PSORIASIS

WHY WE ARE DIFFERENT: SEX ASSOCIATED METHYLATION DIFFERENCES IN PSORIASIS

Mar Llamas-velasco [1] - Ancor Sanz-garcia [2] - Alejandra Reolid [1] - Ester Muñoz-aceituno [3] - Lola Alonso-guirado [4] - Esteban Dauden [1] - Francisco Abad-santos [5] - Maria Carmen Ovejero-benito [5]

Hospital Universitario De La Princesa, Instituto De Investigación Sanitaria La Princesa (iis-ip), Madrid, Spain, Dermatology, Madrid, Spain [1] - Hospital Universitario De La Princesa, Instituto De Investigación Sanitaria La Princesa (iis-ip), Madrid, Spain, Data Analysis, Madrid, Spain [2] - Hospital Universitario De La Princesa, Instituto De Investigación Sanitaria La Princesa (iis-ip), Madrid, Spain, Dermatology, Madrid, Spain [3] - Genetic & Molecular Epidemiology Group, Spanish National Cancer Research Center (cnio), Genetic, Madrid, Spain [4] - Hospital Universitario De La Princesa, Instituto Teófilo Hernando, Universidad Autónoma De Madrid (uam), Instituto De Investigación Sanitaria La Princ, Clinical Pharmacology, Madrid, Spain [5]

Recent studies have shown that psoriasis' severity is higher in males than in females. However, the biologic mechanism underlying this fact is still unknown. Thus, we have analyzed sex-associated differences in DNA methylation in psoriasis patients. For this purpose, we have carried out an epigenome-wide association study in blood samples obtained from 70 moderate-to-severe psoriasis patients treated with anti-TNF drugs. Furthermore, methylation data precedent from 76 healthy subjects were used as controls. Both data sets were analyzed with R Bioconductor with the ChAMP pipeline. We found that there were 564 DMS (differentially methylated sites) between male (n=43) and female (n=27) psoriasis patients. From these sites, only 153 were coincident with the sex-associated DMS found in healthy controls. Thus, a total of 411 sex-associated DMS were exclusively found in psoriasis patients. Among these DMS, 135 (32.8%) were hypomethylated and 276 (67.2%) were hypermethylated in females with respect to males. Several of these sites were located on genes which have been previously related to psoriasis such as APOB, CYP1A1, MTFR1, ZPBP2 and RHCG. Furthermore, 4 more genes showed sex-associated DMS exclusive of psoriasis (C19orf77, FRG1B, PPP1R3G and SCAND3) in different locations. These epigenetic marks were located in the same region (promotor, intergenic region) and showed the same kind of regulation (hypomethylation or hypermethylation) suggesting that they modulate the expression of these genes. Therefore, these findings suggest that the patients' sex should be considered in the management of psoriasis and in the prevention and treatment of its comorbidities.