Localization of the Human Phosphatidylinositol-Specific Phospholipase C \( \beta_3 \) Gene (PLCB3) within Chromosome Band 11q13

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In course of the molecular characterization of a human extragonadal germ cell tumor (EGCT)-associated chromosomal translocation, we identified YACs and cosmids from the 11q13 region. The endclone of one of these YACs appeared to contain a stretch of DNA homologous to part of the human phosphatidylinositol-specific phospholipase C \( \beta_3 \) gene (PLCB3). Since we considered PLCB3 a candidate gene for these EGCTs, we set out to clone the PLCB3 cDNA, from which the 5′ end was still missing, and performed Northern and Southern blot analyses. The localization of PLCB3 to 11q13 was confirmed. In addition, we were able to exclude the gene from involvement in EGCT development.

Recently, we started the molecular characterization of a recurring complex chromosomal translocation, involving breaks in 6p21, 6p22, 6q23, and 11q13, specific for a newly defined subgroup of human extragonadal germ cell tumors (EGCTs) (4). Band 11q13 was chosen as the starting point for our experiments. By using FISH, we were able to narrow the breakpoint region to an interval between loci D11S457 and D11S546 (8). To saturate this genomic region with new probes, sequence-tagged sites (STSS) were generated from single-copy subclones of the breakpoint-bracketing cosmids (cCII-247 and cCII-363, respectively; 10). These STSS, in turn, were used to screen a total human YAC library (CEPH) (1)). This resulted in one positive clone, designated 255H9, with the STS primer set corresponding to cosmids cCII-247 (D11S457). FISH analysis revealed that this YAC gives only one specific hybridization signal on 11q13, indicating that this YAC is non-chimeric. Furthermore, the 255H9 YAC appeared to map proximal to the breakpoint region in EGCTs, as the starting point for our experiments. By using FISH, we were able to narrow the breakpoint region in EGCTs, as the starting point for our experiments. By using FISH, we were able to narrow the breakpoint region in EGCTs, as the starting point for our experiments. By using FISH, we were able to narrow the breakpoint region in EGCTs, as the starting point for our experiments. By using FISH, we were able to narrow the breakpoint region in EGCTs, as the starting point for our experiments. By using FISH, we were able to narrow the breakpoint region in EGCTs, as the starting point for our experiments. By using FISH, we were able to narrow the breakpoint region in EGCTs, as the starting point for our experiments. By using FISH, we were able to narrow the breakpoint region in EGCTs, as the starting point for our experiments. By using FISH, we were able to narrow the breakpoint region in EGCTs, as the starting point for our experiments. By using FISH, we were able to narrow the breakpoint region in EGCTs, as the starting point for our experiments. By using FISH, we were able to narrow the breakpoint region in EGCTs, as the starting point for our experiments. By using FISH, we were able to narrow the breakpoint region in EGCTs, as the starting point for our experiments. By using FISH, we were able to narrow the breakpoint region in EGCTs, as the starting point for our experiments.

FIG. 1. (A) The 5′ sequence of cDNA clone c7. The translation initiation site is shown in boldface. The position where the previously known PLCB3 sequence begins (3) is underlined. (B) Amino acid alignment of the N-terminal regions of the three phosphatidylinositol-specific phospholipases C: PLCB1; PLCB2; PLCB3. The asterisks below the sequences indicate identical amino acids; the dots indicate conservative changes. The position where the previously known PLCB3 sequence begins (3) is underlined.
the chromosomal localization of the PLCB3 gene (Fig. 2B, lane 1). No aberrantly hybridizing fragments were observed in EGCT DNAs (Fig. 2B, lanes 4 and 5). Together with the mRNA studies, this result indicates that the PLCB3 gene can be excluded as a candidate in the development of this group of germ cell tumors. However, since the 11q13 region is involved in a number of other neoplastic disorders (2, 5, 8–10), the gene must be considered a candidate for either one of them.

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REFERENCES


