

INFLUENCE OF JAK/STAT SINGLE NUCLEOTIDE POLYMORPHISMS AND CARDIOVASCULAR EVENTS DURING TREATMENT OF RHEUMATOID ARTHRITIS PATIENT IN A TERTIARY LEVEL HOSPITAL.

A. MARTÍN ROLDÁN¹, N. MÁRQUEZ PETE², M.D.M. SÁNCHEZ SUAREZ³, A. JIMÉNEZ MORALES⁴.

¹HOSPITAL CLÍNICO UNIVERSITARIO DE VALLADOLID, PHARMACY, VALLADOLID, SPAIN.

²HOSPITAL UNIVERSITARIO DE TOLEDO, CLINICAL ANALYSIS DEPARTMENT, TOLEDO, SPAIN.

³HOSPITAL COMARCAL DE BAZA, PHARMACY, GRANADA, SPAIN.

⁴HOSPITAL UNIVERSITARIO VIRGEN DE LAS NIEVES, PHARMACY, GRANADA, SPAIN.

□ Background and importance

Patients with rheumatoid arthritis(RA) are at higher risk of cardiovascular disease(CVD) due to systemic inflammation and treatment-related factors. The JAK/STAT signaling pathway plays a central role in immune modulation. Genetic variability in this pathway may influence cardiovascular outcomes during treatment in RA patients.

□ Aim and objective

To evaluate the potential association between five single nucleotide polymorphisms (SNPs) (rs10119004, rs7857730, rs2274472, rs2230722, rs2230724) in JAK2 gene involved in the JAK/STAT pathway and the development of cardiovascular disease during treatment in patients diagnosed with RA.

□ Matherial and methods

Ambispective observational cohort study in 115 RA patients who had been treated with JAKi. Genotypes were determined by Taqman PCR Real Time. Quantitative variables: age, body mass index(BMI), disease duration, previous biologic therapies (BTs), Charlson Comorbidity Index(CCI). Qualitative variables: sex, first JAKi used, rheumatoid factor, Anti-cyclic citrullinated peptide antibody (ACPA, development of CVD during treatment, previous hypertension or antihypertensive treatment. Data were collected from electronic prescriptions and medical records, and analyzed with R Commander.

□ Results

Population

115 patients

94 women(81.7%)

Median age: 43 years[33–51]

ACPA-positive (82.6%)

RF-positive(74.8%)

CCI was 1.5[0–3]

BMI 27.3[24.3–31.2]

2 prior biologic therapies[1.0-3.2]

Median treatment duration 21 months[13-40]

Previous hypertension was present in 34 patients (29.5%) with 29(25.2%) receiving antihypertensive therapy prior to JAKi treatment

The bivariate analysis revealed that patients with rs2230722 SNP in JAK2 gene showed a statistically significant association with cardiovascular outcomes. Patients carrying the T allele had a notably lower risk of developing cardiovascular disease compared to those with the C allele ($p = 0.002$; OR = 8.44; 95% CI 95%: 2.26–55.02).

□ Conclusions and relevance

Our findings suggest that certain polymorphisms within the JAK/STAT pathway, may influence the risk of CVD during treatment. These preliminary results support further investigation into pharmacogenetic profiling as a tool to stratify cardiovascular risk in RA patients and guide personalized therapeutic strategies.