OPEN ACCESS Freely available online

Advancements in Genetic Engineering

ISSN: 2169-0111

Opinion

Rhodotorula Diobovata Lipid Producer: Optimizing Lipid Accumulation for Biodiesel Production

Nesma Mamdouh*

Department of Obstetrics and Gynecology, Shunde Hospital of Medical University, foshan, China

Introduction

There is a remarkable variety of human facial appearances, almost exclusively the result of genetic differences, as exemplified by the striking resemblance of identical twins. Despite intensive research on the genetics of craniofacial morphology using animal models and human craniofacial syndromes, the genetic variation that underpins normal human facial appearance is still largely elusive. As a part of efforts on detecting genomic variants affecting normal craniofacial appearance, we have implemented a targeted candidate gene approach by selecting 1,319 Single Nucleotide Polymorphisms (SNPs) in over 170 candidate genes and intergenic regions. This list has been further expanded with additional 4,732 tag polymorphisms, representing extended haplotype. All the markers were genotyped in 587 DNA samples using a massively parallel sequencing approach. We used 3-Dimentional (3D) facial scans and direct cranial measurements to calculate 104 craniofacial anthropometric distances, which were analysed for associations with 2,332 polymorphisms.

Postnatal craniofacial morphogenesis

Due to over-conservative nature of the Bonferroni correction, we also report the associations that reached the traditional genome-wide p-value threshold (<5.00E-08) as suggestive. Based on the genome-wide significance threshold, 8 craniofacial phenotypes demonstrated significant and mostly novel associations with 33 intergenic and extragenic SNPs, potentially involved in gene regulation. This study identified a large number of genetic variants associated with normal craniofacial morphology variation, including confirmation of the two previously reported genes. These results enhance our understanding of the craniofacial genetics affecting normal craniofacial appearance and will be of particular value for clinical diagnostics and forensic molecular phenotyping.

The human face is probably the most commonly used descriptor of a person and has an extraordinary role in human evolution, social interactions, clinical applications as well as forensic investigations.

The influence of genes on facial appearance can be seen in the striking resemblance of monozygotic twins as well as amongst first degree relatives, indicating high heritability. Uncovering the genetic background for regulation of craniofacial morphology is not a trivial task. Human craniofacial development is a complex multistep process, involving numerous signalling cascades of factors that control neural crest development, followed by a number of epithelial-mesenchymal interactions that control outgrowth, patterning and skeletal differentiation. The mechanisms involved in this process include various gene expression and protein translation patterns, which regulate cell migration, positioning and selective apoptosis, subsequently leading to development of specific facial prominences. These events are precisely timed and are under hormonal and metabolic control. Most facial features of the human embryo are recognizable from as early as 6 weeks post conception, developing rapidly in utero and continuing to develop during childhood and adolescence. Development of the face and brain are interconnected and occur at the same time as limb formation. Facial malformations therefore, frequently occur with brain and limb abnormalities and vice versa. Consequently, the development of both craniofacial and limb segments is likely to be regulated by the same genes and epistatic interactions. Genetic regulation of craniofacial development involves several key morphogenic factors such as HOX, WNT, BMP, FGF as well as hundreds of other genes and intergenic regulatory regions, incorporating numerous polymorphisms.

CONCLUSION

The loci involved in the craniofacial syndromes may in fact influence the extraordinary variety of human facial appearances, in the same way that genes responsible for albinism have been shown to be involved in normal pigmentation phenotypes. Additionally, non-genetic components such as nutrition, climate and socio-economic environment may also affect human facial morphology via epigenetic regulation of transcription, translation and other cellular mechanics. To date, both the genetic and even more so, the epigenetic regulation of the craniofacial morphology are poorly understood.

***Correspondence to:** Nesma Mamdouh, Department of Obstetrics and Gynecology, Shunde Hospital of Medical University, foshan, China, E mail: nesmamamdouh555@gmail.com

Received: 01-Mar-2022, Manuscript No. MAGE-22-21436; **Editor assigned:** 04-Mar-2022, PreQC No. MAGE-22-21436 (PQ); **Reviewed:** 18-Mar 2022, QC No. MAGE-22-21436; **Revised:** 25-Mar-2022, Manuscript No. MAGE-22-21436 (R); **Published:** 31-Mar-2022, DOI: 10.35248/2375 4508.22.S1.005.

Citation: Mamdouh N (2022) Rhodotorula Diobovata Lipid Producer: Optimizing Lipid Accumulation for Biodiesel Production. Advac Genet Eng. 11:005