
8. Graham Ewing. Are We so Obsessed with Technology that We Fail to Apply Basic Logic to What We See? Has the Accumulation of Data Excluded Consideration of the Quality of the Data? Human Genet Embryol.
9. VY Phanet al. Antoine La Pregnancy after the Calcium Ionophore Activation and Aneuploid Screening Using A-CGH in Globozoospermia Patient Human Genet Embryol.
10. Thomas Mabey andSittisakHonsawek. Genome Wide Association Studies and Next Generation Sequencing Technologies in Osteoarthritis Next GeneratSequenc&Applic.
11. Srilakshmi Srinivasan and JyotsnaBatra. Four Generations of Sequencing- Is it Ready for the Clinic Yet? Next GeneratSequenc&Applic.
12. Dal Rye Kim et al. Identification and Characterization of 1,4-β-D-GlucanGlucohydrolase for the Saccharification of Cell Oligomers from Paenibacillus sp. HPL-001 J Bioprocess Biotech. 2015; 5:209.
13. Satyanarayana KG. Recent Developments in Green Composites based on Plant Fibers-Preparation, Structure Property Studies J Bioprocess Biotech. 2015; 5:206.
14. Mohamed E Selim et al. El-Gammal Evaluation and Characterization of Some Egyptian Fusariumoxysporum Isolates for their Virulence on Tomato and PCR Detection of (SIX) Effector Genes J Bioprocess Biotech. 2015; 5:204.
15. Kojic DD et al. CAD-CAM Ceramic Crown Retention of Resin Cements J BiotechnolBiomater 2014; 4:164.
16. Sherkhane AS et al. VS Quantitative Immunoproteomics Approach for the Development of MHC Class I Associated Peptide Antigens of Alpha-Cobra Toxin from Najakaouthia J BiotechnolBiomater 2014; 4:169.
17. Dimitris S Argyropoulos. Towards Thermoplastic Lignin Polymers: Progress in the Utilization of Kraft Lignin for the Synthesis of Heat Stable Polymer Melts. J BiotechnolBiomater. 2013; 3:e123.
18. Murrr LE. Some Comments on Orthopaedic Implant Infection: Biomaterials Issues. J BiotechnolBiomater. 2013; 3:e119.
19. Basel Khraiwesh. Environmental Biotechnology Under A Changing Climate. J BiotechnolBiomater. 2012; S8: e001.
20. Nivedita Mishra and Krishna Sundari. S Native PGPM Consortium: A Beneficial Solution to Support Plant Growth in the Presence of Phytopathogens and Residual Organophosphate Pesticides J Bioprocess Biotech. 2015; 5:202.
21. Xiaosheng Wang. An Exploration of Mutation Status of Cancer Genes in Breast Cancers Next GeneratSequenc&Applic.
22. Fei Ye et al. Detection of Mitochondrial Mutations in Cancer by Next Generation Sequencing Next GeneratSequenc&Applic.
23. Tomoko Ohta. Epigenetics and Evolutionary Mechanisms Human. Genet Embryol. 2013; 3:113.
24. Israel Gomy. Hereditary Cancer Risk Assessment: How Best can we Achieve it? Hereditary Genet 2013; S2:003.
25. Mohammad Al-Haggar. Evolving Molecular Methods for Detection of Mutations Gene Technology 2013; 2:e104.
26. Luca Galluzzi. DNA-Based Molecular Detection of Toxic Phytoplankton in Water Samples: Different Tools to Get Reliable Information Gene Technology. 2012; 1:e101.

27. Shunyuan Xiao. Protecting Crops from Pathogens: Novel Approaches to an Old Problem Gene Technology 2012; 1:e103.
28. Soraya L. Valles Chances in the Brain Cells, From Epigenetic To the Future Gene Technology 2014; 3: e108.
29. VeyselSabriHancer. Genetics of Antiphospholipid Syndrome Human Genet Embryol 2011; 1: e103.
30. Roger Laine and M. Tino. A Dopamine Gluconamine That Binds D1/D5 Receptors and Has Anti-Parkinsonian Effects in Three Animal Models, is Transported across the Blood Brain Barrier.J BiotechnolBiomater. 2012; 2:5
31. Li A andTanzi RE. Pleiotropy of Presenilins. Hereditary Genet. 2012; 2: e105.
32. Bosco C and Eugenia D. Effects of Maternal Alcoholism on Placental Function and Lung Fetal Development. J Cell SciTher. 2014; 5: 178.
33. Srinivasan H et al.Amniotic Band Syndrome: A Case Series. J Preg Child Health. 2014; 1: 109.
34. Berthelot-Ricou A et al. New Multidisciplinary Approach of Conservative Surgical Management of Placenta PercretaAntenatally Diagnosed. Surgery Curr Res. 2014; 4: 195.
35. Moodley S. Transplacental Infection of HIV-1 and the Associated Risk Factors In Utero. J Clin Cell Immunol.2014; 5: 195.
36. Matsuda Y et al. Prognosis of the Babies Born from Placental Abruption - Difference between Intrauterine Fetal Death and Live-Born Infants. GynecolObstet (Sunnyvale).2013; 4: 191.
37. Chhabra A Cancer Immunotherapy: Targeting Checkpoint Blockade. Adv Genet Eng. 2015; 4: 118.
38. Zhong N et al.Long Non-Coding RNAs, Ubiquitin Proteasome System, Collagen Degradation and Preterm Premature Rupture of Membrane. Adv Genet Eng.2015; 4: 117.
39. Mastinu, Adv Genet Eng 2015; 4:1
40. Muthuswamy S et al. Co-existence of CFTR and SPINK1 Gene Mutations in an Idiopathic Chronic Pancreatitis Case. Gene Technology. 2015; 4: 116.