CONCLUSIONS

Ultrasound is reliable prognostic and diagnostic tools in identifying plasma leakage, hence predicting the severity of diseases and progression of the diseases. Its also shown that when bedside ultrasound findings is combined with POCT result, the sensitivity and predictive values of diagnosing and classifying dengue severity is further enhanced. This is in contrast to using existing laboratory markers in isolation. Henceforth, such patients with evidence of plasma leakage should be managed as severe dengue and merits for intensive care monitoring to minimize the complication.

OP 9
GENETIC VARIANTS THAT ARE ASSOCIATED WITH NEUROPSYCHIATRIC SYSTEMIC LUPUS ERYTHEMATOSUS: A META-ANALYSIS

Roger Ho[1]
[1]Department of Psychological Medicine, Yong Loo Lin School of Medicine National University of Singapore, Singapore

OBJECTIVE

While genetic risks have been implicated in systemic lupus erythematosus (SLE), the roles of various genotypes in neuropsychiatric SLE remain uncertain. The present meta-analysis aimed to combine data from different studies and evaluate the association between each genotype and the risk of developing NPSLE.

METHODS

Studies were searched and retrieved from online databases (PubMed, EMBASE, BIOSIS and Science Direct). Case-control studies containing available genotype frequencies of the gamma Fc region (FCgR) receptors II-A, III-A, and III-B; tumour necrosis factor–alpha (TNF-α); mannan-binding lectin (MBL); integrin alpha M (ITGAM); interleukin–1 (IL-1), IL-1β, and IL-6; IL-10 promoter; and vitamin D genes were chosen. The odds ratio (OR) with a 95% confidence interval (CI) was used to assess the strength of this association between NPSLE and SLE patients.

RESULTS

A total of 33 studies were considered in this meta-analysis. The results suggest that the homozygous FCgR IIIa 158 FF genotype (OR=1.89, p=0.03 for FF vs VV=FV), heterozygous FCgR IIIb NA1/2 genotype (OR=2.14, p=0.03 for NA1/2 vs NA 1/1; OR=1.81, p=0.04), and homozygous ITGAM rs1143679 HH genotype (OR=3.39, p=0.04 for HH vs RH; OR=3.11, p=0.048, for HH vs RR+RH) demonstrated a significant association with NPSLE. Polymorphisms of the TNF-α, MBL2, IL-1, IL-1β, IL-6, IL-10 promoter and vitamin D receptor genes did not show a statistically significant association with the risk of developing NPSLE (p>0.05).

DISCUSSION

This meta-analysis indicates that polymorphisms in the pathways of immune complex clearance, such as the FcγRIIIa, FcγRIIIb and ITGAM genotypes, are potential susceptibility genes for NPSLE.