ANTI-CARBAMYLATED PROTEIN ANTIBODIES’ LEVELS ARE NEGATIVELY CORRELATED WITH CIRCULATING EFFECTOR T-CELLS IN A COHORT OF PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS

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Background/Purpose Anti-carbamylated protein antibodies (anti-CarP) were detected in a large cohort of patients with Systemic Lupus Erythematosus (SLE) in correlation with erosive arthritis but not with disease activity indexes. In animal models, T-cells may be activated by carbamylated epitopes playing a role in the development of arthritis. The imbalance between circulating regulatory (Treg) and CD28- effector T-cells was described in active SLE patients, explaining its involvement in disease’s pathogenesis. Actually, no data are available about the possible correlation with these T-cell subpopulations and anti-CarP levels in SLE.

Methods Eight SLE patients with a median (10th-90th percentile) SLEDAI-2K=0 (0–4), anti-dsDNA levels=34.1 (15.6–427.4) UI/ml (nv<7), SDI=1 (0–1.3) were enrolled. Serum anti-CarP levels were evaluated using a home-made ELISA (nv<340 AU/ml) and peripheral blood T cell immunophenotyping was done using Flow Cytometry (Beckman Coulter). Treg were defined as CD4+CD127lowCD25high T-cells.

Results Enrolled patients showed levels of anti-CarP=189.38 (93.5–341.1) AU/ml, Treg=2.2 (0–9.1) (% of CD4+), CD4+CD28=7.7 (4.8–22.5) (% of CD4+) and CD4+CD28=30.3 (17.2–35.6) (% of CD8+). Analyzing possible correlations among different T-cell subtypes and anti-CarP levels, a significant inverse correlation was found between these autoantibodies and CD4+CD28- T cells (r=-0.8, p<0.01; Spearman rank correlation). No correlations were found between autoantibodies and other T-cell subpopulations or disease activity/damage indexes.

Conclusions In a small cohort of patients with serologically active SLE, anti-CarP autoantibodies were found as negatively correlated to circulating CD4+CD28- T-cells, which were described in association with disease damage, independently of age, gender, disease duration and activity. This suggest a potential role of anti-CarP as marker of SLE with a minor extent of T-cell activation and, consequently, with a possible better prognosis.

THE COMBINED TYPE-I INTERFERON AND NEUTROPHIL GENE SCORES IDENTIFY HIGHLY ACTIVE SYSTEMIC LUPUS ERYTHEMATOSUS PATIENTS AND PERFORMED BETTER THAN CLASSICAL SEROLOGICAL MARKERS

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Background In SLE, heterogeneous clinical expression and activity may reflect diverse pathogenic and/or effector mechanisms. We dwelled into SLE heterogeneity by assessing the expression of three gene sets representative of type I interferon (IFN-I), neutrophil-(PMN) and plasmablast-(PB) signatures in a well characterized, multidisciplinary cohort of SLE patients. We further assessed whether individual gene products could be representative of these three signatures.

Methods Whole blood, serum and clinical data were obtained from 140 SLE individuals. Gene expression was assessed by NanoString® technology, using a panel of 37 probes allowing the computation of six IFN-I, one PMN and one PB scores.

Protein levels were measured by ELISA.

Results High IFN-I gene expression was found in 45 to 50% of SLE individuals, depending on the score used. All 6 IFN-I scores were significantly associated with active skin involvement and 2 of 6 with arthritis. Interferon-induced GTP-binding protein Mx1 (MX1) correlated with IFN-I score (p<0.0001) and was associated with a similar clinical phenotype. High PMN gene expression was found in 25% of individuals in association with SLE fever, serositis, leukopenia and glucocorticoid use. PB gene expression was highly influenced by immunosuppressant agents with no association with SLE features. The combined IFN-I and PMN gene expression was significantly associated with high disease activity and overperformed anti-dsDNA, anti C1q and complement levels to predict SLE activity.

Conclusions The IFN-I and PMN gene scores segregate with distinct SLE clinical features and their joint expression identify high disease activity. MX1 protein levels perform similarly to IFN-I gene expression.

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