

Analysis of Gene Expression Modulated by Indole-3-carbinol in Dimethylbenz[a]anthracene-induced Rat Mammary Carcinogenesis

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Abstract

Our previous finding that pre-initiation treatment of indole-3-carbinol (I3C) represents a chemopreventive effect in dimethylbenz[a]anthracene (DMBA)-induced mammary carcinogenesis has prompted us to test the global expression of genes at an early stage. Rats were continuously fed 300 ppm I3C in their diet at 6 weeks of age and were injected with DMBA at 7 weeks of age, and were sacrificed at 8 weeks of age. Global gene expression analysis using oligonucleotide microarrays was conducted to detect altered genes in DMBA- or DMBA plus I3C-treated mammary glands. Altered genes were identified by fold changes of 1.2 and by t-test ($P < 0.05$) from the log ratios of the hybridization intensity of samples between control (Group 1) and DMBA (Group 2), and from those of samples between DMBA (Group 2) and DMBA plus I3C (Group 3). From these genes, we chose altered genes that were up- or down-regulated by DMBA treatment and recovered to the control level by I3C treatment. For early stage of carcinogenesis, I3C treatment induced the recovery to normal levels of several genes including cell cycle pathway (cyclin B2, cell division cycle 2 homolog A), MAP signaling pathway (fibroblast growth factor receptor 1, platelet derived growth factor receptor, beta polypeptide), and insulin signaling (protein phosphatase 1, regulatory (inhibitor) subunit 3B and flotillin 2), which were up-regulated by DMBA treatment. In addition, I3C treatment induced the recovery to normal levels of several genes including those of MAPK

signaling (transforming growth factor, beta receptor 1 and protein phosphatase 3, catalytic subunit, beta isoform), which were down-regulated by DMBA treatment. These results suggest that the targeting of these genes presents a possible approach for chemoprevention in DMBA-induced mammary carcinogenesis.

Keywords: Dimethylbenz[a]anthracene (DMBA), Microarray, Rat, Mammary gland

Daily contact with some environmental carcinogens is virtually unavoidable, and this is closely associated with the occurrence of cancer^{1,2}. Primary prevention of cancer means preventing the occurrence of cancer by removing causes or providing inhibitory materials. Secondary prevention involves reducing mortality by finding cancer at an earlier stage. To achieve primary prevention of cancer, the application of several naturally occurring compounds from fruits and vegetables has many advantages³, and the consumption of cruciferous vegetables such as cabbages and broccoli has been associated with cancer chemopreventive effects in humans⁴.

Indole-3-carbinol (I3C), a component of cruciferous vegetables, has been suggested to have chemopreventive potential in experiments with animals and humans. I3C is produced endogenously from naturally occurring glucosinolates found in a wide variety of plant food substances, when they are crushed or cooked, and the acid environment of the gut easily converts them into a range of polyaromatic indolic compounds⁵.

It has been reported that I3C has considerable potential as a natural prophylactic anticancer agent against some neoplasms such as in liver⁶, colon⁷ and uterus⁸ when it is applied prior to or concurrently with exposure to the carcinogen. In the mammary gland, I3C treatment inhibited chemically-induced mammary tumors induced by 7,12-dimethylbenz[a]anthracene (DMBA) in a rodent model^{9,10}, as well as naturally occurring mammary gland tumors¹¹.

This chemopreventive effect has been associated with the induction of phase I enzymes such as CYP1A1

and CYP1A2^{12,13}, and phase II enzymes such as glutathione *S*-transferase, NAD(P)H: quinone oxidoreductase, glutathione reductase, glutathione *S*-hydrolase^{14,15}; increased 2-hydroxylation in estrogen metabolism¹⁶; pathways of cell cycle arrest^{17,18}, apoptosis of tumor cells¹⁹, and the inhibition of cancer cell metastasis²⁰.

In our previous study, we found that post-initiation treatment of I3C did not inhibit either *N*-methyl-*N*-nitrosourea (MNU)-induced mammary carcinogenesis²¹ and another study found that I3C did not suppress or DMBA-induced one²². In other organ models, post-initiation treatment of I3C did not inhibit tumor formation, and it promoted tumor multiplicities in some cases^{23,24}.

As I3C and its several metabolites act to induce aryl hydrocarbon receptor mediating response and have an estrogenic effect^{16,25}, they may also have a carcinogenic effect in some situations, especially when initiated cells or tumor cells are growing. These findings have led us to consider time points of carcinogen exposure and the types of carcinogens and cellular circumstances when chemicals are applied.

It is reasonable that I3C induces the removal of a carcinogen before initiation. However, it is not clear which pathway(s) is affected by pre-initiation treatment with I3C. To gain a better understanding of the chemopreventive mechanisms of I3C in mammary carcinogenesis, we performed oligonucleotide microarray analyses using mammary glands of rats treated with I3C or normal diet and DMBA as a carcinogen, and compared the global gene alterations of I3C-treated mammary glands with those of DMBA-treated ones.

Microarray Analysis

A hierarchical analysis revealed that each group was well classified and there was more similarity between the patterns of Groups 1 and 3 than between those of Groups 2 and 3 (Figure 1).

We extracted 179 genes showing a significant increase by comparison between Groups 1 and 2, yet no difference by comparison between Groups 2 and 3 (i.e. recovery to control level); 33 of selected genes had biological relevance to the KEGG pathway (Table 1). These included cell cycle-related genes such as cyclin B2 (*Ccnb2*) and cell division cycle 2 homolog A (*Cdc2a*); MAPK signaling-related genes such as fibroblast growth factor receptor 1 (*Fgfr1*), platelet derived growth factor receptor, beta polypeptide (*Pdgfrb*) and protein phosphatase 5 catalytic subunit (*Ppp5c*); insulin signaling-related genes such as protein phosphatase 1, regulatory (inhibitor) subunit 3B (*Ppp1r3b*) and flotillin 2 (*Flot2*).

In addition, we extracted 83 genes displaying a sig-

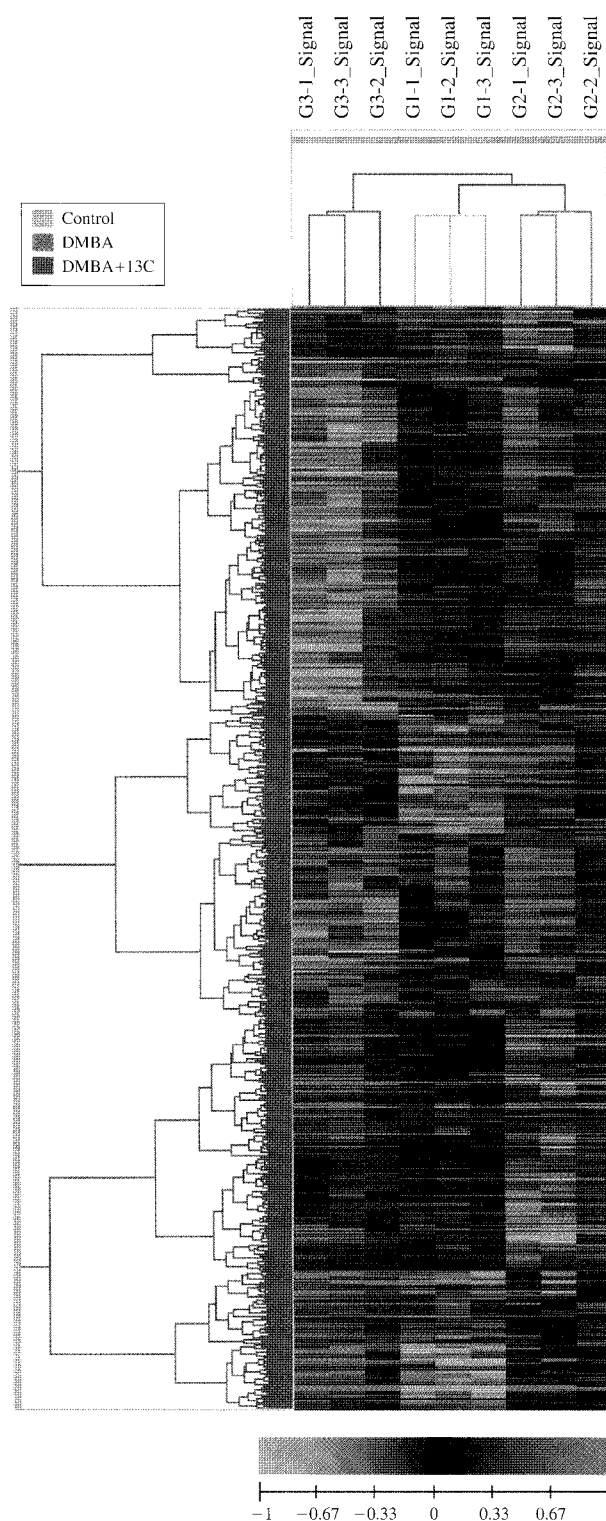


Figure 1. Gene expression in mammary gland from F344 rats treated with DMBA and/or I3C 300 ppm. Three categories of control, DMBA and DMBA plus I3C were classified, and analyzed. Clustering analysis of genes induced by control, DMBA and DMBA plus I3C, showing clear classification of three groups.

Table 1. Gene analysis from down-regulated genes by I3C treatment.

Gene symbol	Gene title	RefSeq Transcript ID	Fold change G1 vs G4	Fold change G1 vs G5	KEGG_Definition
Itgb1	integrin beta 1 (fibronectin receptor beta)	NM_017022	1.423767262	0.904607586	Axon guidance; Focal adhesion; ECM-receptor interaction; Cell adhesion molecules (CAMs); Leukocyte transendothelial migration; Regulation of actin cytoskeleton; Small cell lung cancer
Esam	endothelial cell adhesion molecule	NM_001004245	1.653743325	0.905095962	Cell adhesion molecules (CAMs); Leukocyte transendothelial migration
Lmna	lamin A	NM_001002016	1.616442662	1.12254556	Cell Communication
Ccnb2	cyclin B2	NM_001009470	1.531405666	0.842172108	Cell cycle; p53 signaling pathway
Cdc2a	cell division cycle 2 homolog A (S. pombe)	NM_019296	1.883328503	0.972959955	Cell cycle; p53 signaling pathway; Gap junction
Sdhb_predicted	succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (predicted)	XM_001071846 /// XM_216558	1.383089324	0.896158092	Citrate cycle (TCA cycle); Oxidative phosphorylation
Sdhc	succinate dehydrogenase complex, subunit C, integral membrane protein	NM_001005534	1.542282627	0.691292095	Citrate cycle (TCA cycle); Oxidative phosphorylation
Sord	sorbitol dehydrogenase	NM_017052	1.305630803	0.717887177	Fructose and mannose metabolism
Gls	glutaminase	NM_001109968 /// NM_012569	1.443925125	0.95289679	Glutamate metabolism; D-Glutamine and D-glutamate metabolism; Nitrogen metabolism
Mgll	Monoglyceride lipase	NM_138502	2.467841377	1.068977435	Glycerolipid metabolism
Pigt_predicted	phosphatidylinositol glycan, class T (predicted)	NM_001106540 /// XM_001070371 /// XM_215919	1.497070332	0.904013987	Glycosylphosphatidylinositol (GPI)-anchor; Glycan structures-biosynthesis 2
Bmp7	bone morphogenetic protein 7	XM_001053727 /// XM_342591	1.73674282	0.943554856	Hedgehog signaling pathway; TGF-beta signaling pathway
Hs6st1_predicted	heparan sulfate 6-O-sulfotransferase 1 (predicted)	NM_001108210 /// XM_001056379 /// XM_237060	1.22036299	0.851871069	Heparan sulfate biosynthesis; Glycan structures-biosynthesis 1
Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B	NM_138912	2.676959168	1.382218155	Insulin signaling pathway
Flot2	flotillin 2	NM_031830	1.236616077	0.830879979	Insulin signaling pathway
Ppp5c	protein phosphatase 5, catalytic subunit	NM_031729	1.665770521	0.813983619	MAPK signaling pathway
Fgfr1	Fibroblast growth factor receptor 1	NM_024146	1.333484141	0.983644108	MAPK signaling pathway; Adherens junction; Regulation of actin cytoskeleton; Prostate cancer; Melanoma
Pdgfrb	platelet derived growth factor receptor, beta polypeptide	NM_031525	1.597176777	1.01302539	MAPK signaling pathway; Calcium signaling pathway; Focal adhesion; Gap junction; Regulation of actin cytoskeleton; Colorectal cancer; Glioma; Prostate cancer; Melanoma
Ephx1	epoxide hydrolase 1, microsomal	NM_001034090 /// NM_012844	1.212957639	0.727577668	Metabolism of xenobiotics by cytochrome P450
Ghrhr	growth hormone releasing hormone receptor	NM_012850	2.664307623	1.834264471	Neuroactive ligand-receptor interaction
App	amyloid beta (A4) precursor protein	NM_019288	1.456437373	0.962542624	Neurodegenerative Disorders; Alzheimer's disease
Psen2	presenilin 2	NM_031087	1.557210776	0.758243204	Neurodegenerative Disorders; Notch signaling pathway; Alzheimer's disease
Man2c1	mannosidase, alpha, class 2C, member 1	NM_139256	1.676106514	1.058965068	N-Glycan degradation; Glycan structures-degradation

Table 1. Continued.

Gene symbol	Gene title	RefSeq Transcript ID	Fold change G1 vs G4	Fold change G1 vs G5	KEGG_Definition
Rfng	Radical fringe gene homolog (Drosophila)	NM_021849	1.895552393	0.845579829	Notch signaling pathway
Atp5d	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit	NM_139106	1.364155715	0.987882253	Oxidative phosphorylation
Hmox2	heme oxygenase (decycling) 2	NM_024387	1.207129677	0.856866091	Porphyrin and chlorophyll metabolism
Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	NM_199256	1.422523021	0.826330601	Protein export
Ppp1r12b_predicted	Protein phosphatase 1, regulatory (inhibitor) subunit 12B (predicted)	NM_001107178 /// XM_001062402 /// XM_222656	1.514661346	1.006185822	Regulation of actin cytoskeleton
Gabarap	gamma-aminobutyric acid receptor associated protein	NM_172036	1.246270728	0.926827978	Regulation of autophagy
Stx5a	syntaxin 5a	NM_031704	1.347428762	0.938503805	SNARE interactions in vesicular transport
Rab13	RAB13, member RAS oncogene family	NM_031092	1.616463875	0.900301066	Tight junction
Epb4.11l	erythrocyte protein band 4.1-like 1	NM_021681 /// NM_172090	2.321635953	1.375053451	Tight junction
Sh3gl1	SH3-domain GRB2-like 1	NM_031239	1.932571423	0.654449616	Tyrosine metabolism; Phenylalanine metabolism; Glycerophospholipid metabolism; 1- and 2-Methylnaphthalene degradation; Benzoate degradation via CoA ligation; Limonene and pinene degradation; Alkaloid biosynthesis II

nificant decrease by comparison between Groups 1 and 2, yet no difference by comparison between Groups 2 and 3 (i.e. recovery to control level), and selected 7 genes having biological relevance to the KEGG pathway (Table 2). These included MAPK signaling-related genes such as transforming growth factor, beta receptor 1 (Tgfb1), and protein phosphatase 3, catalytic subunit, beta isoform (Ppp3cb).

In the histopathological examination of the mammary glands, morphological differences were not observed between the control and treated groups (data not shown).

Discussion

In this study, we investigated the chemopreventive effect of I3C in DMBA-induced mammary carcinogenesis at an early stage using a microarray technique. We found that I3C treatment induced the recovery of altered genes induced by DMBA to control levels, including genes of cell cycle, MAPK signaling pathway, insulin signaling pathway, and TGF-beta pathway.

The microarray technique can provide a powerful tool to analyze many genes in a shorter time and to

access a broad range of carcinogenesis research^{26,27} and to obtain profiles induced by several chemicals²⁸⁻³⁰.

As the microarray analysis of rainbow trout treated with I3C revealed increases in genes related to estrogen metabolism³¹, I3C itself may exert estrogenic action in the mammary gland. It is known that estrogen or its metabolites can promote mammary tumors³²; however, the treatment can inhibit mammary carcinogenesis, depending on the treatment time³³. These data suggest that it is important to remind the cellular environment when chemicals are applied³⁴.

Even though treatment with I3C showed chemopreventive effects when it was applied prior to or simultaneously with carcinogen exposure²⁴, it was not effective when applied after carcinogen exposure²³. Based on the finding that I3C had no effect on the rate of removal of DNA adducts when it was incorporated into the diet after carcinogen exposure³⁵, it would appear that it is important to repair the damage induced by carcinogens at an early stage.

In this study, I3C treatment inhibited cell cycle-related genes that were up-regulated by DMBA treatment. It has been reported that I3C treatment induces G1 arrest in a breast cancer cell line¹⁷, and combination therapy with tamoxifen induces suppression of the growth of human breast cancer cells¹⁸. In this study,

Table 2. Gene analysis from up-regulated genes by I3C treatment.

Gene symbol	Gene title	RefSeq Transcript ID	Fold change G1 vs G4	Fold change G1 vs G5	KEGG_Definition
Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	NM_017042	-1.24149791	-0.957642996	MAPK signaling pathway; Calcium signaling pathway; Apoptosis; Wnt signaling pathway; Axon guidance; VEGF signaling pathway; Natural killer cell mediated cytotoxicity; T cell receptor signaling pathway; B cell receptor signaling pathway; Long-term potentiation
Tgfr1	transforming growth factor, beta receptor 1	NM_012775	-1.429215699	-1.06411593	MAPK signaling pathway; Cytokine-cytokine receptor interaction; TGF-beta signaling pathway; Adherens junction; Colorectal cancer; Pancreatic cancer; Chronic myeloid leukemia
Crebbp	CREB binding protein	NM_133381	-1.237478963	-0.907236654	Neurodegenerative Disorders; Cell cycle; Wnt signaling pathway; Notch signaling pathway; TGF-beta signaling pathway; Adherens junction; Jak-STAT signaling pathway; Long-term potentiation; Melanogenesis; Huntington's disease; Renal cell carcinoma; Prostate cancer
Pik3c2b_predicted	phosphoinositide-3-kinase, class 2, beta polypeptide (predicted)	NM_001105951 /// XM_001060466 /// XM_213879	-1.876854528	-0.773322896	Phosphatidylinositol signaling system
Vamp4_predicted	vesicle-associated membrane protein 4 (predicted)	NM_001108856 /// XM_001070325 /// XM_344168	-1.409909017	-1.103830892	SNARE interactions in vesicular transport
Ddx52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	NM_053525	-1.366772065	-1.008179366	Starch and sucrose metabolism; Folate biosynthesis
Sp1	Sp1 transcription factor	NM_012655	-1.235411929	-0.949305052	TGF-beta signaling pathway

Ccnb2 and Cdc2a were suggested as cell cycle-related genes, which may be involved in cancer inhibition by I3C at an early stage.

Furthermore, I3C treatment inhibited MAPK signaling pathway-related genes, such as Fgfr1 and Pdgfrb, which were also up-regulated by DMBA treatment. Fgfr1 is a transmembrane receptor that mediates the signal transduction of fibroblast growth factor and part of the tyrosine kinase receptor, that is related to tumor formation and affects cellular regulation such as proliferation, apoptosis, cell movement, and angiogenesis³⁶. Moreover, Pdgfrb binds to the platelet-derived growth factor BB homodimer, which is related to the formation of breast cancer³⁷. Although Ppp5c acts as a phosphatase and inactivates atrial natriuretic peptide receptor/guanylyl cyclase³⁸, no relationship with tumor formation has been reported until now.

Additionally, I3C treatment inhibited insulin signaling pathway genes such as Ppp1r3b and Flot2, which were up-regulated by DMBA treatment. Ppp1r3b is a subunit of protein phosphatase-1 that is involved in hepatic glycogen-related activity³⁹; however, no relationship with tumor formation has been reported. Also

Flot2 is a GPI-related cell adhesion molecule and is related to the metastasis of squamous cell carcinoma in head and neck⁴⁰.

On the other hand, I3C treatment induced recovery to control level of Tgfr1 and Ppp3cb which were down-regulated by DMBA treatment. TGF-beta binds to TGF-beta receptor and acts as an important factor in cell cycle, cell differentiation, matrix formation, growth inhibition, angiogenesis, immune suppression and apoptosis. Tgfr1, as a TGF-beta receptor, inhibits liver tumor formation^{41,42}. It has also been thought that Ppp3cb is a protein phosphatase⁴³, however, no clear association with tumor formation has been reported.

Taken together, we have identified several genes involving the cell cycle, MAPK signaling pathway, insulin signaling pathway, and TGF-beta signaling pathway, as implicated in the chemopreventive effect of I3C in mammary carcinogenesis at an early stage. Further studies are thus warranted to analyze the functions of these genes using siRNA in DMBA-induced carcinogenesis, such that any chemopreventive strategy will be based on a firm foundation.

Materials & Methods

Animals and Chemicals

Five week-old female Sprague-Dawley (SD) rats were obtained from Charles River Japan, Inc. (Atsugi, Japan), and housed in a room maintained on a 12-h light/dark cycle, at constant temperature and humidity. They were allowed free access to pellet chow (MF-1, Oriental Yeast Co., Tokyo, Japan) during the experiment. I3C and DMBA were purchased from Sigma Chemical Co. (St. Louis, MO, USA).

Treatments

Nine SD rats were divided randomly into three groups (n=3 per group). Animals of Groups 1 and 2 were maintained on MF-1 basal diet throughout the period. Animals of Group 3 were given a diet containing 300 ppm I3C from 6 weeks of age. At 7 weeks of age, animals of Groups 2 and 3 were orally intubated with DMBA (10 mg/rat) solved in sesame oil; animals of Group 1 were injected with sesame oil only. All animals were sacrificed at 2 weeks after I3C treatment.

Animals were fed with or without 300 ppm I3C in their diet and were sacrificed at 8 weeks of age. At necropsy, the mammary glands from each group were fixed in 10% phosphate-buffered formalin and processed routinely for embedding in paraffin, and 4- μ m sections were stained with hematoxylin and eosin for histopathological examination. Mammary gland samples from all animals were also snap-frozen in liquid nitrogen for RNA extraction and subsequent analysis.

RNA Isolation, cRNA Preparation and Microarray Hybridization

Approximately 100 mg of frozen tissue was homogenized, and total RNA was isolated using ISOGEN (Nippon Gene Co. Ltd, Tokyo, Japan), isopropanol precipitated, dissolved in DEPC-treated distilled water, and stored at -80°C until use. RNA concentrations were determined by spectrophotometry (Ultraspec 3000, UV/visible spectrophotometer; Pharmacia Biotech, Tokyo, Japan). The quality of the isolated RNA was assessed by the absorbance at 260 nm, the A260/A280 ratio (1.7-2.0), and evaluation of the integrity of 28S and 18S RNA bands on 1% agarose gels.

A 12- μ g aliquot of total RNA was processed for cDNA synthesis using a cDNA synthesis kit (Affymetrix, Santa Clara, CA, USA) according to the manufacturer's protocol. Biotin-labeled antisense cRNA was synthesized by the *in vitro* transcription reaction (IVT) using an RNA transcript labeling kit (Affymetrix), purified and fragmented, and then hybridized to an oligonucleotide microarray (Affymetrix Gene Chip[®],

Rat Genome 230 2.0 Array) for 16 h at 45°C according to the manufacturer's instructions. The arrays were washed and stained with R-phycoerythrin conjugated streptavidin (Molecular Probes, Eugene, OR, USA) using a Fluidics station 450 (Affymetrix) and then scanned with an Affymetrix GeneChip Scanner 3000.

Raw data were converted into cell intensity measurements using the Affymetrix GeneChip Operating System and then standardized using the MARS 5.0 algorithm. Gene expression data from the microarray were input to GenPlex software ver 3.0 (ISTECH Inc., Korea). Gene expression patterns were analyzed by hierarchical clustering, using genes extracted from each group, by one-way ANOVA ($P < 0.05$). The signal log ratio values, which represent the ratios of hybridization signals between Groups 1 and 2 or Groups 2 and 3, were calculated. Altered genes were defined as those differing by over 1.2-fold with significance ($P < 0.05$) using the unpaired Welch's t-test, and common genes were extracted by Venn diagram.

The classification of associated pathways for interesting genes was performed using the KEGG pathway database. The selected genes were annotated based on NetAffx (<http://www.affymetrix.com>).

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