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### 厚生科学研究費補助金 (厚生科学特別研究事業)

### 分担研究報告書

細胞周期のチェックポイントに関係するホメオボックス遺伝子の各転移性腫瘍における意義 Six と HAT (Histone Acetyl Transferase)

### 分担研究者 川上 潔 自治医科大学 教授

転写因子SixファミリーのうちのひとつhSix1が、骨髄CD34陽性細胞ではGM-CSFによる分化をした方が、Epo, Tpoによる分化よりもより発現していた。また多方向に分化する株細胞 UT-7 を用いてノザン解析を行うと、GM-CSF によって刺激した場合により hSix1 が発現していた。

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### A. 研究目的

癌に対して多くの手術療法や化学療法、放射線療法が開発され、行われている。手術後や化学療法後に早期に再発する症例も依然として存在することも事実である。各種臓器の原発とするがんに対して特異的なマーカーである抗原や遺伝子の発見は、多くの期待を持って今後の癌の臨床経過や予後を推測させ、早期に対処できるようになることが期待される。しかし現実にはまだ多くの症例での検討や基礎的意味付けの必要な部分が多く残での検討や基礎的意味付けの必要な部分が多く残っている。そこで社会のニーズに答えるような臨床的検討から、微小残存病変や微小転移病変の有無の評価やその結果を生かして予後を推測することに生かせれば患者さんへの恩恵や社会への貢献度が高いと考えられる。そのための基礎的および臨床的研究を行う。

1. 病変における細胞の特性の研究

### B. 研究方法

増殖と分化に関係する転写因子 Six ファミリーの ひとつ hSix1 について遺伝子の発現と分化の方向 での検討を行った。ほ乳類細胞での検討の前に、 zebrafish で検討した。

### C. 結果

まず骨髄 CD34 陽性細胞では GM-CSF による分化をした方が、Epo, Tpo による分化よりもより発現していた。また多方向に分化する株細胞 UT-7 を

用いてノザン解析を行うと、GM-CSFによって刺激した場合により hSix1 が発現していた。

### D. 考察

増殖と分化に関係する転写因子 Six ファミリーのひとつhSix1 について遺伝子の発現と分化の方向での検討を行った。ほ乳類細胞での検討の前に、zebrafish で検討した。分化の方向によっては発現が増強される遺伝子がある事がわかった。

### E. 結論

転写因子 Six ファミリーのひとつ hSix1 について 遺伝子の発現と分化の方向での検討を行った。特 に GM-CSF による分化によって増強した。

F. 健康危険情報 特にありません。

### G. 研究発表

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岡見 次郎, 中森 正二, 左近 賢人, 門田 守人 外科治療(0433-2644)84 巻 6号 Page966-971(2001.06)

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Impaired interactions between mouse Eya1 harboring mutations found in patients with branchio-oto-renal syndrome and Six, Dach and G proteins

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Abstract Mutations in EYA1 gene are responsible for branchio-oto-renal (BOR) syndrome as well as for other ocular defects. Most of the mutations are located within or in the vicinity of the Eya domain, which is highly conserved among Eya protein family. The EYA domain is required for protein-protein interaction, which is important to the biological function of EYA proteins. To determine how EYA1 mutations cause BOR syndrome and/or ocular defects, we tested the effects of Eya1 mutations on interactions with Six, Dach and G proteins by mammalian two-hybrid and GST-pulldown assays. Defective interactions were noted between BOR type mutations S486P and L504R of Eya1 and Dach1, G proteins and some of Six proteins. These mutations impaired the activation of transcription from a Six-responsive gene, myogenin, with Six5. S486P and L504R showed altered digestion pattern with trypsin and L504R also decreased the sensitivity to V8 protease digestion and produced a peptide fragment with a different Mr. Our results suggest that defective proteinprotein interactions of the mutations in the Eya domain underlie BOR syndrome and that SIX, DACH and/or G proteins are possibly involved in the pathogenic processes.

Key words BOR syndrome, EYA1, EYA domain, Six, Dach, G protein, mammalian two-hybrid assay, GST-pulldown

### Introduction

EYA family genes are homologues of *Drosophila eyes absent* (eya) which is required for compound eye formation. A clue for molecular functions of EYA family gene products has been given by analyses using *Drosophila* system. Loss-of-function mutations of eya, as well as those of sine oculis (so, one of *Drosophila Six*) and dachshund, result in a reduction or a complete loss of compound eye development in the fly (Bonini et al. 1993; Cheyette et al. 1994; Mardon et al. 1994), while ectopic expression of so or dachshund with eya synergistically induced compound eye formation (Pignoni et al. 1997; Chen et al. 1997). These genetic interactions were shown to be mediated through physical interactions between their gene products (Pignoni et al. 1997; Chen et al. 1997).

EYA1 was originally isolated as a gene responsible for branchio-oto-renal (BOR) syndrome, a human autosomal dominant disorder characterized by hearing impairment, branchial arch deformation and variable severity of renal anomaly (Abdelhak et al. 1997b). In a recent report, EYA1 mutations were also found in certain ocular defects such as cataract and iris anomaly (Azuma et al. 2000). To date, more than 20 mutations of EYA1 have been identified in patients with BOR syndrome or ocular defects, most of which are located in the EYA domain of the product (an amino acid substitution, a truncation or a frame-shift) (Abdelhak et al. 1997a,b; Azuma et al. 2000; Kumar et al. 1998).

The EYA domain is conserved among EYA family gene products and is required for protein-protein interaction. For example, in *Drosophila*, Eyes absent forms a

complex with So and/or Dachshund through the Eya domain synergistically to induce compound eye formation (Pignoni et al. 1997; Chen et al. 1997), and mouse Eya forms a complex with Six and synergistically activate the target gene promoter through nuclear translocation of Eya by Six, for which the Eya domain is indispensable (Ohto et al. 1999). These facts suggest that the protein-protein interaction mediated by EYA domain is important for functions of EYA proteins and for normal organogenesis.

To gain insight into the molecular basis of how EYA1 mutations cause BOR syndrome, we analyzed the effects of EYAI mutations on such protein-protein interactions. For this purpose, we used the substitution and truncation mutations of EYAI identified in patients with BOR syndrome (R275X, L472R and R514G), ocular defects (E330K and S454P) or both (G393S) (Abdelhak et al. 1997b; Azuma et al. 2000) based on the following reasons. 1) Amino acid residues at these mutations are conserved (E330K, G393S and L472R) or homologous (R275X, S454P and R514G) among EYA family genes, suggesting that the molecular functions of these residues are common to EYA gene family. 2) In frame-shift mutations, sequences and lengths of thereafter amino acid stretches are not generally conserved and these stretches might have unexpected gain-of-function. The observations that human EYA1 and mouse Eya1 are highly homologous (99.6% identity in EYA domain, 98.7% identity in the whole molecule) and that mice carrying mutations in Eyal manifest BOR syndrome-like phenotype (Xu et al. 1999; Johnson et al. 1999), suggest that mouse Eya1 functions in the same molecular context as human EYA1. Thus we introduced the corresponding mutations found in human EYA1 into mouse Eya1 (R307X, S486P) and L504R for BOR type, E362K and R546G for ocular type and G425S for complex type) and performed molecular characterizations. We hypothesized that *Eya1* mutations impair molecular interactions with cofactors mediated by EYA domain and analyzed the interaction of these mutations with the known cofactors, Six, Dach and G proteins.

We tested these interactions by mammalian two-hybrid assays and/or GST-pulldown assays. Furthermore, to examine whether the impaired interaction influences the transactivation function of Eya1 with Six, we performed reporter gene assays using a promoter of a Six-responsive gene, *myogenin*. Structural analyses of Eya1 mutations were also performed by protease digestion.

### Materials and methods

### Construction of plasmids

pHM6Eya1R307X, pHM6Eya1E362K, pHM6Eya1G425S, pHM6Eya1L504R, pHM6Eya1R546G and pHM6Eya1S486P were constructed by introducing corresponding point mutations into pHM6Eya1 (Ohto et al. 1999) by cassette mutagenesis using the following sets of PCR primers: 5'-

CGTGGCCGAGGCTGAAGAAACAATA-3' and 5'-

TATTGTTTCTTCAGCCTCGGCCACG-3' (R307X); 5'-

GGACTACGAATGAAAGAGATGATTT-3' and 5'-

AAATCATCTCTTTCATTCGTAGTCC-3' (E362K); 5'-

ACTGGTGTCCGAAGTGGTGTGGACT-3' and 5'-

AGTCCACACCACTTCGGACACCAGT-3' (G425S); 5'-

CAAAGGTTTGGAGGGAAAGTGGTAT-3' and 5'-

ATACCACTTTCCCTCCAAACCTTTG-3' (R546G); 5'-

CTGAAGGCCCTCCCCCTCATCCACT-3' and 5'-

AGTGGATGAGGGGGGGCCTTCAG-3' (S486P); and 5'-

CAACTACGCAGCGCATCCCAGCATT-3' and 5'-

AATGCTGGGATGCGCTGCGTAGTTG-3' (L504R). The point mutations introduced are underlined.

pMEya1 was constructed as follows. The initiation codon (154)-HindIII (654) fragment was amplified by PCR so as to generate an EcoRI site at 5'-terminus. The resulting EcoRI-HindIII fragment was inserted into the EcoRI/SalI sites of pM (Clontech Laboratories, Palo Alto, CA) together with the HindIII (654)-XhoI (3'-terminus) fragment of pHM6Eya1.

pMEya1R307X was constructed by replacing the *Kpn*I (661)-*Pst*I (3'-terminus) fragment of pMEya1 with the *Kpn*I (661)-*Pst*I (3'-terminus) fragment of pHM6Eya1R307X. pMEya1E362K, pMEya1G425S, pMEya1L504R, pMEya1R546G and pMEya1S486P were constructed by replacing the *Bam*HI fragment (1199 to 3'-terminus) of pMEya1 with the *Bam*HI fragment (1199 to 3'-terminus) of pHM6Eya1E362K, pHM6Eya1G425S, pHM6Eya1L504R, pHM6Eya1R546G and pHM6Eya1S486P, respectively.

pfSix1 was constructed as follows. Six1 cDNA was cloned from mouse mammary cancer cell SC-3 cDNA library and the coding region was amplified by

PCR using the following set of primers to generate a *Kpn*I site at 5'-terminus and an *Xba*I site at 3'-terminus: 5'-GGGTACCCATGTCGATGCTGCCGTCGT-3' and 5'-GCTCTAGATTAGGAACCCAAGTCCACCA-3'. The resulting PCR fragment was digested with *Kpn*I and *Xba*I and inserted into the *KpnI/Xba*I sites of pFLAG-CMV-2 (Eastman Kodak, New Haven, Conn.).

pVP16Six1, pVP16Six2, pVP16Six4 and pVP16Six5 were constructed as follows. The full length of the insert of pfSix1 was excised as the *Bam*HI (blunt-ended)-*Xba*I fragment and inserted into the *Bam*HI (blunt-ended)/*Xba*I sites of pVP16 (Clontech) (pVP16Six1); the full length of the insert of pfSix2 (Ohto et al. 1999) was excised as the *Bss*HII (blunt-ended)-*Sma*I fragment and inserted into the *Sal*I (blunt-ended) site of pVP16 (pVP16Six2); the full length of the insert of pfSix4 (Ohto et al. 1999) was excised as the *Bgl*II (blunt-ended)-*Xba*I fragment and inserted into the *Bam*HI (blunt-ended)/*Xba*I sites of pVP16 (pVP16Six4); the full length of the insert of pfSix5 (Ohto et al. 1999) was excised as the *Xba*I (blunt-ended)-*Bgl*II (blunt-ended) fragment and inserted into the *Sal*I (blunt-ended) site of pVP16 (pVP16Six5).

pfDach1 was constructed as follows. pBSmdac (kindly provided by S. Krauss) was engineered to generate a *HindIII* site 5' adjacent to the initiation codon (266). The *HindIII-SspI* (2520) fragment was once cloned into the *HindIII/EcoRV* sites of pBluescript KS+ (Stratagene, La Jolla, CA). Then the insert was excised as the *HindIII-XbaI* fragment and inserted into the *HindIII/XbaI* sites of pFLAG-CMV-2.

pVP16Gz and pVP16GzQ205L were constructed as follows. The *Nco*I (13)-XbaI (3'-terminus) fragments from pCMV5Gz and pCMV5GzQ205L (Itoh et al. 1986) were excised, blunt-ended and inserted into the *Eco*RI (blunt-ended) site of

pVP16. pVP16Gi2 and pVP16Gi2Q205L were constructed as follows. The 262 bp *Hae*III fragments (34-295) from pCMV5Gi2 and pCMV5Gi2Q205L (Itoh et al. 1986) were inserted into the *Bam*HI (blunt-ended) site of pVP16. *Eco*RI (5'-terminus)-*Bst*XI (216) fragments of these plasmids and *Bst*XI (216)-*Xba*I (3'-terminus) fragments of pCMV5Gi2 and pCMV5Gi2Q205L were simultaneously ligated to *Eco*RI/*Xba*I sites of pVP16, respectively.

pGEXSix1 was constructed as follows. The full length of the insert of pfSix1 was excised as the *Eco*RV-XbaI (blunt-ended) fragment and inserted into the *Sma*I site of pGEX-6P-1 (Amersham Pharmacia Biotech, Buckinghamshire, UK).

pGL3MG-1.7 was constructed by inserting the *HindIII* fragment (5' upstream 1.7 kb region of *myogenin* gene promoter) of pMGNLacZ (Fujisawa-Sehara et al. 1993) into the *HindIII* site of pGL3-Basic (Promega, Madison, WI).

### Cell culture and reporter gene assays

293 and NIH3T3 cells were grown in Dulbecco's modified Eagle's medium supplemented with 4.5 g glucose/l, 10% fetal bovine serum with 100 units/ml penicillin and 100 μg/ml streptomycin at 37°C under 5% CO<sub>2</sub>. For mammalian two-hybrid assays, transfections into 293 cells were performed by the standard calcium phosphate method as described previously (Murakami et al. 1998) in 3.5 cm-diameter dishes. For coactivation activity of Eya1, transfections into NIH 3T3 cells were performed by SuperFect Transfection Reagent (QIAGEN, Hilden, Germany) in 24-well plates. Two days after the transfection, cells were collected and lysed for

luciferase assays. All values were normalized by the internal controls of  $\beta$ -galactosidase activities.

### GST-pulldown assays

GST, GST-Six2, GST-Six4 and GST-Six5 fusion proteins were prepared as described previously (Kawakami et al. 1996a,b). GST-Six1 fusion protein was prepared using pGEXSix1 by the same procedure. pHM6Eya1 and its mutations were applied to TNT Quick Coupled Transcription/Translation Systems (Promega, Madison, Wis.) to obtain HA-tagged Eya1 and its mutation proteins labeled with [35S]methionine (Amersham Pharmacia Biotech).

GST, GST-Six1, GST-Six2, GST-Six4 and GST-Six5 fusion proteins bound to Glutathione Sepharose beads in the binding buffer (50 mM K-PO<sub>4</sub>, pH 7.5, 150 mM KCl, 1 mM MgCl<sub>2</sub>, 10% glycerol, 1% Triton X-100) were incubated with <sup>35</sup>S-labeled HA-Eya1 and its mutations at 4°C for 2 h with rotation. Supernatants were recovered as unbound fractions. Beads were washed five times with the binding buffer and dissolved in SDS sample buffer, followed by SDS-PAGE and fluorography.

### Protease digestion

<sup>35</sup>S-labeled Eya1 proteins and their mutations were incubated with V8 protease or trypsin (Sigma, St. Louis, MO.) in a digestion buffer (50 mM Tris-HCl, pH 7.6, 25mM NaCl, and 2 mM EDTA) at 4°C for 30 min. After digestion, samples were