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دومین بهایش مین الللی و دہمین بهایش ملی سر میں اللہ میں اسلامی ایران مو مکمور کی اسلامی ایران

۷–۹ شىھريور ما*ہ* ۱۳۹۶ كرج، سالن همایش های موسسه تحقیقات اصلاح و تهیه نهال و بذر

#### Introduction

 $\beta$ -Thalassemia is one of the most common hereditary hemoglobinopathy disorders with a high frequency in Iran with high risk of .For couples transmitting a genetic defect, Preimplantation Genetic Diagnosis (PGD) can be an alternative way to the select healthy embryo/s before implantation in the uterus. Homozygosity mapping with the help of STR markers in conjunction with direct sequencing can be a very powerful technique to select best embryo. Using highly the polymorphic marker is very helpful in detecting the very important event of "Allele Drop out" in PGD procedure. This study aimed to find polymorphic STR markers linked to the b-globin gene for use in homozygosity mapping studies in of PND (Prenatal Diagnosis) & PGD studies.

individuals 50 unrelated were the allele genotyped to assess frequencies, heterozygosity of the selected markers. Polymorphic STR markers were selected from Tandem Repeats Finder and Sequence-based Estimation of Repeat Variability databases. Suitable primers were designed to be to set up a multiplex-PCR Genotyping of reaction. each individual were performed using fragment analysis by ABI Genetic Analyzer 3130.

Statistical analysis was performed using GenAlEx6.03 softwere.

# Frequency & heterozygosity assessment of STR markers linked to $\beta$ globin gene applicable in PND &PGD

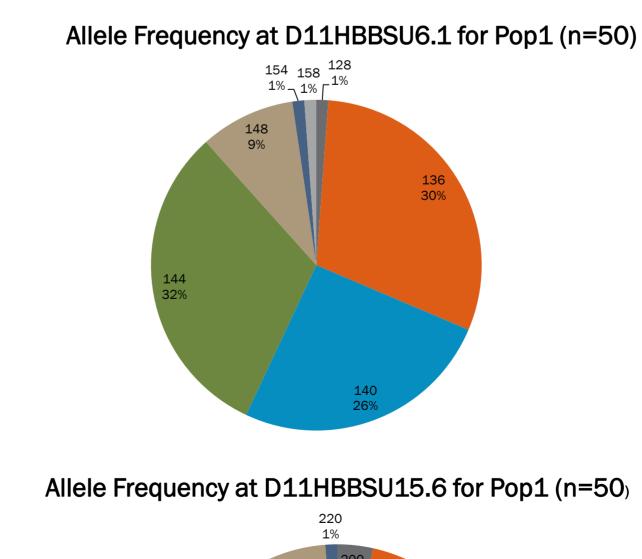
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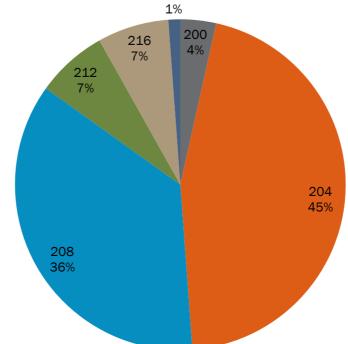
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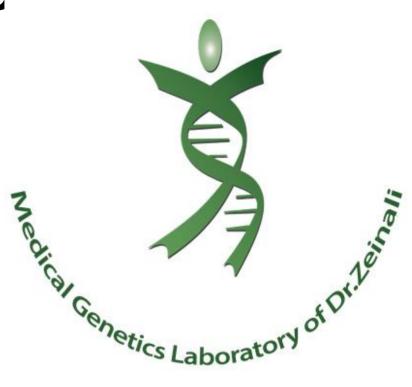
#### **Methods**

### Results

Our results showed that the heterozygosity of selected markers were between 67%-80%. Totaly, 43 alleles were observed. The highest heterozygosity was observed for D11HBBSU6.1 and the lowest for D11HBBSU15.6.7 ,6,7,5,11,6 different allele were seen for D11HBBSD3.3, D11HBBSU2.9,D11HBBSU6.1,D11HBBS D11.2, D11HBBSU11, D11HBBSU15.6 respectively.







All studied loci were in Hardy-Weinberg equilibrium except for D11HBBSU11 and D11HBBSD3.3. The deviation could be because of high number of alleles in these loci.

Conclusion

