عنوان مقاله:

Genetics of endometriosis:genetic risk factors for endometriosis in different levels of the whole systems biology

محل انتشار:

سومین کنگره بین المللی چالش های بالینی در مامائی، زنان و نازائی (سال: 1398)

تعداد صفحات اصل مقاله: 2

نویسنده:

Yasamin Ghaffari - *Faculty of life sciences and biotechnology, Shahid Beheshti University, Tehran, Iran*

خلاصه مقاله:

Background and Aim : Endometriosis is a heritable complex disorder that is influenced by multiplegenetic and environmental factors.In all,16 genomic regions have been associated with endometriosis riskin one or more populations, no independent associations were identified from direct genotyping of commonand low frequency protein coding variants. This suggests most common genetic risk factors contributing toendometriosis risk are located in regulatory DNA sequences and alter the regulation of gene transcription.Functional studies are needed to understand pathways increasing endometriosis risk and help identify noveltargets for interventions to improve diagnosis and treatment.Methods : Genetic risk factors GWAS compares the frequencies of many thousands of single nucleotidepolymorphisms (SNPs) across the genome and the approach is agnostic to assumptions about underlyingdisease biology implicit in the selection of candidate genes in earlier studies Genome-wide associationstudies A recent study in the Icelandic population with replication in Danish samples reported associationwith rs17773813 on chromosome 4q12 (P = 3.8 × 10-11, OR=1.28) upstream of Kinase Insert DomainReceptor (KDR) encoding vascular endothelial growth factor receptor 2 (VEGFR2), and with rs519664 onchromosome 9p22 (P = 4.8 × 10-10), OR=1.29) in the Tetratricopeptide Repeat Domain 39B gene(TTC39B). Replication studies There is generally strong and consistent replication of results from theGWAS studies taking these considerations in mind. Lack of replication in some studies is most likely dueto stochastic fluctuations that typically can be seen between individual datasets . Results for associationon chromosome 12 near vezatin (VEZT) have been replicated in an Italian study and for SNPs onchromosome 2q14 near Interleukin 1 Alpha. Post-GWAS functional analysis Genetic markers atchromosome 1p36.12 show consistent association with endometriosis risk. The association signal includesa block of SNPs spanning the genes WNT4, CDC42 and LINC00339. The key SNP on chromosome 1 islocated within an intron of WNT4, a gene essential for development of the female reproductive tract.Results : Results supported association for the two regions identified previously (chromosomes 7p15 and9p21), confirmed association near the gene for Wnt Family Member 4 (WNT4) on chromosome 1p36, andidentified four novel associations on chromosomes 2 (two regions), 6 and 12.One of the difficulties oftranslating results from the ... world-wide effort on complex disease mapping into clinically relevant outcomesis that there is no compr

کلمات کلیدی:

functional studies,Genetics risk factors, GWAS, gene expression