

**Abstract:**

Cyclin D1, encoded by the CCND1 gene, is a key regulator of the cell cycle at the G1/S phase checkpoint. A common A/G single nucleotide polymorphism (SNP) at nt870 of the CCND1 gene has been associated with outcome in patients with lung tumours and head and neck cancer. The aim of this study was to ascertain the genotype and allele frequency of the CCND1 polymorphism in five distinct ethnic populations. Polymerase chain reaction–restriction fragment length polymorphism (PCR–RFLP) analysis was carried out on genomic DNA from 505 subjects from five distinct ethnic populations (i.e. Caucasian, South-west Asian, Ghanaian, Kenyan and Chinese subjects). Marked differences in genotype were apparent between the ethnic populations, with homozygosity for the G allele ranging from 13.6% in the Chinese subjects to 62.4% amongst Kenyan individuals ( $P < 0.001$ ). Whereas the East and West African populations demonstrated almost identical allele frequencies, both populations differed significantly from each of the remaining populations. The allele frequencies for the South-west Asian population fell between that of the Caucasian and Chinese populations but did not differ significantly from either, while the Caucasian and Chinese subjects displayed significant differences in CCND1 alleles ( $P = 0.003$ ). These marked variations in SNP frequencies between ethnic groups may have a significant impact on prognosis of cancer in these populations, because the CCND1 genotype appears to influence prognosis in each tumour type examined to date.