

## RESEARCH ARTICLE

# Loss of Heterozygosity at the Calcium Regulation Gene Locus on Chromosome 10q in Human Pancreatic Cancer

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### Abstract

**Background:** Loss of heterozygosity (LOH) on chromosomal regions is crucial in tumor progression and this study aimed to identify genome-wide LOH in pancreatic cancer. **Materials and Methods:** Single-nucleotide polymorphism (SNP) profiling data GSE32682 of human pancreatic samples snap-frozen during surgery were downloaded from Gene Expression Omnibus database. Genotype console software was used to perform data processing. Candidate genes with LOH were screened based on the genotype calls, SNP loci of LOH and dbSNP database. Gene annotation was performed to identify the functions of candidate genes using NCBI (the National Center for Biotechnology Information) database, followed by Gene Ontology, INTERPRO, PFAM and SMART annotation and UCSC Genome Browser track to the unannotated genes using DAVID (the Database for Annotation, Visualization and Integration Discovery). **Results:** The candidate genes with LOH identified in this study were *MCU*, *MICU1* and *OIT3* on chromosome 10. *MCU* was found to encode a calcium transporter and *MICU1* could encode an essential regulator of mitochondrial Ca<sup>2+</sup> uptake. *OIT3* possibly correlated with calcium binding revealed by the annotation analyses and was regulated by a large number of transcription factors including *STAT*, *SOX9*, *CREB*, *NF- $\kappa$ B*, *PPARG* and *p53*. **Conclusions:** Global genomic analysis of SNPs identified *MICU1*, *MCU* and *OIT3* with LOH on chromosome 10, implying involvement of these genes in progression of pancreatic cancer.

**Keywords:** pancreatic cancer - loss of heterozygosity - single-nucleotide polymorphism

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### Introduction

Loss of heterozygosity (LOH) is a common genetic alteration in cancer genomes, which derives from heterozygous deletion of one of the two alleles, or duplication of a maternal or paternal chromosome or chromosomal region and concurrent loss of the other allele (Frampton and King, 2013). LOH on chromosomal regions containing key tumor suppressor genes has been considered as a significant contributor to drive cancer progression by inactivating the suppressor genes of tumor (Baker et al., 2009), including pancreatic cancer. For example, *p53* tumor suppressor gene is identified to experience LOH accompanied by mutation in pancreatic cancer cell lines (Butz et al., 2003). Cooperating with mutation and/or loss of *p53*, the LOH of *BRCA1* and *BRCA2* may contribute to the progression of pancreatic cancer (Lucas et al., 2013). Besides, LOH in *THBS2* (6q), *p16* (9p) and *APC* (5q) are also demonstrated to carry the worst prognosis for resected pancreatic ductal and ampullary adenocarcinomas (Franko et al., 2008). By using genome-wide LOH maps in pancreatic cancer, LOH is found with high frequency at various chromosomes

such as 3p, 6p, 6q, 8q, 9p, 9q, 12q, 13q, 17p, 18q and 22q (Lin et al., 2008). However, candidate genes with LOH in pancreatic cancer remains rarely investigated.

Hybridization to single-nucleotide polymorphism (SNP) arrays is an efficient method to detect genome-wide cancer LOH by identifying the absence of heterozygous loci (Beroukhim et al., 2006; Staaf et al., 2008). Thus, the goal of this study was to further identify candidate genes with LOH in pancreatic cancer by performing a genome-wide analysis of LOH using the SNP arrays deposited in public database by Donahue et al. (2012), followed by annotation analysis and transcription factors screening in an attempt to explain the involvement of these genes in pancreatic cancer.

### Materials and Methods

#### *SNP expression profiling data*

The SNP expression profiling data GSE32682 (Donahue et al., 2012) of human pancreatic samples including 25 human pancreatic cancer and 7 non-malignant pancreas samples snap-frozen during surgery were downloaded from the GEO (Gene Expression

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Omnibus) database that is developed as a repository of microarrays, chips, hybridization arrays and high throughput gene expression data. The gene expressions of these samples were investigated by Affymetrix Genome-Wide Human SNP 6.0 Array (GPL6801).

*Data processing and screening of candidate genes with LOH*

Affymetrix CEL files were analyzed using Genotype Console software (version 4.0; Affymetrix) for initial intensity quality control (QC) with the criterion of recommended contrast  $QC > 0.4$ , followed by generating SNP genotype calls using the Affymetrix Birdseed algorithm and filtering SNPs loci with the excluded thresholds of no-call rate  $\geq 10\%$ , minor allele frequency  $< 0.05$  and Hardy Weinberg Equilibrium (HWE) P-value  $0.001$ . Then, copy-neutral LOH (CN-LOH) analysis was performed with the threshold of  $MAPD < 0.04$  to identify the SNP loci of LOH that existed in over 50% of the pancreatic cancer samples while not in control samples. The candidate genes with LOH were screened based on the genotype calls, SNP loci of LOH and dbSNP database (Day, 2010).

*Gene annotation of Candidate genes*

The candidate genes with LOH were annotated by using Gene database in NCBI (the National Center for Biotechnology Information) and the unannotated

genes were inputted into DAVID (the Database for Annotation, Visualization and Integration Discovery) for Gene Ontology (GO), INTERPRO, PFAM and SMART annotation (Sherman et al., 2007).

*Transcription factors screening of unannotated genes*

UCSC Genome Browser track that displays all analyzed transcription factor binding sites (TFBS) was performed to identify the transcription factors of the unannotated genes using DAVID database (Fujita et al., 2010), which was then visualized by constructing regulatory network using Cytoscape software (Kohl et al., 2011).

**Results**

*Intensity QC filtration*

The intensity QC of each sample was analyzed using Genotype Console software (Figure 1). The samples with contrast  $QC < 0.4$  (GSM811149\_17T.CEL and GSM811154\_14T.CEL) were excluded in the following research.

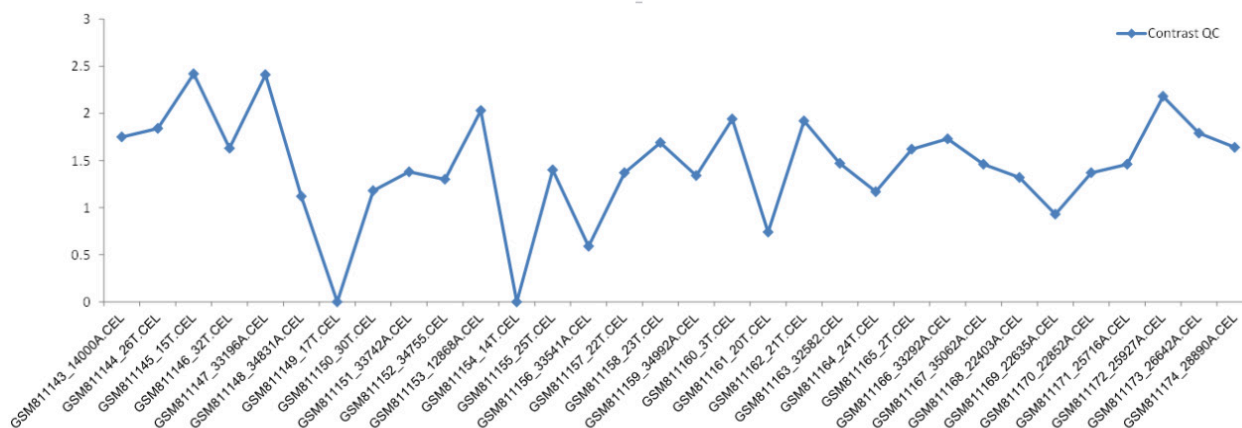
*Candidate genes with LOH*

The candidate genes with LOH identified in this study were *MCU* (mitochondrial  $Ca^{2+}$  uniporter), *MICU1* (mitochondrial calcium uniporter regulator 1) and *OIT3* (oncprotein induced transcript 3) on chromosome 10

**Table 1. Partial results of LOH\_SNP\_gene**

Probe_id	Chr	Pos	CN_state	SNP_ID	Gene_ID
SNP_A-8465056	10	74321221	2	rs7921361	<i>MICU1</i>
SNP_A-2002554	10	74334758	2	rs6415911	<i>MICU1</i>
SNP_A-8423526	10	74378437	2	rs10823937	<i>MICU1</i>
SNP_A-8716423	10	74417164	2	rs9415071	-
SNP_A-1882206	10	74442817	2	rs3009560	-
SNP_A-8631561	10	74490023	2	rs2921448	<i>MCU</i>
SNP_A-8397978	10	74512727	2	rs2894214	<i>MCU</i>
SNP_A-2163625	10	74514615	2	rs7086453	<i>MCU</i>
SNP_A-2120808	10	74522284	2	rs16930097	<i>MCU</i>
SNP_A-2027945	10	74522494	2	rs16930102	<i>MCU</i>
SNP_A-2140867	10	74541864	2	rs11000413	<i>MCU</i>
SNP_A-2297049	10	74570913	2	rs7097134	<i>MCU</i>
SNP_A-8486874	10	74606261	2	rs12785228	<i>MCU</i>
SNP_A-4259678	10	74672399	2	rs11000445	<i>OIT3</i>
SNP_A-8465056	10	74321221	2	rs7921361	<i>MICU1</i>
SNP_A-2002554	10	74334758	2	rs6415911	<i>MICU1</i>
SNP_A-8465056	10	74321221	4	rs7921361	<i>MICU1</i>
SNP_A-2002554	10	74334758	4	rs6415911	<i>MICU1</i>
SNP_A-8423526	10	74378437	4	rs10823937	<i>MICU1</i>
SNP_A-8716423	10	74417164	4	rs9415071	-
SNP_A-1882206	10	74442817	4	rs3009560	-
SNP_A-8631561	10	74490023	4	rs2921448	<i>MCU</i>
SNP_A-8397978	10	74512727	4	rs2894214	<i>MCU</i>
SNP_A-2163625	10	74514615	4	rs7086453	<i>MCU</i>
SNP_A-2120808	10	74522284	4	rs16930097	<i>MCU</i>
SNP_A-2027945	10	74522494	4	rs16930102	<i>MCU</i>
SNP_A-2140867	10	74541864	4	rs11000413	<i>MCU</i>
SNP_A-2297049	10	74570913	4	rs7097134	<i>MCU</i>
SNP_A-8486874	10	74606261	4	rs12785228	<i>MCU</i>
SNP_A-4259678	10	74672399	4	rs11000445	<i>OIT3</i>

Chr, chromosome; Pos, the loci of SNP on chromosome; CN\_state, the copy numbers; SNP\_ID, the ID of SNP in dbSNP database; Gene\_ID, the ID of gene corresponding to the SNP; LOH, loss of heterozygosity; SNP, single-nucleotide polymorphism

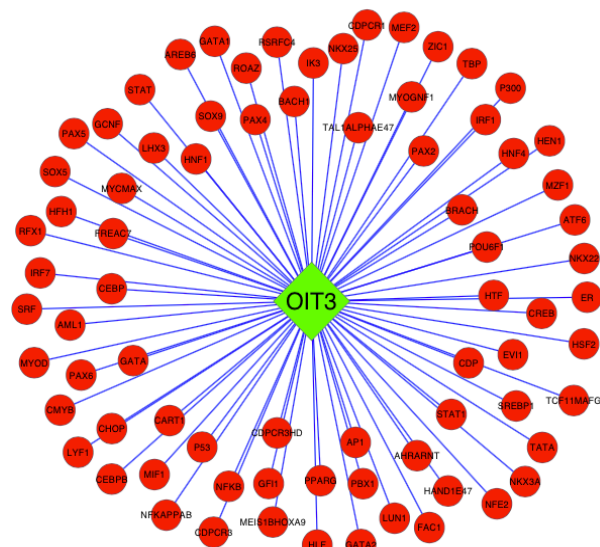


**Figure 1. The Intensity QC in Each Sample.** The X-axis represents file names of samples and the Y-axis represents the value of contrast QC. QC, quality control

**Table 2. The Annotation Results of *OIT3***

ID	<i>OIT3</i>
Gene Name	oncprotein induced transcript 3
GOTERM_CC_FAT	GO:0005635~nuclear envelope,GO:0012505~endomembrane system,GO:0031967~organelle envelope,GO:0031975~envelope
GOTERM_MF_FAT	GO:0005509~calcium ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding
INTERPRO	IPR000152:EGF-type aspartate/asparagine hydroxylation conserved site,IPR001507:Endoglin/CD105 antigen,IPR001881:EGF-like calcium-binding,IPR006209:EGF,IPR006210:EGF-like,IPR013032:EGF-like region, conserved site,IPR017976:Endoglin/CD105 antigen subgroup,IPR017977:Endoglin/CD105 antigen conserved site,IPR018097:EGF-like calcium-binding, conserved site
PFAM	PF00008:227-262,PF00008:EGF,PF00100:Zona pellucida-like domain,PF00100:Zona_pellucida
SMART	SM00179:EGF_CA,SM00181:EGF,SM00241:ZP

\*GO, Gene Ontology; CC, cellular component; MF, molecular function



**Figure 2. The Regulatory Network Between *OIT3* and its Transcription Factors.** The rhombus represents *OIT3* and the surrounding circles represent transcription factors

(Partial results were shown in Table 1). The copy number (CN) in the samples were two or four in this study, probably suggesting LOH resulted from heterozygous deletion of one of the two alleles, or duplication of a maternal or paternal chromosome or chromosomal region and concurrent loss of the other allele.

**Gene annotation**

Gene annotation was performed to identify the

functions of candidate genes with LOH using Gene database in NCBI. Accordingly, *MCU* (Gene ID: 90550) was found to encode a calcium transporter that localizes to the mitochondrial inner membrane and interacts with mitochondrial calcium uptake (Bick et al., 2012; Csordas et al., 2012; Raffaello et al., 2012; Curry et al., 2013; Patron et al., 2013). *MICU1* (Gene ID: 10367) could encode an essential regulator of mitochondrial Ca<sup>2+</sup> uptake under basal conditions. The encoded protein interacts with the mitochondrial calcium uniporter and is essential in preventing mitochondrial Ca<sup>2+</sup> overload that could cause excessive production of reactive oxygen species and cell stress (Mallilankaraman et al., 2012; Arviso et al., 2013; Chen et al., 2013; Hoffman et al., 2013; Logan et al., 2014). *OIT3* didn't obtain any annotated results from Gene database, but get some other annotated messages from GO, INTERPRO, PFAM, SMART annotation analysis provided by DAVID (Table 2). *OIT3*, oncprotein induced transcript 3, was correlated with calcium ion binding, ion binding and cation binding.

**Transcription factors of *OIT3***

By performing UCSC TFBS analysis, this study identified a large number of transcription factors including *STAT* (signal transducer and activator of transcription), *SOX9* (sex determining region Y-box 9), *CREB* (cAMP responsive element binding protein), *NF-kB* (nuclear factor kappa B), *PPARG* (peroxisome proliferator-activated receptor gamma) and *p53*, which had regulatory effects on *OIT3* (Figure 2).

## Discussion

By mapping the SNPs showing LOH in the tumor versus matched normal samples, this study identified three candidate genes with LOH (*MICU1*, *MCU* and *OIT3*) on chromosome 10 in pancreatic cancer, implying an important role for these genes in pancreatic cancer.

*MCU* and *MICU1* are two genes that have been demonstrated to play important roles in mitochondrial  $\text{Ca}^{2+}$  uptake (Perocchi et al., 2010; Baughman et al., 2011; Csordas et al., 2013). The  $\text{Ca}^{2+}$  handling by mitochondria is involved in cell life by triggering or preventing apoptosis probably functioning through the released pro-apoptotic factors such as Bax and Bak from the intermembrane space (Scorrano et al., 2003; Kroemer et al., 2007; Contreras et al., 2010). Thus, it could be speculated that *MCU* and *MICU1* may be related to the cancer progression via affecting cellular apoptosis. As expected, previous study has reported the down-regulation of *MCU* targeted by cancer-related microRNA may increase cancer cell survival and contribute to tumorigenesis in various cancer cells (Marchi et al., 2013). Silencing *MICU1* is also revealed to initiate the mitochondrial pathway for apoptosis by decreasing Bcl-2 expression together with increasing caspase-3 activity and cytosolic cytochrome c contents (Arvizo et al., 2013). Therefore, *MCU* and *MICU1* may be oncogene or tumor suppressor gene and the LOH in them may lead to their lower expression, thus preventing or promoting pancreatic cancer cell apoptosis.

*OIT3* located at 10q22.1 was another gene with LOH found in pancreatic cancer. This gene, also termed as liver-specific zona pellucida domain-containing protein (LZP), is related to hepatocellular function and could be used as a potential diagnostic biomarker for hepatocellular carcinoma (Xu et al., 2003). Also, *OIT3* is reported to experience copy number losses and down-regulation in colorectal cancer (Yoshida et al., 2010). However, the details of the relationships between *OIT3* and cancers are not clear. Herein, *OIT3* was found to be associated with calcium ion binding, probably implying an involvement of this gene in cellular  $\text{Ca}^{2+}$  homeostasis. Moreover, based on the regulatory network in this study, *OIT3* was regulated by a large number of transcription factors including *STAT*, *SOX9*, *CREB*, *NF-kB*, *PPARG* and *p53* which were previously reported to be associated with pancreatic cancer. *STAT-3*, *PPARG* and *NF-kB* signaling pathways are involved in apoptosis and cellular differentiation in pancreatic cancer cells (Elnemr et al., 2000; Sahu and Srivastava, 2009). *CREB* is related to activate *STAT-3* and cyclin D1 expression in pancreatic cancer cells which lead to cell proliferation and tumor progression (Zhang et al., 2010). *SOX9* could initiate and accelerate the formation of premalignant lesions of pancreatic cancer (Kopp et al., 2012). In addition, mutations in *p53* tumor suppressor gene are considered to drive metastasis and contribute to the carcinogenesis of pancreatic cancer (Sato et al., 1996; Amaya et al., 2004; Morton et al., 2010). The LOH of *OIT3* may suggest dysregulated functions of these transcription factors, which may contribute to the progression of pancreatic cancer.

In conclusion, our global genomic analysis of SNPs

provides evidence of LOH in *MICU1*, *MCU* and *OIT3* on chromosome 10 in pancreatic cancer. They may be involved in pancreatic cancer progression by regulating the calcium ion homogenizes and cell apoptosis. However, future mechanistic researches will be required to determine the molecular mechanisms.

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