SNP BASED GENETIC LINKAGE OF LARGE PEDIGREE ASCERTAINED FOR MULTIPLE MOTHERS OF DZ TWINS

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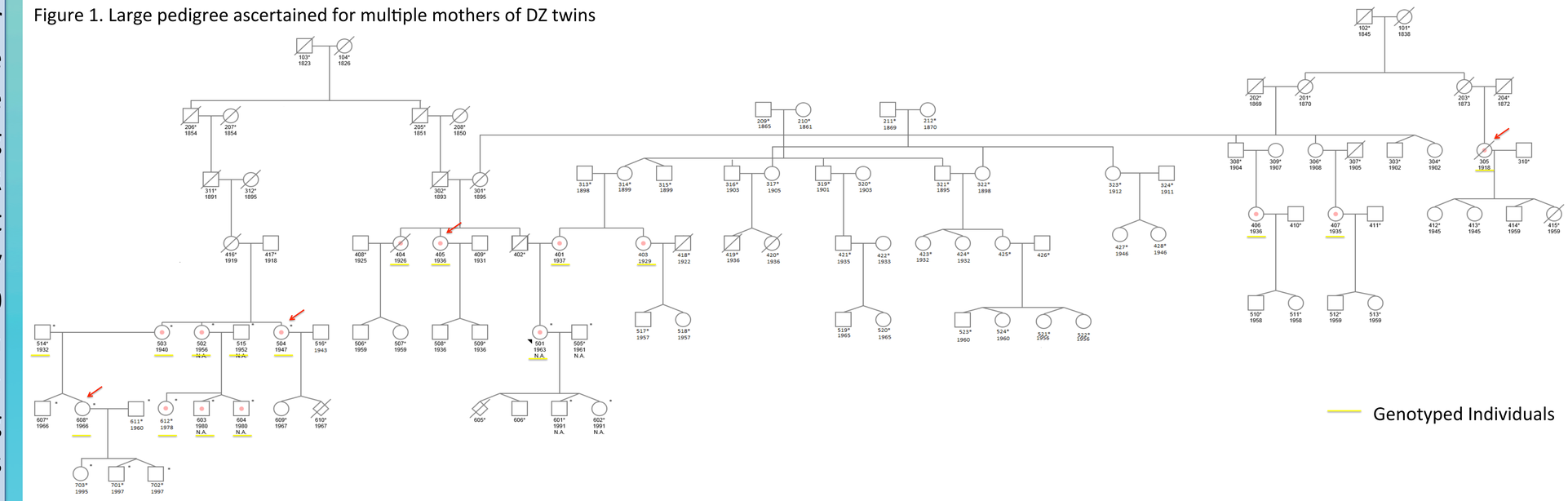
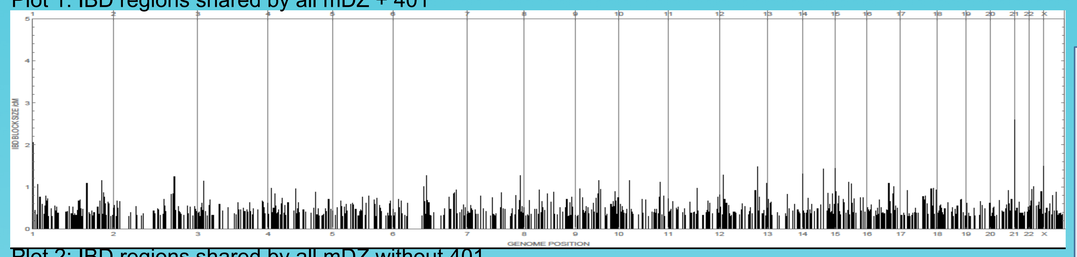
Aim: Based on our previous finding (Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility, Mbarek *et al.* AJHG 2016) we intend to use whole genome sequencing as a follow-up approach to identify new genetic biomarkers that would allow predicting DZ twinning and also related fertility measures in order to improve reproductive ability of infertile couples.

Methods: DNA was available for 17 individuals from a large pedigree ascertained for multiple mothers of DZ twins. Genotyping was performed using Avera-NTR GSA array. Identical By-Descent (IBD) mapping was performed by searching for shared regions in 10 mothers of DZ twins using custom programs written in Mathematica (Wolfram Research, Inc.). Allowing 1 % error rate, all shared regions were reported out and plotted.

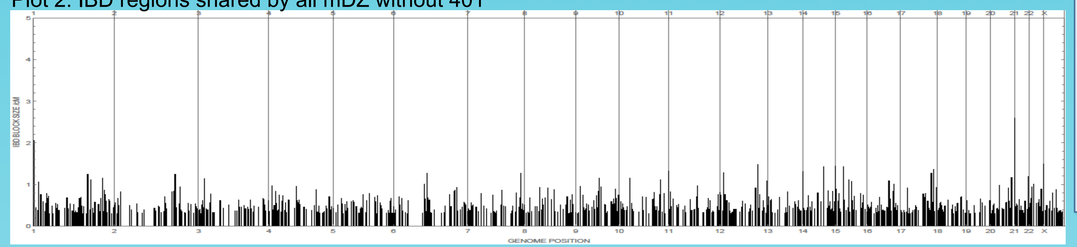
Figure 1. Large pedigree ascertained for multiple mothers of DZ twins



Plot 1: IBD regions shared by all mDZ + 401

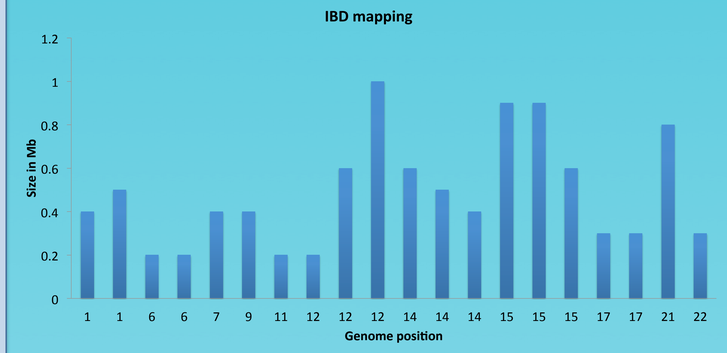


Plot 2: IBD regions shared by all mDZ without 401



Results: Identical-by-descent mapping revealed 11 candidate regions totaling 18.4 Mb on chromosomes 1, 6, 7, 9, 11, 12, 14, 15, 17, 21 and 22 (Figure 2).
Whole genome sequencing (WGS) at a depth of ~ 35X will be performed for the mothers of DZ twins highlighted by red arrow in the pedigree.

Figure 2. IBD mapping delineated 11 candidate regions



IBD regions shared by mDZ from the father's side: {503, 504, 404, 405, 406, 407, 501, 502, 305, 608}