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SEVEN-SINGLE NUCLEOTIDE POLYMORPHISM POLYGENIC RISK SCORE FOR BREAST CANCER RISK PREDICTION IN A VIETNAMESE POPULATION

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Multiple common variations discovered via genome-wide association studies (GWASs) were shown to have a minimal association with breast cancer (BC) risk in Vietnamese women. This study analyzed the cumulative effect in predicting BC risk of ten single nucleotide polymorphisms (SNPs) identified by previous GWAS and were common in Vietnamese. In this case-control research, 240 BC patients and 271 healthy controls were recruited to assess candidate SNPs' association with BC risk. A polygenic risk score (PRS) was then created from SNPs strongly related to the risk of BC among the assessed population. The area under the receiver operating characteristic curve (AUC) was used to assess the effectiveness of the PRS model with BC risk. Logistic regression results showed seven individual SNPs (rs2155209, rs4784227, rs2605039, rs3817198, rs2981582, rs11614913, and rs12325489) were significantly associated with BC risk after multiple testing. These SNPs were then used to create the PRS model. Compared with women in the lowest quartile, women in the highest quartile of PRS had a considerably higher risk (odds ratio 2.65; 95 % confidence interval (95 % CI) 1.61–4.40) with AUC at 71 %. These findings suggest that the 7-SNP PRS would effectively distinguish between women with high and low risk of BC, indicating the genetic marker for BC risk prediction in a Vietnamese population.

Key words: breast cancer risk; polygenic risk score; risk prediction model; single nucleotide polymorphism; Vietnam.

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ВИКОРИСТАННЯ СЕМИ ОДНОНУКЛЕОТИДНИХ ПОЛІМОРФІЗМІВ В ШКАЛІ ПОЛІГЕННИХ РИЗИКІВ ДЛЯ ПЕРЕДБАЧЕННЯ РИЗИКУ РАКУ МОЛОЧНОЇ ЗАЛОЗИ СЕРЕД НАСЕЛЕННЯ В'ЄТНАМУ

Було встановлено, що велика кількість поширених мінливостей, виявлених за допомогою повногеномного пошуку асоціацій (GWAS), мають мінімальне відношення до ризику раку молочної залози серед жінок В'єтнаму. У цьому дослідженні було проаналізовано кумулятивний вплив передбачення ризику раку молочної залози за використання десяти однонуклеотидних поліморфізмів (SNP), ідентифікованих за допомогою попередніх GWAS та поширених серед населення В'єтнаму. Наше дослідження типу «випадок-контроль» залучило 240 пацієнтів, що страждають від раку молочної залози, та 271 здорову особу з метою оцінки асоціації між запропонованими однонуклеотидними поліморфізмами та ризиком раку молочної залози. Потім однонуклеотидні поліморфізми, суттєво пов'язані з ризиком виникнення раку молочної залози серед досліджуваного населення, були використані для створення шкали полігенних ризиків (PRS). Площу під кривою операційних характеристик (AUC) використали для оцінки ефективності моделі PRS щодо ризику раку молочної залози. Після численних тестів результати логістичної регресії продемонстрували сім окремих однонуклеотидних поліморфізмів (SNP) (rs2155209, rs4784227, rs2605039, rs3817198, rs2981582, rs11614913 і rs12325489) були суттєво пов'язані з ризиком раку молочної залози. Визначені SNP використали для створення моделі PRS. Порівняно з жінками з нижньої чверті, жінки у вищій чверті PRS мали значно вищий ризик (співвідношення ризиків 2,65; рівень достовірності 95 % (95 % CI) 1,61–4,40) з AUC при 71 %. Згідно з цими результатами, шкала PRS з семи однонуклеотидних поліморфізмів дозволяє ефективно вирізняти жінок з високим та низьким ризиком раку молочної залози, виступаючи в якості генетичного маркера для передбачення ризику раку молочної залози серед населення В'єтнаму.

Ключові слова: ризик раку молочної залози; шкала полігенного ризику; модель передбачення ризику; однонуклеотидний поліморфізм; В'єтнам.

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