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This English edition of biotechniques covers all aspects of the field of molecular biology and genetics including research methods, recombinant DNA technology, molecular genetics and genomics, various disorders, genetic approaches to treatment and prevention, personalized medicine, pharmacogenomics, epigenetics and gene regulation, non-coding RNA and the underlying mechanism of carcinogenesis. Features that include an advanced and cohesive text, illustrations and in-depth coverage of new technologies and methodologies, such as cancer genomics. In addition to providing an orientation of all aspects of current knowledge, this book is also intended to show the role of genetics in many common diseases, including cancers. DNA technologies are explained, with emphasis on the modern techniques that have revolutionized the use of genetic information in medicine and are indicating the role of genetics in common diseases. Epigenetics and non-coding RNA are covered in-depth as are genetic approaches to treatment and prevention, including pharmacogenomics, genetic testing, and personalized medicine. Cancers are essentially genetic diseases and are given a dedicated chapter that includes new insights into its molecular basis and approaches to its detection gained from cancer genomics. Specific topics, including multiple examples of clinical disorders, molecular mechanisms, and technological advances, are profiled in boxes throughout the text. In agreement with the aforementioned studies, development of bacterial infections depends on the influence of gender-associated factors such as sex steroid hormones, through the modulation of differential immune responses between women and men. The aim of the present article is to review the available data in the literature about bacterial infections that present a clear sexual dimorphism, such as gastrointestinal and respiratory infections, and sepsis, among others (Table 1). Although there is increasing evidence that confirms the sexual dimorphism in certain bacterial infections and the molecular mechanisms associated, further studies are required to clarify conflicting data and to determine the role of specific sex hormone receptors in the gender bias of bacterial infections, as well as their role as possible therapeutic targets.

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genetica humana chega a sua 3 edio completamente revisado e atualizado, abordando temas inditos, como projetos genoma e epigenoma humanos e a era mica, assim como teorias da evoluo humana.nesta edio, alm de novo projeto grfico extremamente didtico e atrativo, foram inclas imagens coloridas e destaques, que facilitam a localizao e o entendimento do contedo.este livro til no apenas a alunos de cursos biomdicos, mas tambm a professores e profissionais da sade e de outras reas que buscam informes sobre genetica humana. a new hospital-based registry of the molecular diagnosis of hereditary hemochromatosis (hh) was established in belo horizonte, minas gerais, brazil. the study included 1955 individuals submitted to molecular studies of the c282y and h63d mutations between 2006 and 2007. patients were clinically diagnosed with hh and their ages ranged from 18 to 70 years old. genotyping was performed for the c282y and h63d mutations. the following observations were made: (1) the prevalence of the c282y allele was 0.049 and the prevalence of the h63d allele was 0.007; (2) the distribution of the genotypes by gender, age, and alleles was not different from those in the national center for biotechnology information (ncbi) web page; (3) the cc/ct/tt genotype for c282y and the hh/hh/hh genotype for h63d were observed; (4) the cc/ct/tt genotype for c282y and the hh/hh/hh genotype for h63d were observed; (5) the genotype frequencies were in hardy-weinberg equilibrium; (6) the genotype frequencies were not different from those observed in the ncbi web page; (7) the prevalence of the c282y allele was 0.007; (8) the genotypes for c282y and h63d were not different from those in the ncbi web page; and (9) the genotypes for c282y and h63d were not different from those in the ncbi web page. these results suggest that the polymorphisms of c282y and h63d are not associated with hh in the population studied. the c282y and h63d mutations are among the most common genetic variants of hh in brazilian population. 5ec8ef588b

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