Role of inflammation gene polymorphisms on pain and response to radiotherapy in multiple myeloma patients with painful bone destructions.

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Background: Previous researches have demonstrated, that the severity of pain perception and it’s response to analgesia is highly dependent on gene polymorphism encoding for cytokines. We evaluated 12 single nucleotide polymorphisms (SNP) in 6 genes encoding for cytokines in multiple myeloma patients (n = 81) and assessed their influence on pain severity and response to palliative radiotherapy. Methods: Pain intensity was assessed by Visual Analogue Scale. The total dose of opioids was converted to a mean morphine-equivalent dose (mg/day). Pain intensity and dose of analgesics were evaluated before radiotherapy and 4, 12 and 24 weeks after the treatment. Analysis of SNP of genes IL6, IL10, TNFA, IL1A, IL1B, ILIRN was carried out. Multivariable regression was used to assess correlations between severe pain and SNP, adjusting demographic and clinical variables. Results: Severe pain was more prevalent among patients with a Karnofsky index ≥ 60% (OR 5.84; 95% CI 1.49 – 22.87) and patients with GG genotype of ILIRN c.1812G > A polymorphism (OR 2.79; 95% CI 1.05 – 7.46). The analysis revealed that patients with IL1A c.889C > T CC genotype had a better response to radiotherapy after 12 and 24 weeks, compared to patients with TT and CT genotypes (p = 0.013 and p = 0.006 respectively). Patients with IL1B c. 3953C > T CC genotype also demonstrated a better response to radiotherapy after 12 and 24 weeks, compared to patients with TT and CT genotypes (p = 0.002 and p = 0.002 respectively). Patients with ILIRN c.11100T > C CC genotype had a faster response (after 4 weeks) to radiotherapy, compared to patients with TT and CT genotypes (p = 0.023). Conclusions: This study provides preliminary evidence, that genes encoding for particular cytokines play a significant role on pain severity and response to radiotherapy in multiple myeloma patients. Clinical trial information: NCT02024815