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# Association of Proinflammatory Gene Polymorphisms with Pain-Related Temporomandibular Disorder

ID 0294

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## AIM

This study aimed to investigate the association between single nucleotide polymorphisms (SNPs) in proinflammatory cytokine (*TNF* and *TGFB1*) and chemokine (*CXCL8*) genes with **painful temporomandibular disorders** (TMDp) (Figure 1).

TACCA[G/T]GTAGC

Figure 1. SNP rs2227307 (*CXCL8*) with single nucleotide variants G or T.

([https://www.thermofisher.com/order/genome-database/details/genotyping/C\\_11748168\\_10?CID=&ICID=&subtype](https://www.thermofisher.com/order/genome-database/details/genotyping/C_11748168_10?CID=&ICID=&subtype))

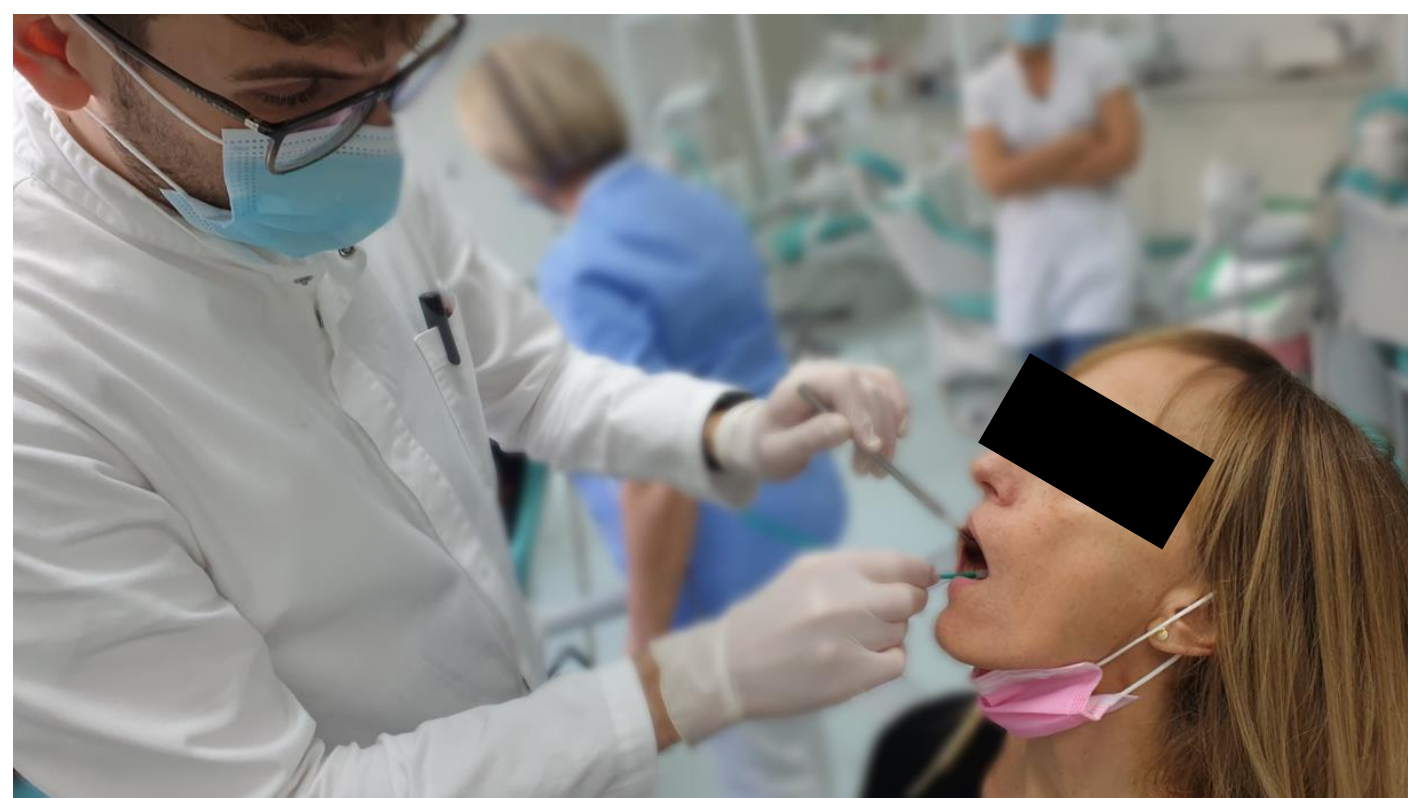


Figure 2. Buccal Mucosa Swabs

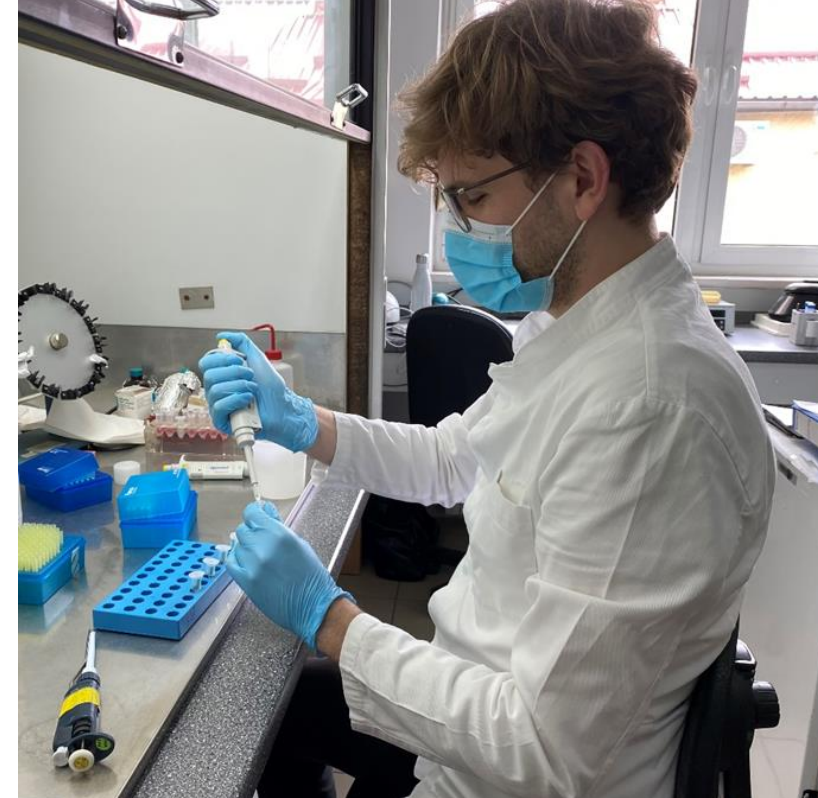


Figure 3. Pipetting DNA Samples for Genotyping

## METHODS

Diagnosis of TMDp involves myalgia and/or arthralgia. The study included **170 individuals**: 85 with diagnosed TMDp and 85 healthy controls (CTR). In the TMDp group, the average age was 29.96, with 76 females (89.41%) and 9 males (10.59%). In the control group, the average age was 26.23, with 62 females (72.88%) and 23 males (27.12%).

Intensity of orofacial pain was measured through Characteristic Pain Intensity (CPI) score from **Graded Chronic Pain Scale**, whereas TMD patients with CPI>50 were considered as a high pain intensity group (HPI).

Genomic DNA was extracted from buccal mucosa swabs (Figure 2). Single nucleotide **polymorphisms** (SNPs) in genes encoding **interleukin 8** (*CXCL8*; rs2227306, rs2227307), **transforming growth factor  $\beta$**  (*TGFB1*, rs4803455) and **tumour necrosis factor-alpha** (*TNF*, rs1800629) were analysed by real time-PCR using Taqman Genotyping assays (Figure 3).

The assessment was performed according to dominant and recessive genetic models where minor allele represented the risk allele. Chi-Square Test, Fisher's Exact Test and Mann-Whitney U test were used for data analysis.

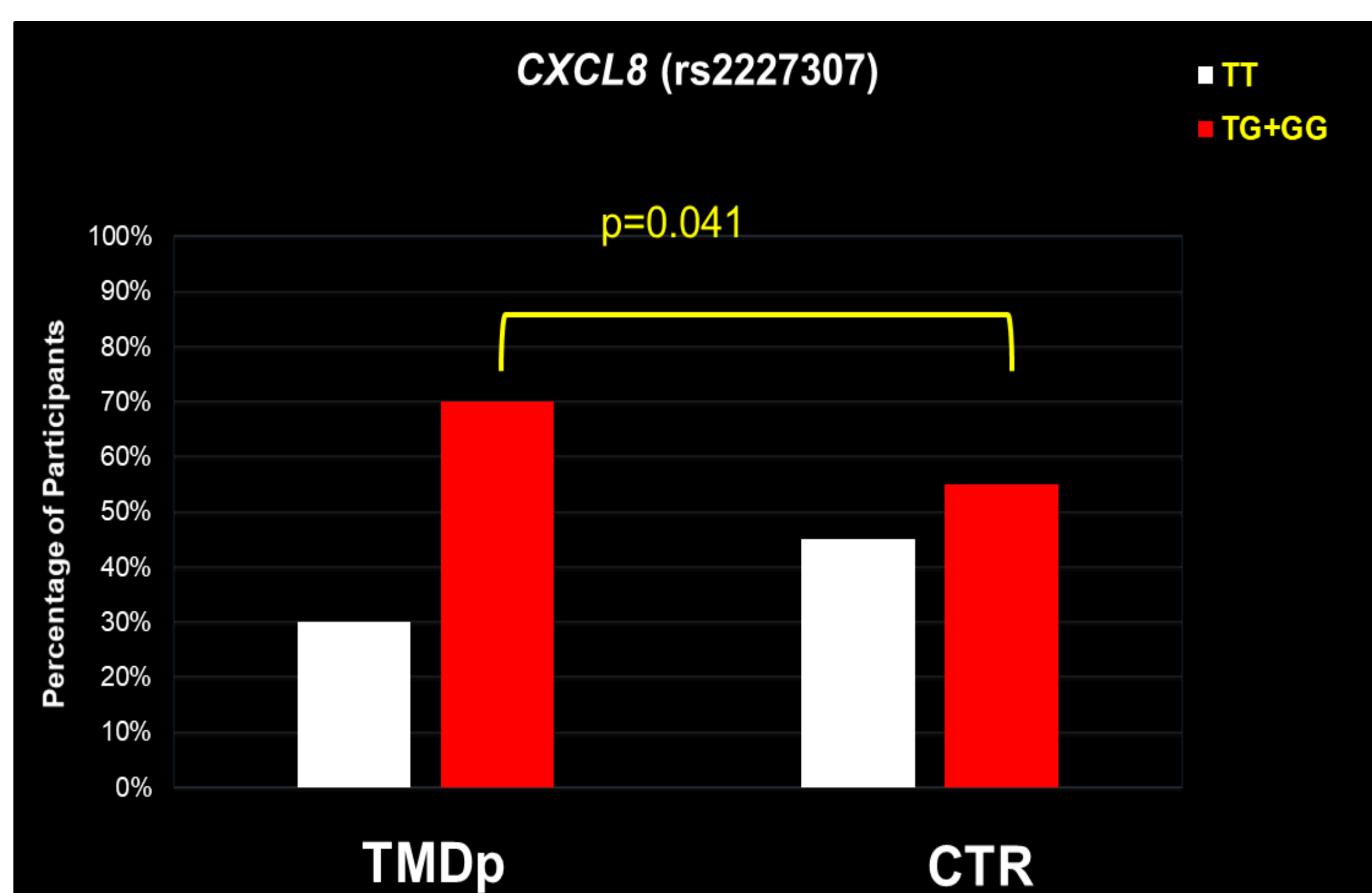


Figure 4. Genotype distribution between Pain-Related Temporomandibular Disorders (TMDp) vs. Controls (CTR) in *CXCL8* (rs2227307)

## FUNDING

Croatian Science Foundation Project IP-2019-04-6211 (PI: Iva Alajbeg) and "Young Researchers' Career Development Project - Training of Doctoral Students" (DOK-2020-01) (student: Marko Zlendić).

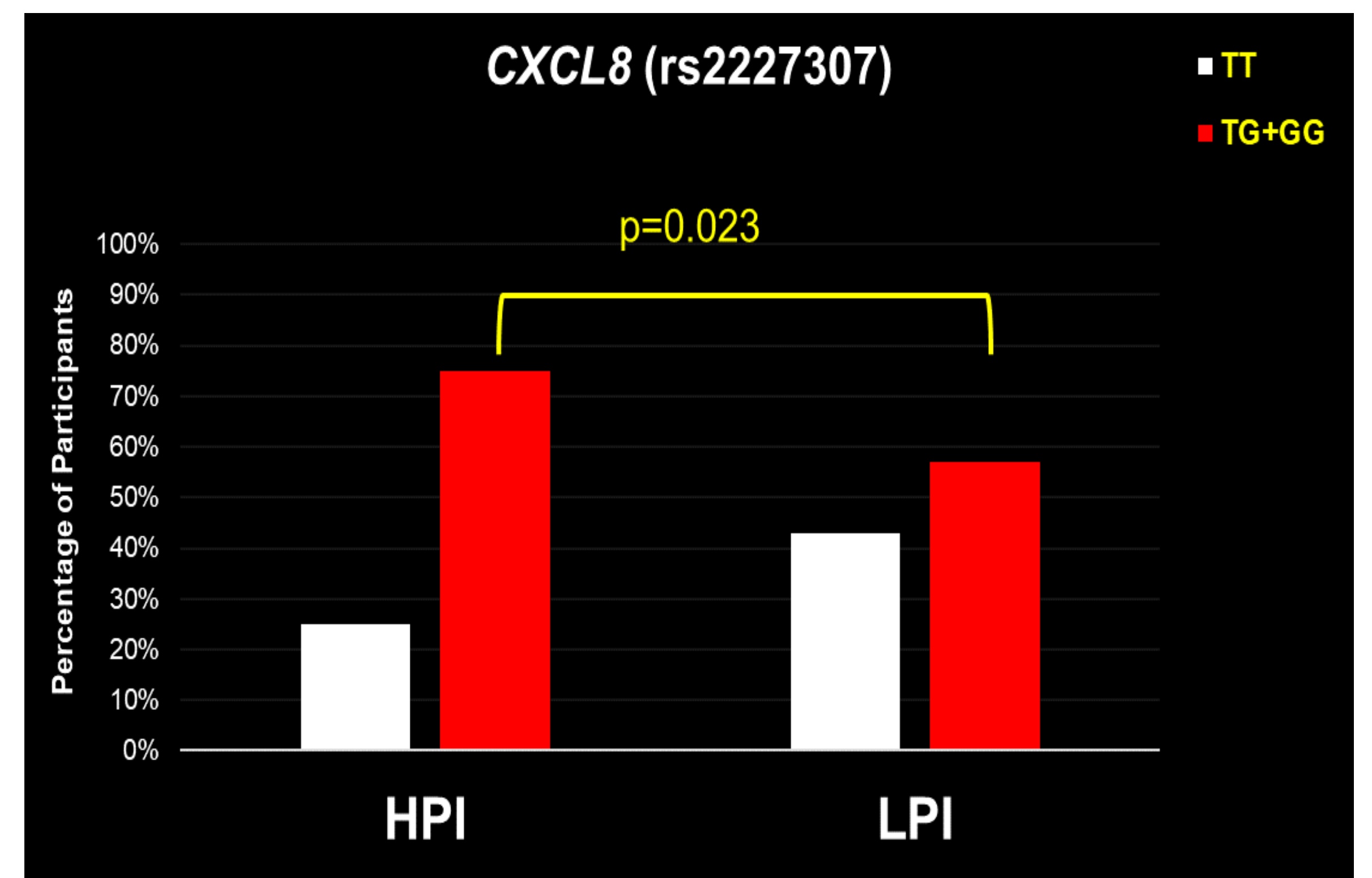


Figure 5. Genotype distribution between patients in high pain intensity (HPI) vs low pain intensity (LPI) group in *CXCL8* (rs2227307)

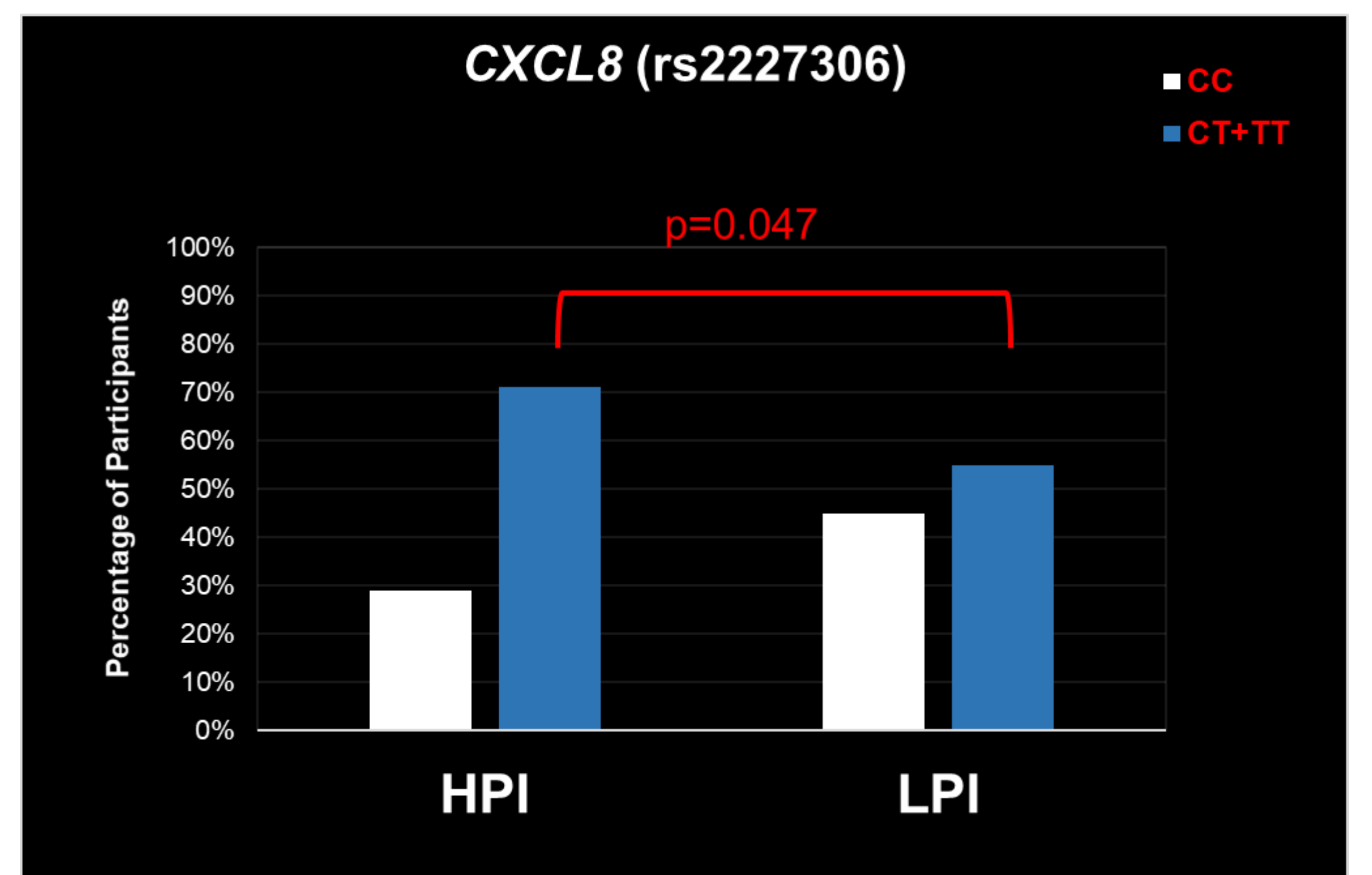


Figure 6. Genotype distribution between patients in high pain intensity (HPI) vs low pain intensity (LPI) group in *CXCL8* (rs2227306)

## RESULTS

The frequency of patients carrying **minor allele G of rs2227307** was **higher in TMDp patients** than in CTRs (70% vs. 55%,  $p=0.041$ ) (Figure 4).

Carriers of **minor allele G and T of rs2227307 and rs2227306** respectively were significantly **more represented in HPI group** when compared to the rest of the participants (75% vs. 57%,  $p=0.023$ ; 71% vs. 55%,  $p=0.047$ , respectively) (Figure 5,6).

Also, TMDp subjects carrying **GG+GT of rs2227307** polymorphism reported significantly **shorter pain duration** in last 6 months (80 vs.112 days,  $p=0.041$ ) and significantly **higher worst facial pain** (7.3 vs. 6.5,  $p=0.031$ ) compared to the subjects with the TT genotype.

## CONCLUSION

**Certain SNPs may predict pain intensity and chronicity in TMDp patients.**

Our results support the association between SNPs in pro-inflammatory chemokine genes (*CXCL8*) and TMDp, highlighting the potential utility of genetic testing in predicting pain severity.

Further research is needed to confirm these findings and explore underlying mechanisms.



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