Rapid and accurate determination of (CAG)n repeats in the androgen receptor gene using polymerase chain reaction and automated fragment analysis.

Abstract:

To develop and evaluate a new method for determination of the CAG repeat length in Exon 1 of the androgen receptor gene. DESIGN AND METHODS: The method is based on PCR amplification of a DNA region encompassing the repeats and analysis of the length of the PCR product on a sequencing gel. One of the PCR primers was labeled with Cy5.5 fluorescent dye to facilitate detection after laser excitation. We used a fully automated system for electrophoretic separation of the PCR product and accurate sizing of the length of the PCR product using fragment analysis. RESULTS: The major advantages of the new technique are its simplicity, speed, accuracy, and reproducibility. Analysis of the CAG repeats in genomic DNAs from 18 males indicated that they were all hemizygous with a mean CAG repeat number of 22 (range 20-30 repeats). Among 60 DNAs from females, 16 were homozygous and 44 were heterozygous. The repeat length ranged from 17-30 with a mean of 22. In both males and females, the distribution of CAG repeats was bimodal. CONCLUSION: We anticipate that this improved method for CAG repeat analysis will find applications in clinical studies involving prostate and breast cancer patients