

HHS Public Access

Author manuscript

Cancer Genet Cytogenet. Author manuscript; available in PMC 2018 February 09.

Published in final edited form as:

Cancer Genet Cytogenet. 2008 October 15; 186(2): 120–121. doi:10.1016/j.cancergencyto.2008.06.011.

Assignment of the *BLID* gene to 11q24.1 by fluorescence in situ hybridization

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BLID (RefSeq number NM_001001786) (alias *BRCC2*, breast cancer cell 2) is an intronless gene. It was originally identified as an ~1.2-kb transcript in human breast carcinoma cells and normal cells (GenBank accession number AF303179) [1]. The longest predictive open reading frame of *BLID* cDNA (862 bp) codes for a protein consisting of 108 amino acids. Current data suggest that BLID functions as a proapoptotic molecule [1]. That is, expression of BLID has a negative impact on cell survival and correlates with caspase activation, chromatin condensation, and DNA fragmentation—hallmarks of cells undergoing apoptosis. Increase in the mitochondrial levels of endogenous BLID occurs in response to doxorubicin and hydrogen peroxide, known cytotoxic agents. An N-terminal deletion mutant of *BLID* lacking a BH3-like domain, or a *BLID* containing mutant BH3-like domain, fails to induce apoptosis, whereas a C-terminal deletion mutant retains the apoptotic activity. Taken together, these findings indicate that *BLID* functions as a proapoptotic tumor supressor molecule.

Cavalli et al.

A putative localization of the *BLID* gene to 11q24.1 was determined, using genomic sequence analysis [1]. Furthermore, Rogaeva et al. [2] reported that *BLID* is located distal to the *SORL1* gene, which maps to 11q23.2~q24.2.

To precisely determine the chromosomal location of the human *BLID* gene, we applied fluorescence in situ hybridization (FISH) mapping. Using the Human Genome Browser at UCSC (http://genome.ucsc.edu), we identified a bacterial artificial chromosome (BAC) clone, RP11-166D19, containing the *BLID* gene sequence. BLAST analysis (http://www.ncbi.nlm.nih.gov) revealed 100% sequence homology. The BAC clone was obtained from BACPAC Resources (Children's Hospital Oakland Research Institute, Oakland, CA) and was grown in our laboratory.

DNA was prepared and labeled with biotin-11-dUTP (PerkinElmer, Waltham, MA) using nick translation, as previously described [3,4]. Biotin-labeled DNA was hybridized to normal human chromosome preparations and was detected with fluoresceine–avidin D-cell sorter (Vector Laboratories, Burlingame, CA). Chromosomes were counterstained with 4',6-diamidino-2-phenylindole (DAPI), which produces a Q-banding pattern. Scoring of metaphases and digital image acquisition were performed using a 100× objective mounted on a Leica DMRBE microscope (Wetzlar, Germany) equipped with optical filters for DAPI and fluorescein (Chroma Technologies, Brattleboro, VT) and a cooled charge-coupled device (CCD) camera (Photometrics, Tucson, AZ) with Nu200 software (Photometrics). Fluorescein and DAPI images were recorded separately and were merged using the software package NIH Image 1.57 (http://rsb.info.nih.gov/nih-image) and band assignment of the fluorescein signal was done.

Image analysis revealed that the *BLID* gene maps to human chromosome 11q24.1. A specific hybridization signal was detected in all the metaphases analyzed, on both chromatids of chromosome 11, at band 11q24.1. No additional hybridization signals were detected. Figure 1 shows a representative metaphase spread hybridized with the BAC RP11-166D19 clone.

Acknowledgments

This work was supported by the Susan G. Komen Breast Cancer Foundation (Award no. BCTR0503829) to B.R.H.

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Cavalli et al.

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Cavalli et al.

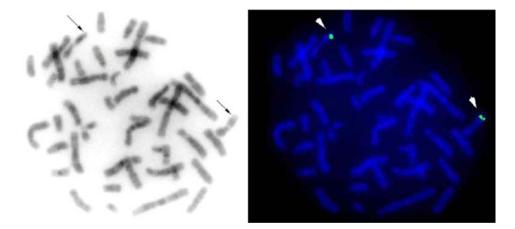


Fig. 1.

A representative metaphase spread hybridized with bacterial artificial chromosome RP11-166D19 clone, showing the assignment of *BLID* to human chromosome 11q24.1 by fluorescence in situ hybridization. The left panel shows an electronically inverted 4['],6- diamidino-2-phenylindole (DAPI) image of the metaphase (inverted DAPI images give a G-band like pattern). Arrows point to the location of *BLID* on 11q24.1. The right panel shows the fluorescein image of the same metaphase spread. Arrowheads point to the FISH signals.

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