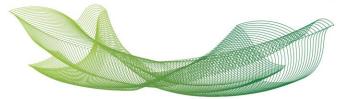


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Tipo	Periódico
Título	The intricate interplay between MSI and polymorphisms of DNA repair enzymes in gastric cancer <i>H.pylori</i> associated
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Resumo	Gastric cancer is the fourth most common type of cancer worldwide. Helicobacter pylori is a well-established risk factor and may cause injuries to genomic integrity through an inefficient DNA repair. This study aimed to examine the influence of polymorphisms in DNA repair enzymes using markers for microsatellite instability (MSI). Polymorphisms of DNA repair enzymes were detected by PCR-RFLP and MSI, by high resolution melt (HRM) analysis. Helicobacter pylori detection and genotyping were accomplished by PCR. MSI was observed in 47.5% of the cases and it was associated with the ERCC1 polymorphic allele, whereas MSI-H was associated with the XRCC3 heterozygous genotype. MSI was more frequent in intestinal gastric cancer (IGC), where it was associated with ERCC1 or RAD51 polymorphic alleles. Also, MSI-H was associated with the XRCC3 heterozygous. In diffuse gastric cancer (DGC), almost all of MGMT polymorphic genotype carriers showed MSI. Helicobacter pylori was positive in 94% of the cases and the most virulent strains were associated with MSI, mainly MSI-H. When the subtypes were considered, these associations were found only in the IGC and associated with more virulent strains. Among the cases with microsatellite instability, IGC showed a correlation between the XPD wild-type and the ERCC1 polymorphic allele, and all of them were infected by the most virulent strains. On the other hand, in DGC, the XPD polymorphic allele was correlated with the XRCC3 wild-type with no prevalence of H.pylori virulence. Our data demonstrated that polymorphisms in repair enzymes can interfere with the efficiency of the repair process, but it differs depending on the





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	histological subtype and H.pylori involvement. Besides nucleotide excision repair, base excision repair and mismatch repair pathway, the homologous recombination are also involved.
Fomento	

