(204) Mild to moderate knee osteoarthritis causes peripheral and central pain sensitization and reduced quality of life

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The purpose of this study was to determine if individuals with mild to moderate knee osteoarthritis (OA) experience hyperalgesia and central sensitization by comparing them to healthy age and sex-matched control subjects and to determine if levels of hyperalgesia and central sensitization are associated with pain intensity at rest and during movement. A secondary purpose was to determine if these individuals experience significantly poorer quality of life than healthy subjects and if pain and function predict their quality of life. Seventy-five knee OA subjects and 25 age and sex-matched healthy controls were enrolled. Quantitative sensory tests (QST), including punctate pain intensity (PPI), pressure pain threshold (PPT), heat pain threshold (HPT), heat pain tolerance (HPTol), and heat temporal summation (TS), measured primary and secondary hyperalgesia and central sensitization. Pain intensity at rest and during movement was assessed on a 10 cm Visual Analog Scale, walking function was measured with the Timed Up and Go (TUG) test and the Medical Outcomes Study Short Form 36 (SF-36) measured quality of life. Significant differences were found for PPI at proximal and distant sites, for PPT and TS at the affected knee, and for all SF-36 scores. QST measures were significantly related to pain intensity at rest and during movement. Pain, but not function, predicted quality of life in knee OA subjects. This study shows that individuals with mild to moderate knee OA are already experiencing peripheral and central pain sensitization which relates to the level of perceived pain. These individuals also have a reduced quality of life which is predicted by the level of perceived pain. These results suggest that aggressive pain management during this early period is indicated to improve the quality of life for these individuals who are not yet candidates for joint replacement.

(206) Variations in inflammatory cytokine genes are associated with persistent severe breast pain after breast cancer surgery

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Persistent pain following breast cancer surgery is a significant problem. Immune mechanisms appear to play a central role in the development and maintenance of persistent pain. Few studies have evaluated for associations between persistent breast pain following breast cancer surgery and variations in genes that encode for inflammatory cytokines. Recently, we used growth mixture modeling to identify latent classes (i.e., subgroups) of patients with distinct trajectories of worst breast pain scores using a 0-10 numeric rating scale (NRS), reported prior to and monthly for 6 months after surgery. Four subgroups were identified: 126 patients (31.7%) with "No Pain", 173 (43.4%) with "Mild Pain" (NRS of ~3 that remained constant), 53 (13.3%) with "Moderate Pain" (NRS of ~2 that increased over time), and 46 (11.6%) with "Severe Pain" (NRS of ~8 that remained constant). The purpose of this study was to evaluate for associations between single nucleotide polymorphisms (SNPs) among 15 cytokine genes and persistent breast pain after surgery (i.e., No Pain GMM group and Severe Pain GMM group). Women in the Severe Pain group, compared to the No Pain group, differed on a number of demographic (i.e., age, years of education, income, ethnicity, comorbidities, functional status), pre-operative (i.e., pain in the breast prior to surgery), intraoperative (i.e., number of lymph modes removed), and post-operative (i.e., worst postoperative pain scores, re-excision or mastectomy within 6 months after surgery) characteristics (all $p<0.05$). After adjustment for severity of worst postoperative pain, three SNPs (i.e., interleukin (IL) 1 receptor 2: rs11674595; IL4 rs2243248; IL13: rs1800925) were associated with pain group membership. These findings suggest a role for cytokine gene polymorphisms in the development of severe persistent pain following breast cancer surgery. These variations may help to identify patients who are predisposed to the development of severe persistent breast pain following breast cancer surgery.

B03 Cancer, AIDS/HIV Pain

(205) Variations in potassium channel genes are associated with severe persistent breast pain after breast cancer surgery

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Persistent pain after breast cancer surgery is common with prevalence rates that range from 25% to 80%. Recently, we used growth mixture modeling to identify latent classes (i.e., subgroups) of patients with distinct trajectories of worst breast pain scores using a 0-10 numeric rating scale (NRS), reported prior to and monthly for 6 months after surgery. Four subgroups were identified: 126 patients (31.7%) with "No Pain", 173 (43.4%) with "Mild Pain" (NRS of ~3 that remained constant), 53 (13.3%) with "Moderate Pain" (NRS of ~2 that increased over time), and 46 (11.6%) with "Severe Pain" (NRS of ~8 that remained constant). Given their role in nociceptive transmission, we previously identified associations between preoperative, post-operative, and persistent mild pain in the breast (i.e., Mild Pain GMM group) with variations in a number of potassium (K+) channel genes. The purpose of this study was to test for associations between single nucleotide polymorphisms (SNPs) in 10 K+ channel genes and severe persistent breast pain after surgery (i.e., Severe Pain GMM group). Compared to the No Pain group, patients in the Severe Pain group differed in several demographic (i.e., age, years of education, ethnicity, annual income), clinical (i.e., functional status, number of comorbidities, pain in the breast prior to surgery), intraoperative (i.e., number of lymph nodes removed, axillary lymph node dissection, and post-operative (i.e., severity of average and worst post-operative pain, re-excision or mastectomy during the 6 months following surgery) characteristics (all $p<0.05$). Significant associations were found between variations in 5 genes [KCND2 (n=4, $p<.05$), KCNJ3 (n=8, all $p<.05$), KCNJ6 (n=3, all $p<.05$), KCNK3 (n=2, all $p<.05$) and KCNK9 (n=1, $p<.05$)] and pain group membership. K+ channel gene variations and specific demographic and clinical characteristics are associated with a novel phenotypic characterization of persistent severe breast pain after breast cancer surgery.

(207) Variations in potassium channel genes are associated with persistent mild breast pain after breast cancer surgery

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Persistent pain after breast cancer surgery is common, and substantial individual variability exists in terms of its severity. Given their role in nociceptive transmission and our previous finding of an association with preoperative breast pain, we hypothesized that variations in potassium (K+) channel genes would be associated with persistent breast pain after breast cancer surgery. Therefore, the purpose of this study was to test for associations of single nucleotide polymorphisms (SNPs) and inferred haplotypes among 10 K+ channel genes and the occurrence of persistent breast pain after surgery. Growth mixture modeling was used to identify latent classes (i.e., subgroups) of patients with distinct trajectories of worst pain scores using a 0-10 numeric rating scale (NRS), reported prior to and monthly for 6 months after surgery. Four subgroups were identified: 126 patients (31.7%) with "No Pain", 173 (43.4%) with "Mild Pain" (NRS of ~3 that remained constant), 53 (13.3%) with "Moderate Pain" (NRS of ~2 that increased over time), and 46 (11.6%) with "Severe Pain" (NRS of ~8 that remained constant). Comparisons were made between the two largest classes (i.e., No Pain and Mild Pain). Compared to the No Pain group, patients in the Mild Pain group were younger ($p<.01$), poorer functioning ($p<.05$), had more lymph nodes removed ($p=.02$), more frequently had reconstruction at the time of surgery ($p<.01$), were pre-menopausal ($p<.05$), and had strange sensations in the breast prior to surgery ($p<.001$). Significant associations were found between variations in 6 genes [KCNA1 (n=1, $p<.01$), KCND2 (n=1, $p<.05$), KCNJ3 (n=6, all $p<.05$), KCNJ6 (n=10, all $p<.05$), KCNK9 (n=3, all $p<.05$) and KCNS1 (n=2, both $p<.05$)] and pain group membership. K+ channel gene variations and distinct demographic and clinical characteristics are associated with a novel phenotypic characterization of persistent breast pain after breast cancer surgery.