Background and aims SLE is a multisystem autoimmune disease, having known HLA-DRB1*15 and DRB1*03 risk alleles and an association with EBV in the Caucasoid population. We compared the association of HLA-DRB1 and EBV in North Indian cohort of adult and paediatric SLE.

Methods We analysed 109 adult SLE (aSLE) and 52 paediatric SLE (pSLE) with 278 age and sex matched control adult (CA) and paediatric (CP) for HLA-DRB1 genotyping by PCR-SSP, EBV-IgM and IgG to VCAgp125, VCAp19, EBNA-1, p22 and EA-D by line blot assay and EBV load by real-time PCR.

Results The frequencies of DRB1*15 and DRB1*03 were higher in SLE (OR=2.57 and 1.67 respectively) compared to controls. aSLE had higher frequencies of DRB1*03 (OR=2.33) and DRB1*04 (OR=7.51) compared to pSLE whereas, pSLE had higher frequency of DRB1*15 (OR=2.42) compared to aSLE. pSLE had more 3+ to 4+ positivity of EBV-IgG to VCAgp125 compared to aSLE (p=0.0008). EBV-IgM to VCAp19, EBNA-1 and EA-D (25%, 12.5% and 6.25% respectively) were present only in pSLE. pSLE had higher EBV load compared to aSLE (p=0.045). IgG to p22 and EA-D were associated with DRB1*03 in aSLE (OR=3.92 and 5.28 respectively) and IgG to VCAgp125, VCAp19, EBNA-1, p22 and EA-D were associated with DRB1*15 in pSLE (OR=4.0, 3.44, 4.6, 4.8 and 4.8 respectively).

Conclusions DRB1*15 and DRB1*03 are risk alleles in North Indian SLE. Both show strong associations with immune response to EBV proteins. pSLE has stronger association with DRB1*15, which is associated with early infection, stronger immune response to EBV proteins and higher EB viral load, which may explain more severity of pSLE.

Background and aims To detect the expression of three SLE-susceptible genes, PNP, PLEKHF2 and ANKRD44 in SLE PBMC and lupus nephritis kidney samples, and to investigate their function.

Methods We collected PBMC from 46 SLE patients and 48 healthy controls, and renal biopsy tissues from 12 lupus nephritis patients and peri carcinomatous tissues from 10 patients with kidney cancer. The mRNA expression levels of PNP, PLEKHF2 and ANKRD44 were detected by qPCR. Their expression levels with the SLE clinical features and IFN scores were analysed. ANKRD44 was tested at different time points in Raw264.7 cells during IFN stimulation. The expression of ANKRD44 was knocked down by using siRNA in Raw264.7 cells. The change of IFIGs and the activation of IFN signalling pathway were detected by Real-time PCR and western blotting.

Results PNP, PLEKHF2 and ANKRD44 were found significantly decreased in SLE PBMCs compared with healthy controls. The mRNA expression of PNP and ANKRD44 were significantly decreased while the expression of PLEKHF2 was increased in kidney of lupus nephritis. The expression of PNP was negatively correlated with IFN score in SLE PBMC samples, while the expression of ANKRD44 was negatively correlated with IFN score in lupus nephritis kidney. ANKRD44, which could be down-regulated by IFN alpha, could inhibit the type I IFN signalling pathway and downregulate the expression of IFIGs.

Conclusions PNP and ANKRD44, expressed abnormally and associated with IFN alpha, might be used as new candidate biomarkers for SLE diagnosis; ANKRD44 could repress the IFN downstream pathway, it would be a potential drug target.