

Assignment of the gene for a ubiquitin-conjugating enzyme (UBE2I) to human chromosome band 16p13.3 by in situ hybridization

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Rationale and significance

We have recently cloned a cDNA encoding a protein which interacts with a transcription factor, MITF (Microphthalmia-associated transcription factor), using the yeast two-hybrid system (Iwata et al., in preparation). The predicted protein called UBE2I (GenBank: U45328) is ~60% homologous to a ubiquitin-conjugating enzyme (E2) of *Saccharomyces cerevisiae* UBC9 (Seufert et al., 1994) and that of *Schizosaccharomyces pombe*: Hus5 (Al-Khodairy et al., 1994). One of the functions of a ubiquitin-conjugating system is to degrade transcription factors such as MAT α 2 (Hochstrasser and Varhavsky, 1990) and Gcn4 (Kornitzer et al., 1994). MITF is a transcription factor which is involved in melanocyte differentiation (Tachibana et al., 1994, 1996). Mutations of the MITF gene appear to cause Waardenburg syndrome type 2 (WS2; MIM193510) in patients from some families (Tassabehji et al., 1995; Nobukuni et al., 1996). Given the association between UBE2I and MITF gene products, we speculate that mutations of the UBE2I gene may cause WS2 or similar diseases. We here localized the UBE2I gene on chromosome 16 band p13.3. Among several diseases mapped to 16p13.3, the autosomal dominant congenital cataract with microphthalmia (Yokoyama et al., 1992; MIM156850) is the one most likely to involve a mutation of the UBE2I gene, since microphthalmia can be caused by mutations of the MITF homolog in mice (Steingrimsson et al., 1994). We

are now analyzing the possible mutation of the UBE2I gene in an individual showing congenital cataract with microphthalmia (Yokoyama et al., 1992).

Materials and methods

Human metaphase cells were prepared from phytohemagglutinin-stimulated lymphocytes. Purified DNA from a P1 clone containing the UBE2I gene was labeled with digoxigenin-dUTP by nick translation and used as a probe. In one-color FISH, digoxigenin-labeled probe was combined with sheared human DNA, and hybridized to metaphase chromosomes in a solution containing 50% formamide, 10% dextran sulfate and 2 \times SSC, and detected with fluorescein-conjugated antidigoxigenin antibodies as described previously (Stokke et al., 1995). Chromosomes were then counter-stained with propidium iodide. For two-color FISH a histin labeled probe specific for the heterochromatic region of chromosome 16 was employed. Chromosome 16 specificity was confirmed by the cohybridization of marker D16S422 (Dr. Valentine, unpublished data). The probe was co-hybridized with UBE2I probe and detected by avidin-Texas red. Chromosomes were then counterstained by 4',6-diamidino-2-phenylindole.

Probe name: UBE2I-P1/9032

Probe type: genomic DNA

Insert size: ~85 kb

Vector: P1 phage

Proof of authenticity: DNA sequencing

Gene reference: Watanabe et al. (1996), Iwata et al. (in preparation) and this report

Results

One-color FISH resulted in specific labeling of the distal short arm of a group E chromosome. Two-color experiments resulted in the specific labeling of the short arm of chromosomes which are co-labeled with the probe specific to chromo-

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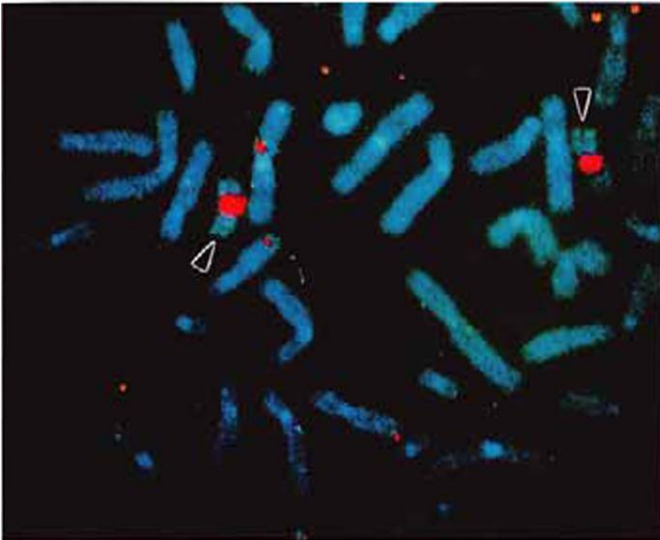


Fig. 1. In situ hybridization of digoxigenin-labeled UBE21-P1/9032 probe to human metaphase cells resulted in specific labeling at the p13.3 region of chromosome 16 (green signals; arrow heads). Note that the chromosome is labeled with a probe specific for the heterochromatic region of chromosome 16 (pink signals).

some 16 (Fig. 1). Measurements of 10 specifically hybridized chromosome 16's demonstrated that the UBE21 gene is located at a position which is 98% of the distance from the centromere to the telomere of chromosome arm 16p, an area that corresponds to band 16p13.3.

Location: 16p13.3

No. of cells examined: 80

No. of cells with specific signals: 68

Most precise assignment: 16p13.3

Location of background signals (sites with > 2 signals): none observed

Note: During the review of the manuscript, a cDNA for UBE21 was cloned from human fetal-brain library and the gene was mapped (Watanabe et al., 1996).

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References

- Al-Khodairy F, Enoch T, Hagan JM, Carr AM: The *Saccharomyces pombe huf5* gene encodes a ubiquitin conjugating enzyme required for normal mitosis. *J Cell Sci* 108:475-486 (1995).
- Hochstrasser M, Varshavsky A: In vivo degradation of a transcriptional regulator: the yeast $\alpha 2$ repressor. *Cell* 61:697-708 (1990).
- Kornitzer D, Raboy B, Kulka RG, Fink GR: Regulated degradation of the transcription factor Gcn4. *EMBO J* 13:6021-6030 (1994).
- Nobukuni Y, Watanabe A, Takeda K, Skarka H, Tachibana M: Analyses of loss-of-function mutations of the MTF gene suggests that haploinsufficiency is a cause of Waardenburg syndrome type 2A. *Am J Hum Genet* 59:76-83 (1996).
- Seufferl W, Fletcher H, Jentisch S: Role of a ubiquitin-conjugating enzyme in degradation of S- and M-phase cyclins. *Nature* 373:78-81 (1994).
- Steingrimsson E, Moore KJ, Lamoreux MI, Ferré-D'Amaré, Burley SK, Zimring DCS, Skow LC, Hodgkinson CA, Arnheiter H, Copeland NG, Jenkins NA: Molecular basis of mouse *microphthalmia (mi)* mutations helps explain their developmental and phenotypic consequences. *Nature Genet* 8:256-263 (1994).
- Stokke T, Collins C, Kuo W-L, Kowbel D, Shadravan F, Tanner M, Kallioniemi A, Kallioniemi O-P, Pinkel D, Deaven L, and Gray JW: A physical map of chromosome 20 established using fluorescent *in situ* hybridization (FISH) and digital image analysis. *Genomics* 26:134-137 (1995).
- Tachibana M, Perez-Jurado LA, Nakayama A, Hodgkinson CA, Li X, Schneider M, Miki T, Fox J, Francke U, Arnheiter H: Cloning of MTF, the human homologue of the mouse *microphthalmia* gene, and assignment to human chromosome 3, region p14.1 → p12.3. *Hum molec Genet* 3:553-557 (1994).
- Tachibana M, Takeda K, Nobukuni Y, Urahe K, Long JE, Meyers KA, Aaronson A, Miki T: Fetal-specific expression of MTF, a gene for Waardenburg syndrome type 2, converts fibroblasts to cells with melanocyte characteristics. *Nature Genet* 14:50-54 (1996).
- Tassabehji M, Newton VE, Read AP: Waardenburg syndrome type 2 caused by mutations in the human microphthalmia (MTF) gene. *Nature Genet* 18:251-255 (1994).
- Watanabe TK, Fujiwara T, Kawai A, Shimizu F, Takami S, Hirano H, Okuno S, Ozaki K, Takeda S, Shimada Y, Nagata M, Takauchi A, Takahashi E, Nakamura Y, Shio S: Cloning, expression, and mapping of UBE21, a novel gene encoding a human homologue of yeast ubiquitin-conjugating enzymes which are critical for regulating the cell cycle. *Cytogenet Cell Genet* 72:16-89 (1996).
- Yokoyama Y, Narahara K, Tsuji K, Ninomiya S, Seino Y: Autosomal dominant congenital cataract and microphthalmia associated with familial t(2;16) translocation. *Hum Genet* 90:177-178 (1992).