Exploring and managing inequalities in RMD healthcare

SomeONE LIKE ME: THE EFFICACY OF A PEER MENTORING INTERVENTION ON DISEASE SELF-MANAGEMENT AND HEALTH-RELATED QUALITY OF LIFE AMONG AFRICAN AMERICAN WOMEN WITH SYSTEMIC LUPUS ERYTHEMATOSUS (SLE)

Keywords: Quality of life, Systemic lupus erythematosus, Self-management

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Background: Disease self-management indicates practical ways to deal with pain, fatigue, and stress and can include better nutrition, exercise, understanding treatment options, and better communication. Evidence-based self-management interventions designed to enhance social support and provide health education, among lupus patients, have demonstrated significant improvements in health distress, self-reported global health, and activity limitation, but African Americans and women are still disproportionately impacted by systemic lupus erythematosus (SLE).

Objectives: The purpose of this study was to determine whether participation in a new, culturally tailored peer mentoring intervention was associated with improvements in disease self-management and health related quality of life (HRQOL) among African American women with systemic lupus erythematosus (SLE).

Methods: The Peer Approaches to Lupus Self-Management (PALS) study was a randomized controlled trial wherein modeling and reinforcement of disease self-management skills by peers (mentors) to other African American women with SLE (mentees) was achieved through a combination of educational and informal phone or video interactions with each other. The control condition included small support groups that met on the same schedule as peer mentoring sessions. The Lupus Quality of Life questionnaire (LUP-QOL), which incorporates the Medical Outcomes Study (MOS) Short Form 36 Health Survey (SF-36) and the Functional Assessment of Chronic Illness Therapy-Fatigue (FACIT-F), was used to determine HRQOL, and the Patient Activation Measure (PAM) assessed disease self-management or an individual's knowledge, skill, and confidence for managing their health and healthcare. Generalized Linear Mixed Models were used to determine whether the intervention produced a greater change in these main outcomes from baseline, controlling for education, income, and age, reported.

Results: Of the 314 enrolled PALS participants, 138 were mentored (experimental), 132 participated in small support groups (controls), and 44 served as mentors. Although not statistically significant, there were incrementally improving trends in patient activation as the intervention progressed, among mentors and experimental participants and decreasing trends in depression and anxiety among experimental participants. Measures of social functioning (from the LUP-QOL) and coping (or lupus self-efficacy) significantly improved from baseline, among experimental participants (both p < 0.05).

Conclusion: Our findings suggest that participation in a peer mentoring intervention led to improvements in disease self-management and HRQOL, in areas of social functioning, coping, depression, and anxiety, among African American women with SLE. Since these factors are related to disease activity and morbidity/damage, future investigations should consider ways in which this approach can augment clinical care on a larger scale.
Clinical and molecular differences across sexes in Rheumatic Disease

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Background: Juvenile idiopathic arthritis (JIA) encompasses a group of childhood onset rheumatic diseases that primarily affect females. JIA has been reported to occur in females and males with a 2:1 ratio, however, systemic JIA is reported more frequently in male patients. Genetic risk factors may contribute to the sex dimorphism in JIA incidence, however this contribution has yet to be defined.

Objectives: To investigate, using sex dimorphism analysis, whether genetic risk factors for JIA differ in males and females.

Methods: High quality genotype data was available on 3356 JIA cases (females = 2209, males =1147) and 9196 controls (female =4059, males =5137). Our primary analysis combined sex-specific GWAS summary statistics using the GWAMA software package. Summary statistics were calculated using logistic regression with three principal components as covariates using PLINK. The sex-differentiated p-value (psex) provided overall evidence for association to JIA allowing for differences between males and females, and the heterogeneity p-value (phet) provided evidence to support a difference in effect estimates between sexes. As a secondary analysis we performed a logistic regression, as above, on all samples and included sex as an interaction term (pint) provided sex specific differences.

Results: A total of 6571296 SNPs were analysed after quality control. The strongest signal detected using a logistic regression in females was rs9469137 (p = 1.7x10^-5) and in males it was rs11666910 (p = 9.7x10^-5). GWAMA supported evidence of sex heterogeneity for these SNPs, rs9469137 psex = 2.2x10^-10, ORfemale = 2.6, ORmale = 5.3, rs11666910 psex = 1.8x10^-14, ORfemale = 4.0, ORmale = 1.6. The strongest signal from the sex-specific GWAS was rs9266716, psex = 1.9x10^-17, ORfemale = 7.7x10^-16, ORmale = 1.2, ORfemale = 0.6. These SNPs all map to the HLA region, providing strong evidence for sex dimorphism in this region, therefore sex-specific HLA fine mapping was conducted. This analysis revealed that residues at position 13 of HLA-DRB1 were strongly associated with JIA in females (pint = 1.8x10^-15). Glycine at position 13 of HLA-B27 is a well-established risk factor for ERA, where males are predominately affected. Outside of the HLA region, the strongest associated SNP was rs9469137 phet = 4.0, ORfemale = 1.9, ORmale = 0.6. These SNPs all map to the HLA region, providing strong evidence for sex dimorphism in this region, therefore sex-specific HLA fine mapping was conducted. This analysis revealed that residues at position 13 of HLA-DRB1 were strongly associated with JIA in females (pint = 1.8x10^-15). Glycine at position 13 of HLA-B27 was detected as strongly associated with JIA in male patients (pint = 5.4x10^-14, ORmale = 3.8, ORfemale = 5.2x10^-5, ORfemale = 1.6). An association test with sex as an interaction term revealed glycine at position 13 as sex dimorphic, p = 4.3x10^-11. Associations of residues at position 13 of HLA-DRB1 have previously been reported in JIA, where the cohort consisted of oligoarthritis and rheumatoid factor negative polyarthritis individuals. These ILAR subtypes have a greater frequency in females. HLA-B27 was detected as strongly associated with JIA in females (pint = 6.3x10^-8, ORfemale = 3.8, ORmale = 0.7). This SNP is located near the BPN2 gene and had a greater effect size in males.

Conclusion: This analysis reveals that there are several sexually dimorphic genetic risk factors that may affect JIA development in males and females. For the first time markers within the HLA region have been detected as sex dimorphic. Understanding the genetic risk factors to JIA development will help to further define the disease, which may aid in disease classification and diagnosis in the future. In particular, the substantial differences in effect estimates observed between males and females suggests that sex-specific polygenic risk scores should be considered when HLA signals are incorporated into these efforts.

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SEX DIMORPHISM ANALYSIS IN A COHORT OF JIA PATIENTS REVEALS DIFFERING GENETIC RISK FACTORS FOR FEMALES AND MALES

Keywords: Inflammatory arthritides, Genetics/Epigenetics, Gender/diversity issues

Figure 1.

Phenotypic outcomes in JIA patients are affected by varying genetic factors, and sex plays a significant role in the development and susceptibility to these conditions. Understanding the genetic basis of JIA is crucial for personalized treatment approaches.

Figure 1 illustrates the phenotypic outcomes in JIA patients, highlighting the importance of genetic factors and the impact of sex differences. The figure underscores the need for further research into genetic risk factors that may affect JIA development in males and females.

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