Group 2 included 112 patients who underwent open gastroctomy or open colectomy and postoperative continuous epidural analgesia. In both groups, patients with chronic pain or severe systemic disease, patients who took any analgesics, psychotherapeutic drugs, anti-anxiety drugs, or anticonvulsants were excluded. There was no difference in age, body height or weight between patients with or without the minor G allele of the rs3845336 SNP in both groups. Carriers of the minor G allele had higher opioid requirements in Group 1, while reporting higher pain scores in Group 2. Altogether, carriers of the minor G allele exhibited enhanced pain-related phenotypes after gastrointestinal surgery, in contrast to reduced pain-related phenotypes after orthognathic surgery. These results suggest that this SNP enhances pain-related phenotypes after gastrointestinal surgery, possibly through impairment of CaV2.3 VACCs responsible for activation of visceral inflammatory pain stimulus-elicited antinociception.

PT636
Association between the rs7583431 single-nucleotide polymorphism close to the activating transcription factor 2 (ATF2) gene and the analgesic effect of fentanyl in the preoperative cold pressor-induced pain test
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Abstract
Background: Activating transcription factor 2 (ATF2) is a member of the leucine zipper family of DNA-binding proteins and is widely distributed in tissues. Several recent studies have demonstrated that this protein is involved in mechanisms related to pain and inflammation. However, polymorphisms of the ATF2 gene is unclear that encodes the human ATF2 influence pain sensitivity. The ATF2 gene is known to be highly polymorphic. Thus the present study examined associations between the analgesic effect of fentanyl in the preoperative cold pressor-induced pain test and polymorphisms in the ATF2 gene in 355 Japanese patients who underwent orthognathic surgery.

Result: In the present study, 39 single nucleotide polymorphisms (SNPs) were polymorphic, and a total of 2 linkage disequilibrium blocks with 7 Tag SNPs (rs1153711, rs1153702, rs7583431, rs2302663, rs3845744, rs1205399, and rs268214) were observed in the region within and around the ATF2 gene. Thus, we further analyzed associations between these seven SNPs and clinical data. Result of multiple testing such as Bonferroni adjustments, for the rs7583431 SNP, the analgesic effect of fentanyl in the preoperative cold pressor-induced pain test of the subjects in the AA group was significantly greater than in the AC + CC group (Mann-Whitney U-test, P = 0.007).

Conclusions: The present findings may contribute to adequate postoperative pain relief in individual patients. Although more research on the genetic factors that influence opioid sensitivity is necessary, postoperative analgesic requirements may be predicted before surgery by analyzing the ATF2 SNP, together with other polymorphisms in the genes that are reportedly associated with opioid sensitivity, such as OPRM1 and GIRK2.

PT637
[11C-](R)-PK11195 positron emission tomography in patients with complex regional pain syndrome: a pilot study
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Abstract
Complex regional pain syndrome is characterized by severe and chronic pain, but the pathophysiology of this disease are not clearly understood. The primary aim of our study was to explore neuroinflammation in patients with complex regional pain syndrome (CRPS) using positron emission tomography (PET), with an 18kDa translocator protein (TSPO) specific radioligand [11C-](R)-PK11195. [11C-](R)-PK11195 PET scans were acquired for eleven patients with CRPS (age: 30–55 years) and twelve control subjects (age: 30–52 years). Parametric image of distribution volume ratio (DVR) for each participant was generated by applying a relative equilibrium-based graphical analysis. The DVR of [11C-](R)-PK11195 in the caudate nucleus (t21 = −3.209, p = 0.002), globus pallidus (t(21) = −2.045, p = 0.027), putamen (t21 = −2.492, p = 0.011), nucleus accumbens (t21 = −2.218, p = 0.019), thalamus (t21 = −2.395, p = 0.013), postcentral gyrus (t21 = −1.996, p = 0.03) and precentral gyrus (t21 = −1.839, p = 0.04) were significantly higher in CRPS patients than in healthy controls. In patients with CRPS, there was a strong positive correlation between the DVR of [11C-](R)-PK11195 in the caudate nucleus and the pain score, the Visual Analogue Scale (r = 0.639, p = 0.034) and affective subscales of McGill Pain Questionnaire (r = 0.604, p = 0.049). We demonstrated that neuroinflammation in CRPS patients from basal ganglia (BG) to cortical region. Our results suggest that microglial pathology can be an important pathophysiology of CRPS. Association between the level of caudate nucleus and pain severity indicated that neuroinflammation in this region might play a key role. These results may be essential for developing effective medical treatments.

PT638
Translational research of chronic pain patients using human blood-induced microglia-like (iMG) cells
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Abstract
Fibromyalgia is a refractory disease characterized by chronic pain, the cause of which has not yet been elucidated due to its complex pathology. Recently, activation of immune cells in the brain called microglia has attracted attention as a potential underlying pathological mechanism in chronic pain. Until recently, however, technological and ethical considerations have limited the ability to conduct research using human microglia. We have developed a technique to create human-induced microglia-like (iMG) cells from human peripheral blood monocytes.

This study was conducted to observe microglia activation in patients with fibromyalgia at the cell level using iMG technique. iMG cells were created from 14 patients with fibromyalgia and 10 healthy individuals, and analyzed at the molecular cell level. No significant difference in phagocytic capacity was observed between iMG cells derived from healthy participants and patients with fibromyalgia. Interestingly, however, TNF-α gene expression level and protein concentrations significantly increased in ATP-stimulated iMG cells from patients with fibromyalgia compared to cells from healthy individuals. Moreover,