

Oncogenic mutations in IDH1 affect the MLL1-mediated NF- κ B pathway activation

Ya Gao¹, Maurice de Wit¹, Iris de Heer¹, Jory Prince¹, Eduard Struys³, Cassandra Verheul², Gajja S. Salomons³, Peter Sillevius Smitt¹, Martine Lamfers², Pim J. French¹

Departments of ¹ Neurology and ² Neurosurgery, Erasmus Medical Center, Rotterdam, the Netherlands; ³ Department of Clinical Chemistry, VU University Medical Center, Amsterdam the Netherlands

Under revision

ABSTRACT

Background

The gene encoding isocitrate dehydrogenase 1 (*IDH1*) is frequently mutated in gliomas. *IDH1*^{R132H} is the most common mutation in *IDH1*, resulting in a neomorphic enzyme that produces D-2-hydroxyglutarate (D2HG). The elevated level of D2HG inhibits a number of pathways that ultimately causes cells to remain in an undifferentiated stem-like state. It is however unclear whether all pathways affected by mutant IDH1 have been identified.

Methods

We performed a biotin pull-down assay followed by mass spectrometry to identify potential binding partners of IDH1. The interaction was confirmed for both IDH1-wildtype (IDH1^{wt}) and IDH1-mutants (IDH1^{R132H}, IDH1^{R132C} and IDH1^{G70D}) using western blot analysis and proximity ligation assays. An NF-κB luciferase reporter assay was used to determine NFκB pathway activation. Proliferation was measured using an IncuCyte (Essen bioscience).

Results

Our data show that IDH1^{R132H}, but not IDH1^{wt}, inhibited the TNFα-induced NF-κB pathway activation. We demonstrate that this inhibition was mediated by D2HG and was MUL1 dependent. In IDH1^{wt}-expressing cells, TNFα induces an immediate transient growth arrest. In contrast, IDH1^{R132H}-expressing cells continue to grow following stimulation with TNFα stimulation. We show that this reduced growth attenuation was also observed in IDH1^{wt}-expressing cells treated with octyl-D2HG and it was dependent on MUL1.

Conclusion

Our data indicate that IDH1 interacts with MUL1 and we show that IDH1 mutations inhibit the MUL1-mediated NF-κB pathway activation. This inhibition ultimately leads to an insensitivity to stimuli that inhibit cell growth.

INTRODUCTION

Somatic mutations in the *isocitrate dehydrogenase 1* (IDH1) gene have been identified in more than 70 % of diffuse astrocytomas, oligodendrogliomas and secondary glioblastomas (sGBMs) (1-3). Mutations are almost always heterozygous and over 90 % of these mutations are missense mutations leading to replacement of arginine 132 by histidine (R132H) within the catalytic domain (IDH1^{R132H}). Mutations in the IDH1 gene also occur in several other tumor types including acute myeloid leukemia, chondrosarcomas and intrahepatic cholangiocarcinomas (4-6). Wildtype IDH1 catalyzes the decarboxylation of isocitrate to α -ketoglutarate (α KG) and produces NADPH, whereas mutant IDH1 reduces α KG to generate D-2-hydroxyglutarate (D2HG) and produces NADP⁺ (7). Mutations in the IDH1 gene are one of the earliest genetic aberrations during oncogenesis of gliomas, especially those of lower grade (lower grade glioma, LGG) (8). IDH1 mutations are clonal and retained as gliomas progress in time to a higher grade, suggesting continuous dependence on the mutation by tumor cells (3, 9). These properties make mutant IDH1 a good target for therapy.

The product of mutant IDH1, D2HG, shares structural resemblance with α KG and the elevated D2HG level interferes with a number of α KG-dependent enzymes (10). Examples include TET2 and KDM4A/JMJD2A, enzymes involved in the demethylation of DNA and histones (10-12). The increased level of D2HG also affects the hydroxylation of HIF-1 α by the Egl nine homolog 1 (EGLN1) prolyl hydroxylase (13), which leads to an upregulation of HIF1 α -inducible genes including vascular endothelial growth factor (VEGF) (14, 15). It should be noted that, due to the different affinities for D2HG, the α KG-dependent enzymes are affected at various levels (10, 12). As a result of the competitive inhibition of α KG-dependent oxygenases, IDH1 mutant cells ultimately remain in an undifferentiated state (16).

Although these studies demonstrate the involvement of mutant IDH1 and the concomitant increase in D2HG during oncogenesis, it is possible that other pathways are also affected by mutant IDH1 and D2HG. In this study, we performed a biotin-pull down and identified mitochondrial ubiquitin E3 ligase 1 (MUL1) as a novel binding partner for IDH1. We show that mutant IDH1 and the elevated D2HG level affects the function of MUL1 in regulating the NF- κ B pathway.

MATERIALS AND METHODS

Constructs and cell lines

IDH1^{wildtype} and *IDH1*^{R132H} were cloned into pEGFP-C2 (Addgene) as described previously (17). Additional mutations were created using site-directed mutagenesis with primers (5'-CTATCATCATAGGTTGTCATGCTTATGGGGATCAATAC-3' and 5'-CCATAAGCATGACAACCTATGATGATAGGTTTTAC-3') for *IDH1*^{R132C} and (5'-AGAAGCATAATGTTGACGTCAAATGTGCCAC-3' and 5'-GTGGCACATTTGACGTCAACATTATGCTTCT-3') for *IDH1*^{G70D}. All the constructs were checked by Sanger sequencing. HEK and U87 cell lines stably expressing *IDH1*^{wt}, *IDH1*^{R132H} and eGFP were cultured in selective DMEM medium with 400 to 600 µg/ml Geneticin (Gibco, Invitrogen, Breda, the Netherlands) as described (18). The *MUL1* clone was a gift kindly provided by Dr. Bae (19). Patient-derived glioma stem cell line was cultured as previous (20). *IDH1* mutation status was confirmed using Sanger sequencing. The use of patient tumor tissue was approved by the Institutional Review Board of the Erasmus Medical Center, Rotterdam.

HEK MUL1 Knockout cells

5x 10⁵ HEK cells were seeded in a well of a 6-well plate 24 hours before transfection. Transfection was performed using FuGENE (Promega, Leiden, The Netherlands) according to manufacturer's protocol with CRISPR/Cas9 constructs targeting the first exon of *MUL1* as described (21) and co-transfected using an eGFP reporter construct. Single cell sorting was applied to the transfected cells by a BD FACS Aria III (Beckton Dickinson, NJ, USA) based on GFP expression. Genotyping was performed when each clone reached about 90 % confluency in a 96-well plate.

Biotin pulldown and mass spectrometry

IDH1^{wt} and eGFP constructs were transfected into HEK cells using Polyethylenimine "Max" (Polysciences, Eppelheim, Germany). *IDH1*^{wt} protein was isolated using Dynabeads (Life Technologies, Carlsbad, USA) and proteins specifically bound to *IDH1*^{wt} were identified as described (18).

Proximity ligation assay (PLA)

HEK cells were seeded in 8-well LabTek glass slide plates (Thermo Fisher Scientific, Rochester, USA) and transfected with *IDH1* constructs using FuGENE (Promega) according to manufacturer's protocol. Primary glioma cells were cultured as described (20) and transferred on glass slides by CytospinTM (Thermo Scientific) at 300 rpm for 5 minutes at room temperature. Cells were fixed with 4 % PFA and permeabilized with 10 % Triton X-100 in PBS for 10 minutes, followed by twice PBS/Tween wash.

The PLA assay was performed according to manufacturer's protocol (DUOLink, Uppsala, Sweden). Antibodies used were IDH1 (1:500, Sigma-Aldrich, Zwijndrecht, the Netherlands), eGFP (1:500, Abcam, Hilversum, The Netherlands) and MUL1 (1:500, Sigma-Aldrich).

Immunoblotting

Western blots were performed as previously described (22). Primary antibodies used were directed against I κ B (1:1000, Cell Signaling), Mul1 (1:1000), IDH1 (1:1000), GFP (1:1000), β -actin (1:5000, Sigma-Aldrich), and HPRT (1:1000, Abcam). Intensity of proteins bands on the blots was quantified using Image Lab 5.1 (BIO-RAD).

Luciferase reporter assay

Cells were plated and transfected with the NF- κ B reporter constructs (accession code EU581860, Promega) along with IDH1 mutant constructs and controls using FuGENE according to manufacturer's protocol. Cells were lysed in 100 μ l lysis buffer followed by incubation with luciferin substrate (Promega). Luciferin unit was quantified by a Dual-Luciferase Reporter Assay System (Promega). Three independent experiments were performed.

Proliferation assay

Proliferation assays were performed using an IncuCyte (Essen Bioscience, Ann Arbor, MI) as described (22). 4×10^5 cells were seeded in each well of a 96-well plate. Cells were stimulated with 1 μ g/ml TNF α when they were at the log growth phase. Growth curves were constructed using the IncuCyte software based on data extracted from Confluency v1.5 metric. Confluency was measured every 2 hours. Growth rate was calculated using confluency at 3 sequential time points before and after TNF α stimulation divided by time (% confluency/ hours). This experiment was performed three times independently. Each experiment included 5 wells per condition as technical replicates. P values were calculated using Student's t-test with even variance.

RESULTS

IDH1 associates with MUL1

To identify binding partners for IDH1, we performed a biotin-pulldown using HEK cells stably expressing IDH1-wildtype (IDH1^{wt}) (18). Subsequent mass spectrometry identified over 90 candidates. We filtered out duplicate hits, proteins that also associated with the control construct (bio-eGFP) and proteins present in > 10 % of CRAPome pulldown results (23). Six candidate IDH1-interacting proteins remained

(Table 1). Although the Mascot score of all IDH1-interacting proteins was low compared to other studies performed in our laboratory (22), MUL1 showed the highest affinity for IDH1^{wt}. We therefore further investigated the potential interaction between these two proteins.

Table 1. Potential binding partners of IDH1^{wt}

Gene symbol	Mascot score	Description
MUL1	283	Mitochondrial ubiquitin ligase activator of NF- κ B 1
FLOT1	194	Flotillin 1
SRP14	184	Signal recognition particle 14 kDa protein
OTUB1	176	Ubiquitin thioesterase OTUB1
CYR61	100	Uncharacterized protein
AAAS	87	Achalasia variant

To validate the mass spectrometry results, we performed an independent biotin pull-down using HEK cells stably expressing IDH1^{wt}, IDH1^{R132H} and eGFP. Subsequent western blot confirmed the association between MUL1 and IDH1 (both IDH1^{wt} and IDH1^{R132H}) but not in control cells expressing eGFP (Fig. 1A). This association was further confirmed using an *in situ* proximity ligation assay (PLA) in which a red fluorescent signal is only present when two proteins are in close proximity. In transiently transfected HEK cells, a strong signal was observed in cells expressing IDH1 (IDH1^{wt} and IDH1^{R132H}) but not in eGFP controls (Fig. 1B). Two additional IDH1 mutation constructs were included in these experiments, IDH1^{R132C} and IDH1^{G70D}. The IDH1^{R132C} mutation has a higher enzymatic activity in producing D2HG than IDH1^{R132H} (24) and IDH1^{G70D} is a loss-of function mutation reported in 10 % of thyroid cancers (7, 25). Increased intracellular D2HG levels were indeed detected in HEK cells expressing IDH1^{R132C} but not IDH1^{G70D} (supplementary Fig. 1). Both IDH1^{R132C} and IDH1^{G70D} mutants also showed specific association with MUL1 (Fig. 1B). The association between IDH1 and MUL1 by PLA was further confirmed in U87 glioblastoma cell lines that stably expressed either IDH1^{wt} or IDH1^{R132H} (Fig. 1C). Moreover, the interaction was also detected in one primary cell lines derived from a IDH1^{wildtype}-GBM and two IDH1^{R132H}-mutated LGG (glioma stem cells, GCS) (Fig. 1D and E). PLA results were validated in three independent experiments. These experiments demonstrate that IDH1, both wildtype and mutant, interact with MUL1 and that the interaction is independent of the ability of IDH1 to produce D2HG.

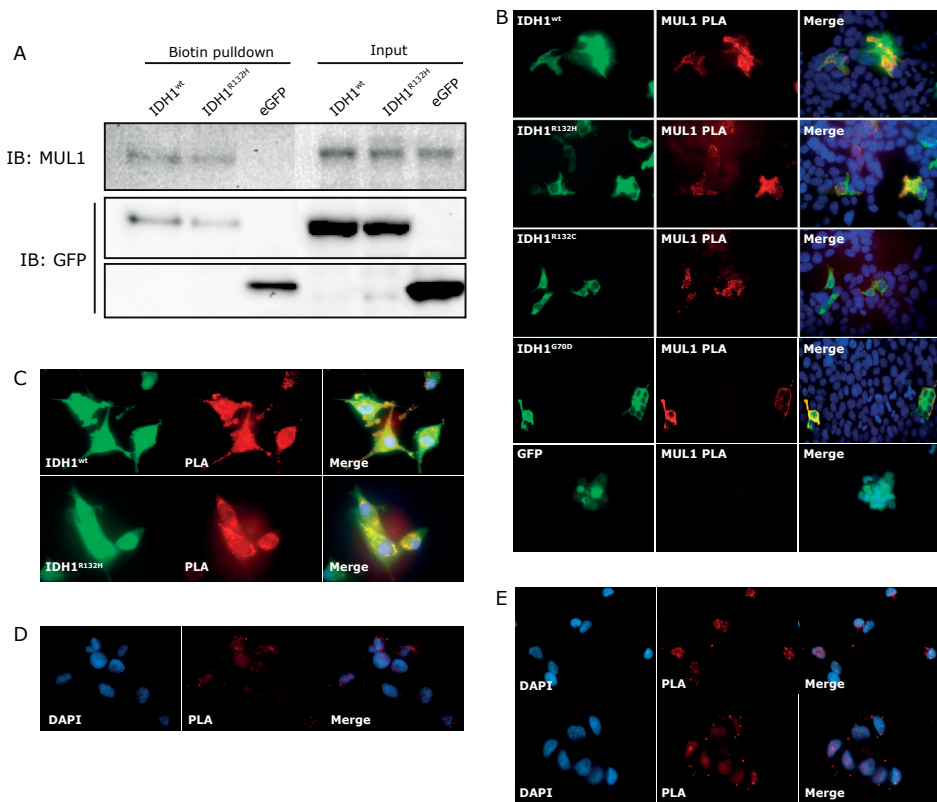


Figure 1. Association between MUL1 and IDH1. MUL1 protein was detected before and after biotin pull-down using HEK cells expressing IDH1 constructs (A). No MUL1 protein was associated with IDH1 in control eGFP-expressing cells. In PLA assays, a red fluorescent signal is seen when two proteins are in close proximity. Proximity ligation assays confirm that MUL1 co-localizes with IDH1 but not with eGFP controls. Results are shown for HEK cells (B) and U87 cells (C). Primary IDH1R132H mutant glioma cells confirmed the co-localization in glioma cells. In this case, the PLA was performed using IDH1 and MUL1 antibodies (D).

MUL1 is involved in the TNF α -induced activation of NF- κ B pathway

MUL1 was initially identified as an activator of NF- κ B pathway in a large-scale screen (26). However, luciferase reporter assays failed to show an activation of the NF- κ B pathway by MUL1 overexpression (Supplementary Fig. 2). We therefore generated MUL1 knockout (MUL1 K.O.) HEK cells using CRISPR/Cas9 (Supplementary Fig. 3) and examined NF- κ B pathway activation. Since I κ B is degraded after activation of the canonical NF- κ B pathway, we determined NF- κ B pathway activation by measuring cellular I κ B levels on western blot. As expected, western blot demonstrated a decreased I κ B level in HEK cells upon TNF α stimulation (Fig. 2a and 2b). Interestingly, the I κ B level was not affected when stimulating MUL1 K.O. cells with TNF α , which indicates that MUL1 plays an important role in the TNF α -induced activation of the NF- κ B pathway.

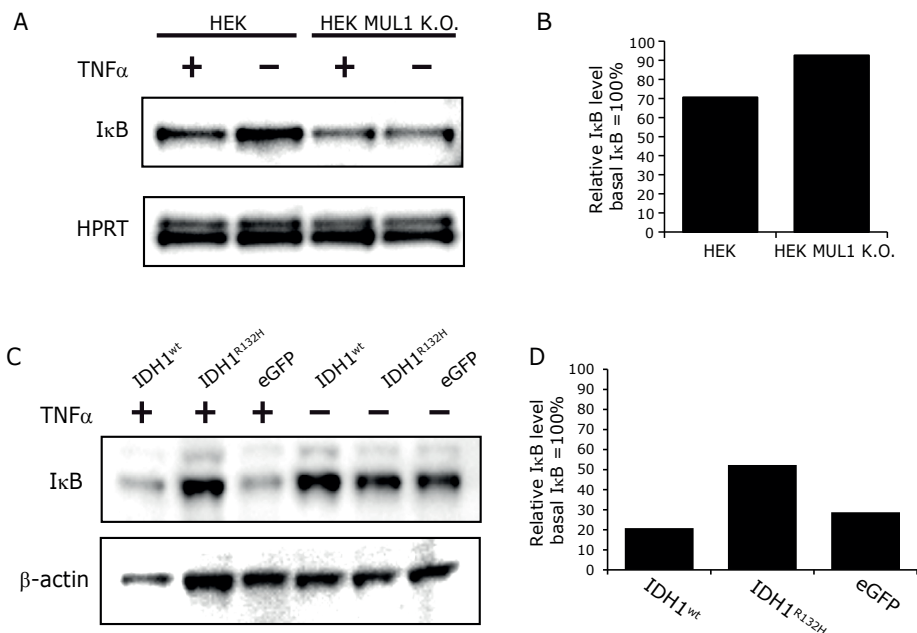


Figure 2. MUL1 depletion and IDH1 mutations results in insensitivity to TNFα stimulation. (A) Western blot showed that stimulation of HEK cells with TNFα results in a degradation of IκB in wildtype HEK cells. This degradation is absent in MUL1 K.O. cells. (B) quantification of protein bands in A. (C) IκB is degraded upon TNFα stimulation in HEK cells expressing IDH1^{wt} but not cells expressing IDH1^{R132H}. (D) Quantification of protein bands in B.

MUL1 is inhibited by D2HG-producing IDH1 mutants

We next measured the IκB levels upon TNFα stimulation in HEK cells stably expressing IDH1^{wt}, IDH1^{R132H} or eGFP (Fig. 2c and 2d). Similar to the eGFP control cells, TNFα induced a decrease in IκB levels in HEK cells expressing IDH1^{wt}. However, TNFα did not induce a decrease in IκB levels in HEK cells expressing IDH1^{R132H}. To determine whether the attenuated NF-κB pathway activation in IDH1^{R132H}-HEK cells was related to the elevated D2HG levels, we measured the IκB level in HEK cells in the presence of octyl-D2HG, a cell permeable analogue of D2HG (Fig. 3a and 3b). Similar to the HEK cells expressing IDH1^{R132H}, normal HEK cells cultured in the presence of octyl-D2HG showed less IκB degradation after TNFα stimulation. Our experiments therefore indicated that the TNFα-induced NF-κB pathway activation was inhibited by IDH1^{R132H} and D2HG.

To examine if NF-κB pathway activity is affected by D2HG in other cell types, we cultured human T lymphocytes in the presence of 300μM octyl-D2HG for 48 hours followed by stimulation with TNFα. Similar to observed in HEK cells, a reduced degradation of IκB was detected in the cells exposed to D2HG compared to cells exposed to PBS controls (Fig. 3c and 3d).

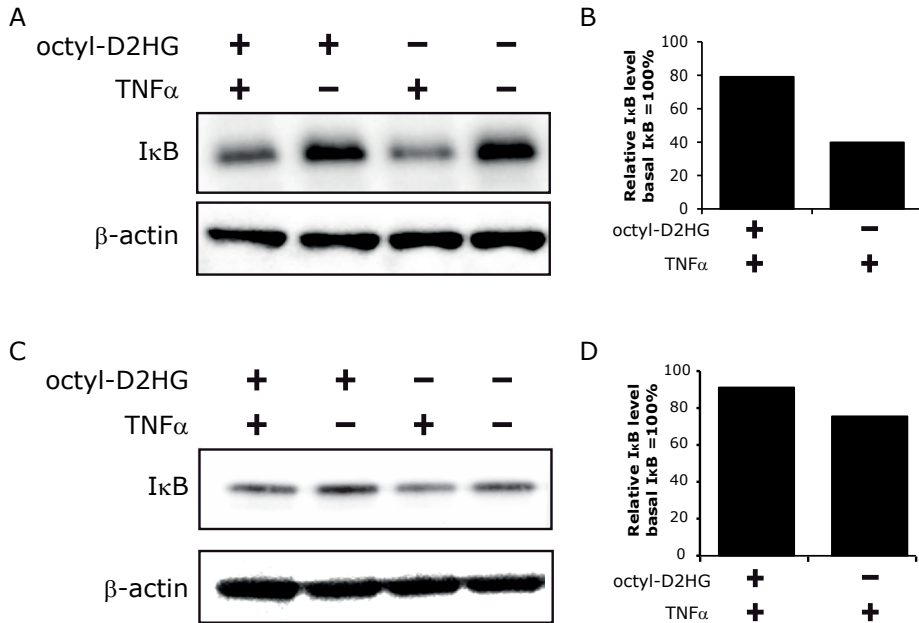


Figure 3. High levels of D-2HG result in insensitivity to TNF α stimulation. Western blot showing I κ B degradation in HEK (A) and T lymphocytes (C) after stimulation with TNF α . This degradation is however reduced when cells are stimulated in the presence of 300 μ M octyl-D2HG. (B and D) Quantification of A and C respectively.

We next investigated NF- κ B pathway activity using luciferase reporter constructs to validate our western blot data. For this, HEK cells stably expressing IDH1^{wt}, IDH1^{R132H} or eGFP control were transfected with the NF- κ B luciferase reporter construct (Fig. 4a). The basal level of NF- κ B activity in HEK cells expressing eGFP control was similar to the HEK cells expressing IDH1^{wt} ($n=4$, $p=0.314$). However, a lower NF- κ B activity was detected in HEK cells expressing IDH1^{R132H} ($n=4$, $p=0.007$). As observed in the western blot for I κ B, our data showed that while TNF α stimulates the NF- κ B pathway in IDH1^{wt} and eGFP cells ($n=4$, $p=0.110$), the NF- κ B pathway was less sensitive to TNF α stimulation in IDH1^{R132H} cells ($n=4$, $p=0.020$). TNF α also resulted in less activation of the NF- κ B pathway when normal HEK cells were cultured in the presence of 300 μ M of octyl-D2HG (Fig. 4b, $p=0.016$). These data therefore confirm that IDH1^{R132H} and D2HG attenuate the TNF α -stimulated NF- κ B pathway activity in HEK cells.

Cellular effects of IDH1 mutations on NF- κ B pathway activation

To determine the cellular effect of IDH1 mutations on NF- κ B pathway activation, we transfected HEK cells with various IDH1-mutation constructs and measured their growth rate before and after TNF α stimulation. HEK cells expressing IDH1^{wt} and

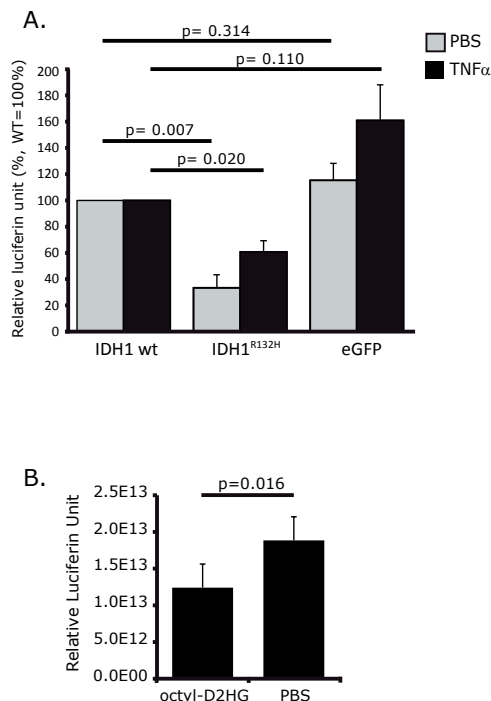


Figure 4. Luciferase reporter assays confirm the attenuated TNF α response in cells expressing IDH1^{R132H} or incubated in the presence of D2HG. HEK cells expressing IDH1^{R132H} showed less NF- κ B activity compared to the controls at both basal and stimulated conditions (A). HEK cells treated with octyl-D2HG also showed less NF- κ B activation compared to controls (B).

IDH1^{G70D} showed a temporary growth arrest after stimulation with TNF α (Fig. 5a and Supplementary Fig. 4a). IDH1^{wt} and IDH1^{G70D} cells grew at a rate of 1.0 % and 1.1 % confluency increase per hour respectively before TNF α stimulation (Supplementary Table 1). After TNF α stimulation, cells almost completely stopped growing and the growth rate reduced to 0.0 % and 0.1 % confluency increase per hour (100 % and 91 % reduction in growth rate). This decrease was highly significant, $p = 0.0004$ and $p = 0.0003$ for IDH1^{wt} and IDH1^{G70D} respectively. The TNF α induced growth arrest lasted for more than 10 hours in both IDH1^{wt} and IDH1^{G70D} cell lines.

Interestingly, HEK cells expressing IDH1^{R132H} or IDH1^{R132C} did not show the complete TNF α -induced growth attenuation (Fig. 5b and Supplementary Fig. 4b). Instead, the IDH1^{R132H} or IDH1^{R132C} cells remained growing albeit at reduced rate. Before TNF α stimulation, IDH1^{R132H} and IDH1^{R132C} cells grew at a rate that was similar to IDH1^{wt} and IDH1^{G70D} cells (1.1 % and 1.0 % confluency increase per hour respectively, Supplementary Table 2). After TNF α stimulation however, the rate was reduced to 0.3 % and 0.5 % confluency increase per hour, which was significantly higher than IDH1^{wt} and IDH1^{G70D} (Fig. 5c, $p = 0.0019$ for IDH1^{R132H} v. IDH1^{wt} and $p < 0.0001$ for IDH1^{R132C} v. IDH1^{wt}, $n = 5$). TNF α also was unable to induce a transient growth arrest in MUL1 K.O. cells (Fig. 5d-f and Supplementary Table 2). This growth arrest was independent

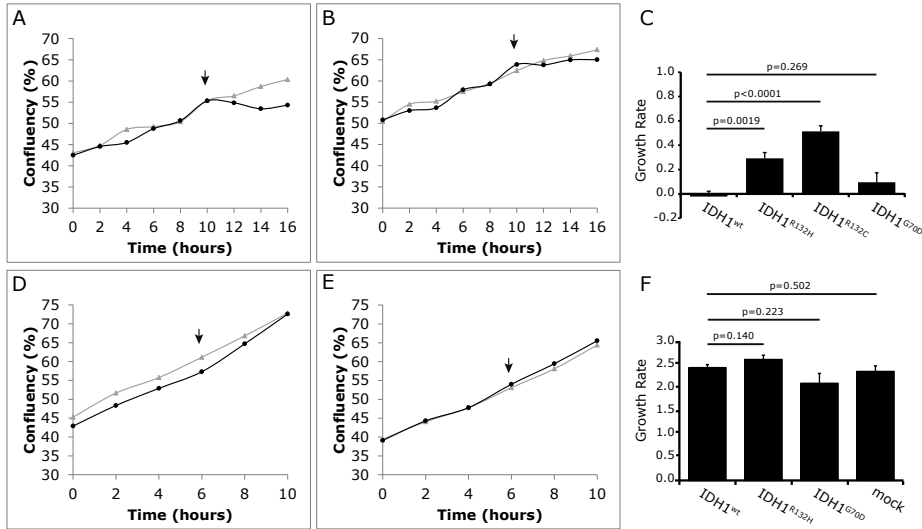


Figure 5. IDH1 mutant cells are insensitive to TNF α -induced growth arrest and this insensitivity is dependent on MUL1. Growth curves of HEK cells expressing IDH1wt (A) and IDH1R132H (B). As shown, the growth of HEK cells expressing IDH1wt was suspended following TNF α stimulation whereas HEK cells expressing IDH1R132H were less susceptible to TNF α -induced growth arrest. Growth rates of HEK cells stimulated with TNF α were calculated using confluency (%) divided by time (hours) (C). As expected, growth rates of HEK cells expressing IDH1wt and IDH1G70D after TNF α stimulation were similar and close to 0 ($n=4$, $p=0.296$). Whereas the growth rates of HEK cells expressing IDH1R132H and IDH1R132C were significantly higher than IDH1wt-expressing cells after TNF α stimulation ($n=4$, $p=0.0019$ and $p<0.0001$ respectively). Growth curves of HEK MUL1 K.O. cells expressing IDH1wt (D) and IDH1R132H (E). As can be seen, the growth of MUL1 K.O. HEK cells does not change following TNF α stimulation, regardless of the presence of IDH1 mutations. The growth rates of HEK MUL1 K.O. cells expressing IDH1wt showed no difference compared to the HEK MUL1 K.O. cells expressing IDH1R132H or IDH1G70D after TNF α stimulation (F, all p values were not significant). Black lines: TNF α stimulation, grey lines: control. The arrow denotes the time point where cells were stimulated with TNF α .

of IDH1 expression as it was absent in MUL1 K.O. cells expressing either IDH1^{wt}, IDH1^{R132H}, IDH1^{G70D} or mock control (Fig. 5d and f, Supplementary Fig. 4c and 4d and Supplementary Table 2). These results demonstrate that the impaired TNF α -induced growth arrest depends on expression of MUL1 and is inhibited by IDH1 mutants that produce D2HG.

DISCUSSION

In this study, our biotin-pull down assay identified MUL1 as a novel binding partner for IDH1. We show that mutant IDH1 and the elevated D2HG level affect the function of MUL1 in inhibiting the activation of the NF- κ B pathway. This ultimately results in an attenuated TNF α -induced growth arrest of cells. Our study therefore identified

the NF- κ B pathway as a pathway that is affected by oncogenic mutations in IDH1 and elevated levels of D2HG.

MUL1 was first identified to be an activator of the NF- κ B pathway in a large-scale screen (26). Although our data failed to show activation of the NF- κ B pathway by MUL1 overexpression, our data do show that MUL1 plays an important role in the TNF α -induced NF- κ B pathway activation as this activation is absent in MUL1 K.O. cells (Fig. 5).

A previous study highlighted a potential tumor suppressor function of MUL1 as it showed significantly decreased expression level in several cancer cell lines compared to normal tissue (27). Moreover, the *MUL1* gene is homozygously deleted at a low but significant frequency in various cancer types including pancreatic cancers (7.3 %) and cholangiocarcinomas (3.4 %) (28). Our data are consistent with MUL1 functioning as a tumor suppressor gene as we show that MUL1 is involved in mediating growth arrest following TNF α stimulation and MUL1 K.O. cells do not show such growth arrest.

Our data show that MUL1 interacted with IDH1, regardless of the presence of oncogenic IDH1 mutants that produce D2HG (Fig. 2). A similar inhibition was observed in normal HEK cells treated with octyl-D2HG, which suggests that D2HG is a key mediator of the inhibition (Fig. 3). Similar to MUL1 K.O. cells, cells expressing IDH1^{R132H} or IDH1^{R132C} continued to grow following TNF α stimulation (Fig. 5b and Supplementary Fig. 4b). It should be noted that MUL1 K.O. cells were completely insensitive to TNF α induced growth inhibition whereas cells expressing IDH1^{R132H} or IDH1^{R132C} showed some arrest in their growth. It is possible that higher D2HG levels are required for a complete inhibition.

The mechanism behind the inhibitory effect of IDH1 on the TNF α -induced growth arrest remains to be elucidated. It is possible that, similar to other pathways affected by mutant IDH1, α KG-dependent enzymes are involved. Nevertheless, our study clearly demonstrates that mutant IDH1, and the concomitant increase in D2HG, are involved in regulating the NF- κ B pathway. The clinical efficacy of inhibiting D2HG production in IDH1 mutated tumors is currently being investigated. Our data suggest that MUL1 is a downstream target for treatment in IDH mutated tumors and may be amenable for targeting.

Accumulated D2HG levels were detectable not only within IDH-mutated tumor cells but also in their extracellular environment (29, 30). It is possible that high extracellular D2HG levels result in elevated D2HG levels within stromal cells surrounding the

tumor (e.g. by passive diffusion or uptake). If D2HG reaches high enough concentrations, it could affect the function of those cells. The TNF α -induced NF- κ B activation is critical for activating T lymphocytes and our data show that this activation was inhibited when culturing T lymphocytes in the presence of D2HG (31-33) (Fig. 3c). These data are in line with a study showing that D2HG decreased expansion of CD4⁺ and CD8⁺ T cells (30). Other studies have also shown a role for D2HG in affecting the immune system. For example, a recent study demonstrated that D2HG suppresses the number of T lymphocytes recruited to the LGGs by inhibiting CXCL10 expression (34).

In conclusion, our data indicated that IDH1 interacts with MUL1 and we show that IDH1 mutations inhibit the MUL1-mediated NF- κ B pathway activation. This inhibition ultimately leads to an insensitivity to stimuli that inhibit cell growth.

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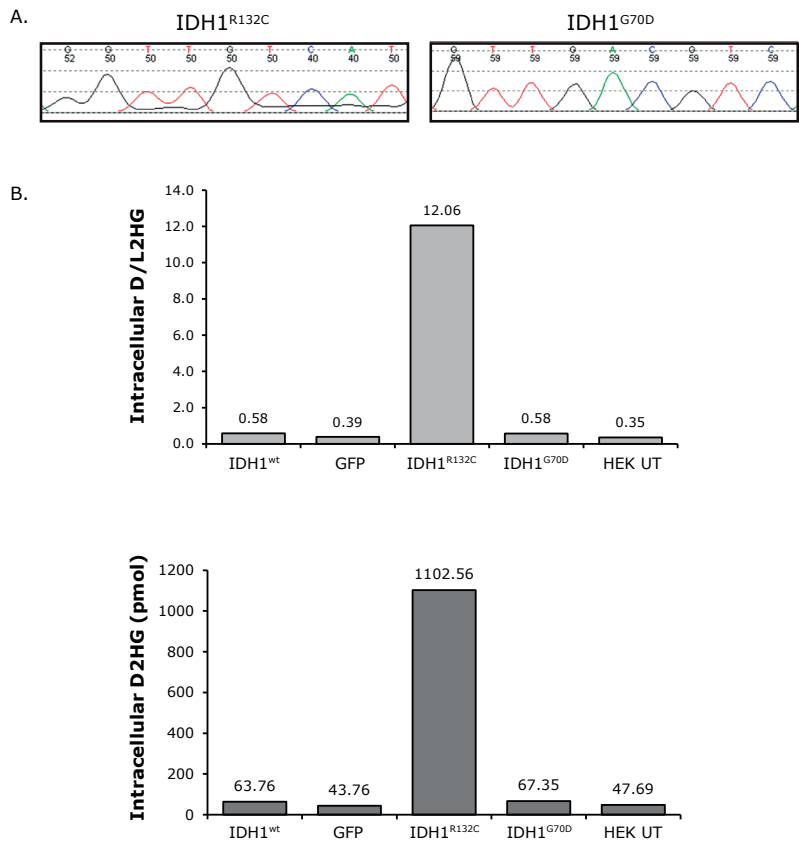
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Supplementary Table 1. Growth rate of HEK cells expressing different IDH1 constructs before and after TNF α stimulation.

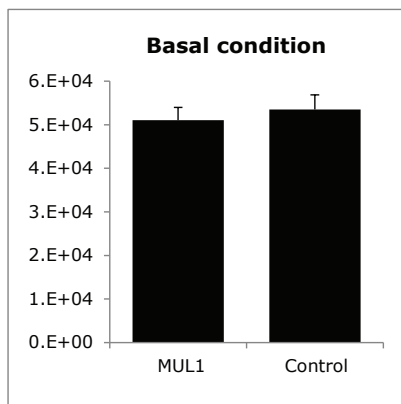
	Before TNF α (\pm SE)	After TNF α (\pm SE)	Reduced growth rate after stimulation with TNF α (%)	Before PBS (\pm SE)	After PBS (\pm SE)	Reduced growth rate after stimulation with PBS (%)
IDH1^{wt}	1.0 \pm 0.094	0.0 \pm 0.043	100	1.1 \pm 0.153	1.0 \pm 0.119	10
IDH1^{R132H}	1.1 \pm 0.049	0.3 \pm 0.048	73	1.0 \pm 0.064	0.9 \pm 0.103	10
IDH1^{R132C}	1.0 \pm 0.111	0.5 \pm 0.045	50	1.2 \pm 0.068	1.1 \pm 0.120	8
IDH1^{G70D}	1.1 \pm 0.040	0.1 \pm 0.078	91	1.0 \pm 0.021	1.0 \pm 0.108	0

Supplementary Table 2. Growth rate of MUL1 Knockout HEK cells expressing different IDH1 constructs before and after TNF α stimulation.

	Before TNF α (\pm SE)	After TNF α (\pm SE)	Reduced growth rate after stimulation with TNF α (%)	Before PBS (\pm SE)	After PBS (\pm SE)	Reduced growth rate after stimulation with PBS (%)
IDH1^{wt}	2.4 \pm 0.092	2.5 \pm 0.066	0	1.9 \pm 0.141	2.3 \pm 0.213	0
IDH1^{R132H}	2.2 \pm 0.098	2.6 \pm 0.091	0	2.0 \pm 0.073	2.5 \pm 0.193	0
IDH1^{G70D}	1.8 \pm 0.123	2.1 \pm 0.215	0	1.9 \pm 0.216	2.0 \pm 0.170	0
mock	2.1 \pm 0.043	2.4 \pm 0.119	0	1.9 \pm 0.044	2.3 \pm 0.161	0

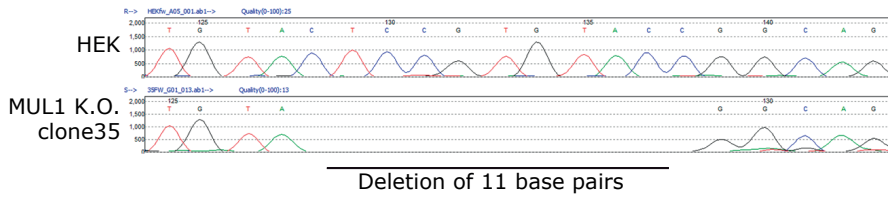


Supplementary Figure 1. Characterization of IDH1 constructs. Sanger sequencing confirmed the IDH1^{R132C} and IDH1^{G70D} (A). Elevated D2HG level was detected in HEK cells expressing IDH1^{R132C} using LC/MS (B). The D2HG level was generalized using L2HG levels in each sample (upper panel). Absolute D2HG concentration of each sample is shown in the lower panel. UT: un-transfected.

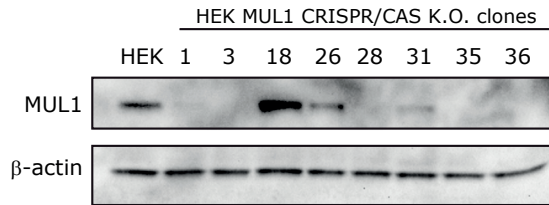


Supplementary Figure 2. Overexpression of MUL1 does not activate NF- κ B pathway in HEK cells stably expressing eGFP.

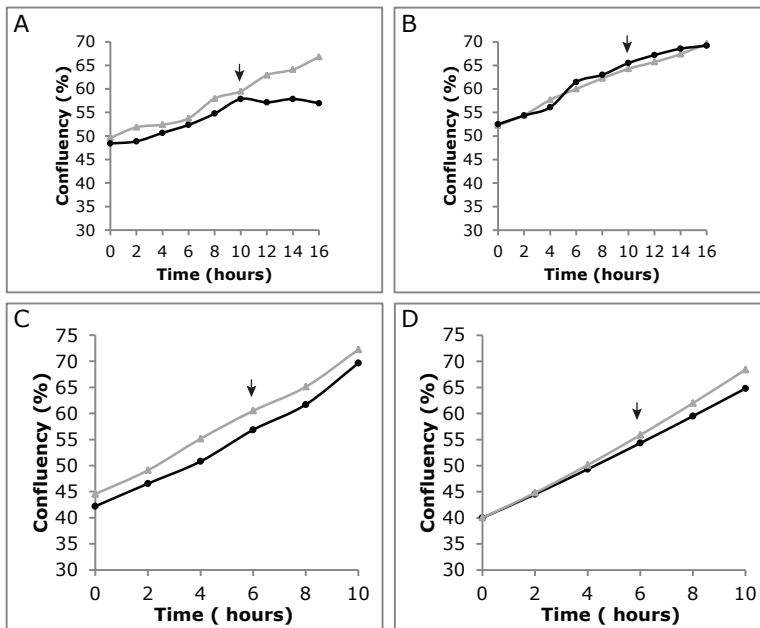
A.



B.



Supplementary Figure 3. Generation of MUL1 knockout (MUL1 K.O.) HEK cell lines using CRISPR/CAS9 system. A. Targeted Sanger sequencing showed 11 base pairs of deletion in the exon 1 of MUL1 K.O. HEK cells. B. Immunoblotting confirmed the depletion of MUL1 in HEK K.O. cells.



Supplementary Figure 4. TNF α -induced growth arrest is inhibited in IDH1R132C-expressing cells or MUL1 K.O. cells. Growth curves of HEK cells expressing IDH1G70D (A) and IDH1R132C (B). As shown, the growth of HEK cells expressing IDH1G70D was suspended following TNF α stimulation whereas HEK cells expressing IDH1R132C were less susceptible to TNF α -induced growth arrest. Growth curves of HEK MUL1 K.O. cells expressing IDH1G70D (C) and IDH1R132C (D). The growth of MUL1 K.O. HEK cells does not change following TNF α stimulation, regardless of the presence of IDH1 mutations. Black lines; TNF α stimulation, grey lines: control. The arrow denotes the time point where cells were stimulated with TNF α .