PAIN OF 500 COMMUNITY REFERRALS FOR SHOULDER PATHOLOGIES: CLUSTER INTO GROUPS WITH DIFFERENT CLINICAL ASSOCIATIONS: DATA FROM A PROSPECTIVE STUDY OF 500 COMMUNITY REFERRALS FOR SHOULDER PAIN

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Background: Shoulder pain is common and its management remains challenging, often resulting in poor outcomes: 50% of people continue to have shoulder pain at 18 months. This may be in part due to inaccurate clinical diagnosis. Ultrasound offers accurate detection of pathology and its use is increasing. However, the relationship between ultrasound findings and clinical phenotype is unclear.

Objectives: A prospective study was undertaken to explore latent class groupings and explore the association between patient reported outcome measures and the different groups.

Methods: 500 primary care patients attending for shoulder ultrasound were prospectively recruited. Radiologists and sonographers underwent training to ensure standardised reporting. Baseline data was collected via self-reported questionnaires. Outcome measures collected included pain, function, quality of life, treatments received, activity, self-efficacy and levels of acceptable symptom states. These measures underwent Rasch analysis. Latent class analysis was undertaken to identify groups.

Results: Mean age was 53.6% and 52% were female. Latent class analysis confirmed the existence of 4 groups: limited bursitis; extensive inflammation; RC tears; limited pathology. The oldest age group were those with RC tears, and the youngest was those with limited bursitis. The rotator cuff tear group had the highest level of pain and disability, and the lowest levels of acceptable symptom states. Those with limited pathology had the highest levels of acceptable symptom states. The extensive inflammation group had the lowest activity scores. Summary statistics for classes obtained prior to covariate adjustment (complete data only)

Conclusions: This study confirms that ultrasound pathologies cluster into groups. These groups appear to differ in symptom associations at baseline; expanding the LCA to include covariates will allow us to formally explore these associations. A longitudinal study will provide understanding of the relevance of these groups to long-term patient outcomes.

Disclosure of Interest: None declared

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OP0075

ASSOCIATION BETWEEN BRAIN-DERIVED NEUROTROPHIC FACTOR GENE POLYMORPHISMS AND FIBROMYALgia IN A KOREAN POPULATION: A MULTI-CENTRE STUDY

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Objectives: Several lines of evidence suggest that brain-derived neurotrophic factor (BDNF) is involved in the pathophysiology of fibromyalgia (FM) and studies have found that FM patients have altered serum and plasma BDNF levels. How-ever, it is not known whether polymorphisms of the BDNF gene are associated with FM. In this study, we explored the association between polymorphisms of the BDNF gene with FM susceptibility and the severity of symptoms.

Methods: The study enrolled 409 patients with FM and 423 controls from 10 medical centres that participated in the Korean nationwide FM survey study. Alleles at 10 positions in the BDNF gene were genotyped: rs2853187 (C>T); rs7103873 (G>C); rs7103411 (C>T); rs10835210 (C>A); rs11301004 (A>G); rs12273539 (C>T); rs11030102 (G>C); rs11030101 (A>T); rs62625 (G>A); and rs7124442 (C>T).

Results: The allele and genotype frequencies of BDNF rs11030104 differed significantly between the FM patients and controls (p<0.031). The GG genotype of rs11030104 had a protective role against FM (p=0.016) and the G allele of rs11030104 was negatively associated with the presence of FM compared with the A allele (p=0.013). In comparison, although the allele and genotype frequencies of BDNF rs12273539 did not differ between the FM patients and controls, the TT genotype of BDNF rs12273539 was associated with susceptibility to FM (p=0.038). Haplotype analyses suggested that some BDNF haplotypes have a protective role against FM. Finally, we found that some genotypes and haplotypes of the BDNF gene contribute to the specific symptoms of FM.

Conclusions: This study is the first to evaluate the associations of BDNF gene polymorphisms with FM. Our results suggest that some BDNF single-nucleotide polymorphisms and haplotypes are associated with susceptibility to, and contribute to the symptoms of, FM.

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