

Diacylglycerol kinase δ regulates protein kinase C and epidermal growth factor receptor signaling

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Diacylglycerol kinases (DGKs) phosphorylate diacylglycerol (DAG) to terminate its signaling. To study DGK δ , we disrupted its gene in mice and found that DGK δ deficiency reduced EGF receptor (EGFR) protein expression and activity. Similar to EGFR knockout mice, DGK δ -deficient pups were born with open eyelids and died shortly after birth. PKCs are activated by DAG and phosphorylate EGFR to reduce its expression and activity. We found DAG accumulation, increased threonine phosphorylation of EGFR, enhanced phosphorylation of other PKC substrates, and increased PKC autophosphorylation in DGK δ knockout cells, indicating that DGK δ regulates EGFR by modulating PKC signaling.

Diacylglycerol kinases (DGKs) catalyze the phosphorylation of diacylglycerol (DAG) to produce phosphatidic acid (1, 2). DAG, the substrate of the DGK reaction, is a key intracellular signaling factor that activates PKCs, Ras guanyl nucleotide-releasing proteins, and some transient receptor potential channels (3, 4). DAG also recruits a number of proteins to membrane compartments, including the chimaerins, PKD, and the Munc13 proteins (3). Its effects on numerous and diverse targets underscores the importance of DAG signaling and indicates that DAG affects a broad array of signaling events. Because the consumption of DAG by DGKs is thought to attenuate these actions, the DGK reaction is biologically important and likely regulates numerous DAG signaling pathways.

Mammalian DGKs differ in their structures, patterns of tissue expression, and catalytic properties. Ten of them have been identified and are classified into five subtypes based on their structural motifs (1, 2, 5, 6). Their structural diversity and distinct expression patterns indicate that each isoform may perform a different biological function. Supporting functional diversity, the DGK knockout mice that have been studied to date have distinct phenotypes, including resistance to seizures in DGK ϵ knockout mice (7), attenuated Ras signaling in DGK ι knockouts (8), and hyperactive T cell signaling in DGK ζ -deficient mice (9).

As a type II DGK, DGK δ has a characteristic pleckstrin homology domain and a sterile α -motif domain (Fig. 1A). To determine its biological function, we generated mice with a targeted mutation of the DGK δ gene. Our data indicate an important role for DGK δ in modulating PKC and EGF receptor (EGFR) signaling.

Results and Discussion

We used mice to make a targeted deletion of the N-terminal portion of the DGK δ catalytic domain (see Fig. 7, which is published as supporting information on the PNAS web site). Southern blot analysis of tail DNA confirmed proper insertion of the targeting vector (data not shown), and RT-PCR demonstrated absence of DGK δ mRNA in homozygous mutant cells (Fig. 7C). Also confirming DGK δ gene inactivation, DGK δ protein was absent in knockout keratinocyte and dermal fibroblast cell lysates (Fig. 7D). Deleting DGK δ did not significantly affect mRNA expression of other DGKs in brain tissue (Fig. 7E). Finally, to establish the expression pattern of DGK δ in WT mice, we performed RT-PCR using mouse tissues and found DGK δ mRNA in most tissues and in developing embryos (Fig. 7F).

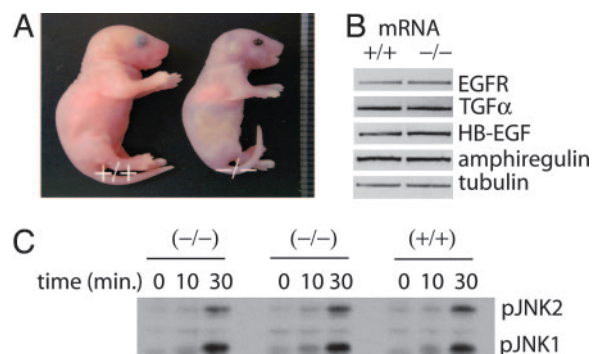


Fig. 1. Morphology of DGK δ -deficient mice, expression of EGFR and its growth factors, and JNK signaling. (A) Newborn DGK δ knockout mice had open eyelids and were smaller than normal littermates. (B) Using mRNA from primary keratinocytes, we detected EGFR, TGF α , HB-EGF, amphiregulin, and tubulin by RT-PCR. (C) DGK δ mutant or WT immortalized embryo fibroblasts were treated with activin B (10 ng/ml) for the indicated times, and phosphorylated JNK1 and JNK2 (pJNK1 and 2) were detected by immunoblotting.

Heterozygous mice (*dgkd*^{+/-}) were viable and fertile, and the genotypes of newborn progeny from *dgkd*^{+/-} intercrosses were consistent with Mendelian inheritance. Unexpectedly, the homozygous null defect was invariably lethal: *dgkd*^{-/-} mice developed respiratory difficulty and died within 24 h after birth. Additionally, most *dgkd*^{-/-} fetuses were smaller than WT and heterozygous littermates: Newborn *dgkd*^{-/-} mice weighed 1.10 \pm 0.21 g ($n = 11$), whereas WT mice weighed 1.39 \pm 0.15 g ($n = 11$). Newborn *dgkd*^{-/-} mice were identifiable by their open eyelids (Fig. 1A). Normally, eyelids fuse at approximately embryonic day (E) 16.5 and do not open until approximately postnatal day 14. In contrast, at E17.5 and at birth, all *dgkd*^{-/-} fetuses that we examined had open eyelids.

Several genetic abnormalities result in the phenotype of open eyelids at birth. In most cases, these mutations have disrupted EGFR signaling. For example, disrupting the genes encoding c-Jun (10, 11), JNK (12), or MEK (MAPK/ERK kinase) kinase 1 (13) resulted in reduced expression of EGFR and/or its growth

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Abbreviations: DAG, diacylglycerol; DGK, DAG kinase; EGFR, EGF receptor; TACE, TNF α converting enzyme; HB-EGF, heparin binding EGF; cPKCs, conventional and novel PKCs; pT EGFR, threonine-phosphorylated EGFR; pY EGFR, phospho-tyrosine EGFR; MARCKS, myristoylated alanine-rich C kinase substrate.

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factor ligands, causing an open-eyelid phenotype. And disrupting TNF α converting enzyme (TACE), which proteolytically releases EGFR ligands from the cell surface, or EGFR itself similarly caused an open-eyelid phenotype (14–16). TACE is predominantly responsible for shedding the six known EGFR ligands (17). We found no differences in *dgkd*^{-/-} and WT embryo fibroblasts in TACE expression or in their ability to shed overexpressed TGF α , heparin binding EGF (HB-EGF), amphiregulin, and betacellulin (data not shown). Nor were there differences in TNF α or p75 TNF α receptor shedding in newborn *dgkd*^{-/-} and *dgkd*^{+/+} liver homogenates (data not shown). Based on these results, we concluded that DGK δ did not regulate TACE activity.

Several mutations that interrupted the JNK signaling pathway reduced mRNA expression of EGFR and/or its growth factors and resulted in the open-eyelids-at-birth phenotype (10–13). Using semiquantitative RT-PCR, we tested expression of mRNA encoding EGFR, HB-EGF, TGF α , and amphiregulin in primary keratinocytes isolated from either WT or DGK δ -null mice and found similar expression of EGFR and growth factor mRNA in knockout cells compared with WT cells (Fig. 1B). We also found identical phosphorylation of JNK1/2 in *dgkd*^{-/-} and *dgkd*^{+/+} embryo fibroblasts treated with activin B (Fig. 1C). Thus, deleting DGK δ did not affect JNK signaling pathways known to cause aberrant mRNA expression of EGFR or its growth factors.

Next, we examined EGFR protein in primary keratinocytes and consistently found reduced EGFR expression in DGK δ -null keratinocytes (Fig. 2A and B). To verify reduced EGFR expression, we immunostained EGFR in paraffin sections from *dgkd*^{-/-} or *dgkd*^{+/-} newborn mice and found reduced levels of EGFR in all layers of the epidermis in *dgkd*^{-/-} mice. EGFR was most significantly reduced in the basal layer of the epidermis (Fig. 2C). These data indicated that DGK δ is necessary for proper expression of EGFR protein. To verify that reduced DGK δ attenuated EGFR protein expression, we used RNAi to knock down DGK δ in SCC-9 cells, a squamous cell cancer line. Consistent with reduced EGFR expression in DGK δ -deficient mice, we found significantly reduced EGFR protein in DGK δ knockdown cells (Fig. 2D and E).

Our data indicated a crucial role for DGK δ in maintaining EGFR protein expression. We considered the possibility that DGK δ might maintain this expression by regulating DAG signaling. PKC enzymes are major targets of DAG and are known to phosphorylate human EGFR at threonine-654 (T654) (18, 19). The consequences of this phosphorylation are twofold. First, it reduces EGFR tyrosine kinase activity by an unknown mechanism (18–20). Second, it induces internalization of EGFR but then causes the silenced receptor to be recycled to the plasma membrane (21–24). Combined, the overall immediate effect of PKC phosphorylation is to blunt EGFR signaling. The negative effects on EGFR are further augmented if PKC activation continues for several hours, at which point, EGFR is degraded, and its levels fall (25).

By consuming DAG, DGKs can reduce PKC activity (26–28), so we reasoned that deleting DGK δ might have increased PKC activity and caused excess T654 EGFR phosphorylation. To explore this possibility, we immunoprecipitated EGFR from newborn mouse brain lysates and then immunoblotted to detect phospho-Thr-X-Arg. In *dgkd*^{-/-} mice, we found increased phospho-threonine EGFR compared with *dgkd*^{-/-} and WT mice (Fig. 3A and B), which suggested that deleting DGK δ activated PKCs that then phosphorylated EGFR. To test whether expressing DGK δ could attenuate EGFR threonine phosphorylation, we expressed DGK δ 1 in embryo fibroblasts, treated the cells with TGF α , and then immunoprecipitated EGFR and measured its threonine phosphorylation by Western blotting. We found that expressing DGK δ 1 reduced the phosphorylation of T654 in

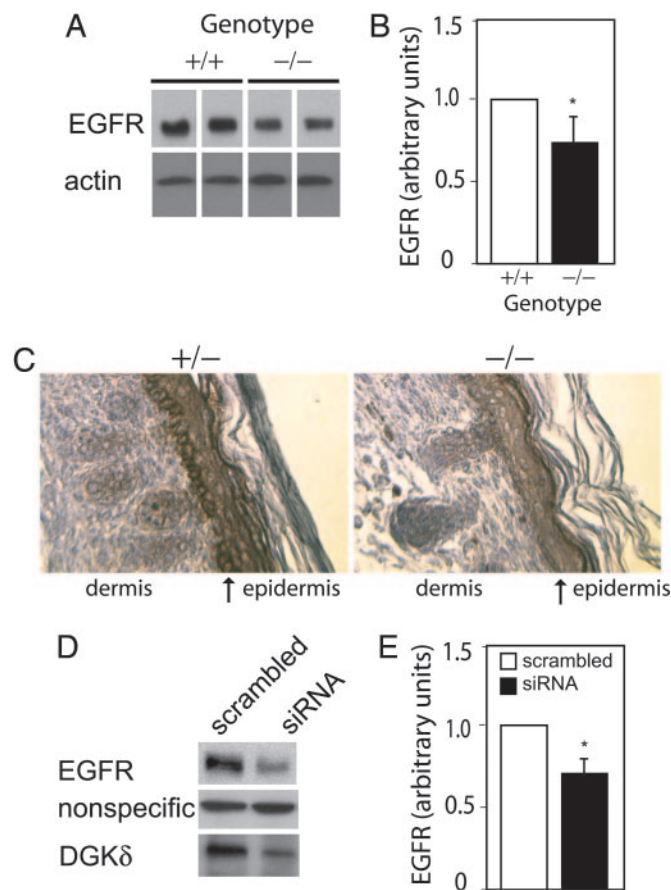


Fig. 2. DGK δ deficiency reduces EGFR expression. (A) EGFR and β -actin protein expression in WT or DGK δ knockout primary keratinocytes was detected by Western blotting. Samples from two WT and two knockout lysates are shown; lane separations were removed from the blot for clarity. (B) Scanning densitometry of EGFR Western blots demonstrated significant reduction of EGFR expression in DGK δ -null cells. Shown are mean values and SD for DGK δ knockout mice compared with WT (*, $P < 0.02$; $n = 12$). (C) Back skin from heterozygous (+/-) and homozygous (-/-) DGK δ mutant mice was immunostained to detect EGFR (brown) and counterstained with hematoxylin. The arrows mark the basal layer of the epidermis. (D) Using siRNA, DGK δ was knocked down in SCC-9 cells. After 48 h, EGFR and DGK δ were detected by immunoblotting. Shown is a nonspecific band detected by the anti-EGFR antibody that did not change upon knockdown of DGK δ . There was also no change in expression of β -actin (not shown). (E) Scanning densitometry of Western blots from six experiments demonstrated that knockdown of DGK δ reduced EGFR expression. Shown are mean values and SD of DGK δ siRNA compared with scrambled control siRNA (*, $P < 0.05$).

EGFR (Fig. 3C and D). Together, our data indicate that DGK δ regulates PKCs that phosphorylate EGFR.

Increased T654 EGFR phosphorylation in *dgkd*^{-/-} mice would be expected to eventually reduce EGFR protein expression levels by causing its degradation. To test whether we could rescue EGFR expression by inhibiting PKCs, we treated *dgkd*^{-/-} keratinocytes with a broad-spectrum PKC inhibitor, bisindolylmaleimide I, for 1 h and found partial rescue of EGFR expression in the cells (Fig. 3E). Other PKC inhibitors, Gö6976 and Gö6983, also increased EGFR expression in *dgkd*^{-/-} keratinocytes and SCC-9 cells treated with DGK δ siRNA (data not shown). Because SCC-9 cells and keratinocytes express at least five PKC isoforms and the inhibitors that we used would not affect all of them, it was not surprising that the inhibitors did not fully restore EGFR expression. Because PKCs participate in endosome formation and trafficking (29, 30) and can phosphorylate and regulate dynamin (31), we explored the possibility that

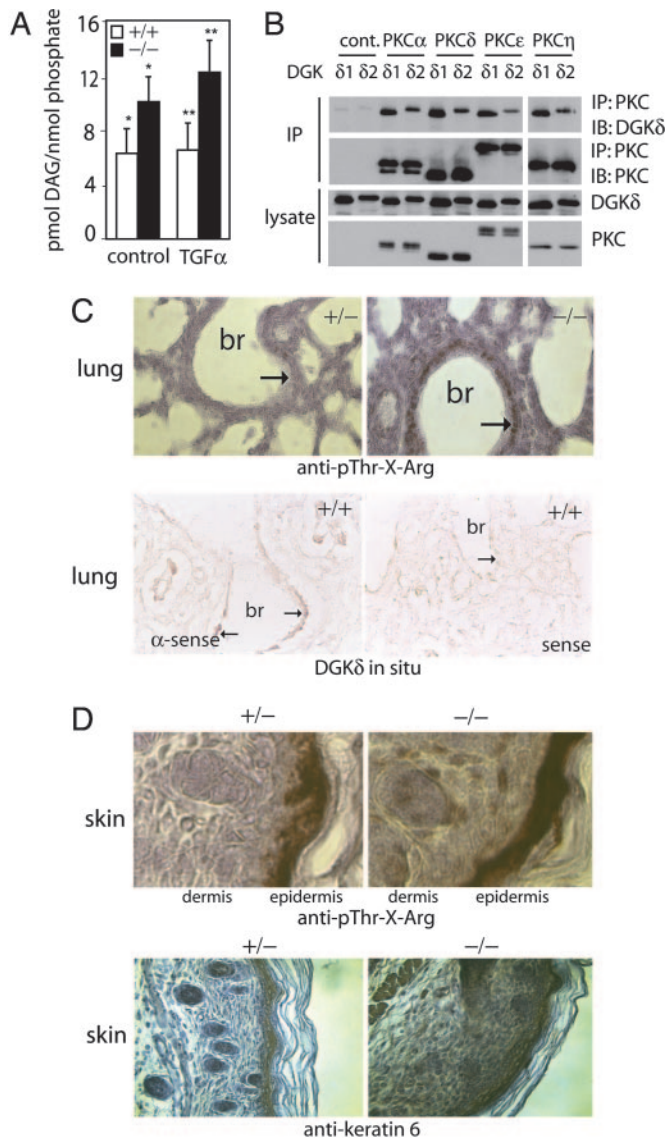


Fig. 5. DAG levels and assessment of PKC activity. (A) DAG quantity in starved or TGF α -treated (10 ng/ml for 15 min), immortalized embryo fibroblasts was normalized to lipid phosphate. Shown are mean values and SD ($n = 4$). * and ** indicate that the changes were significant ($P < 0.05$) as calculated by one-tailed t tests. (B) FLAG-DGK δ 1 or FLAG-DGK δ 2 was cotransfected into MCF-7 cells with either control vector or a PKC isotype with a Myc epitope tag. The PKC was immunoprecipitated with anti-Myc antibodies, and coimmunoprecipitation of DGK δ was detected by immunoblotting using anti-FLAG antibodies. (C Upper) Sections from heterozygous (+/-) or DGK δ -null (-/-) newborn mouse lung that were immunostained to detect phospho-Thr-X-Arg and counterstained with hematoxylin. In *dgkd*^{-/-} mice, there was increased immunostaining (brown, marked by arrows) in the epithelial lining of the major bronchi (br). (C Lower) Lung sections from WT mice processed for *in situ* hybridization by using an antisense (α -sense) probe. Expression of DGK δ mRNA (brown, marked by arrows) in the epithelium of major bronchi is shown. There was minimal *in situ* staining of the epithelium (marked by arrow) with the sense probe. (D) Sections from heterozygous (+/-) or DGK δ -null (-/-) newborn mouse back skin immunostained brown to detect phospho-Thr-X-Arg or keratin 6 and counterstained with hematoxylin.

and keratin 6 immunostaining in *dgkd*^{-/-} mice indicated that deleting DGK δ led to increased PKC activity.

To confirm high levels of PKC activity in cells and tissue from the mice, we immunoblotted primary dermal fibroblast lysates to detect phospho-MARCKS (myristoylated alanine-rich C kinase substrate), a major substrate of PKCs, and found increased

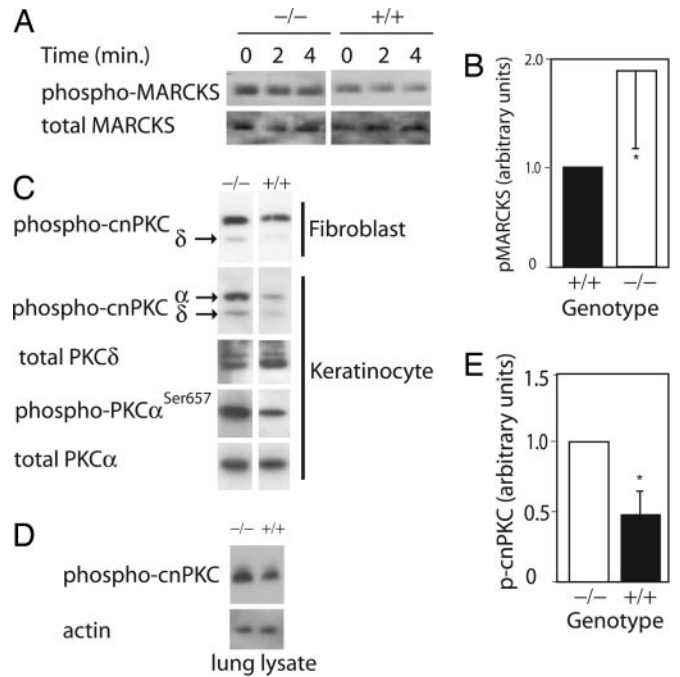


Fig. 6. Indicators of active PKCs. (A) Primary dermal fibroblasts were treated with TGF α (10 ng/ml) for the indicated times. Phospho-MARCKS was then detected in the cell lysates by immunoblotting. Membranes were stripped and reprobed to detect total MARCKS. (B) Western blots of phospho-MARCKS (pMARCKS) were quantified by scanning densitometry. There was a significant increase in pMARCKS in DGK δ -null cells compared with WT cells. Shown are mean values and SD from four experiments (*, $P < 0.05$). (C) Starved primary dermal fibroblast or keratinocyte lysates were immunoblotted to detect hydrophobic motif phosphorylation of cnPKCs (phospho-cnPKC) or phospho-PKC α ^{Ser657}. Blots were stripped and reprobed to detect total PKC α and PKC δ . Bands corresponding to PKCs α and δ are marked by arrows. (D) Lung lysates from DGK δ mutant or WT mice were immunoblotted to detect hydrophobic motif phosphorylation of cnPKCs (phospho-cnPKC). The blot was reprobed to detect β -actin. (E) Western blots of phospho-cnPKC (p-cnPKC) were quantified by scanning densitometry. There was a significant increase in cnPKC phosphorylation in DGK δ -null lung lysates compared with WT cells. Shown are mean values and SD (*, $P < 0.05$; $n = 3$).

MARCKS phosphorylation in *dgkd*^{-/-} cells compared with *dgkd*^{+/+} cells (Fig. 6 A and B). Finally, to assess the abundance of active PKCs, we measured the levels of phospho-PKC in the lysates by immunoblotting with an antibody to detect hydrophobic motif serine/threonine phosphorylation of cnPKCs. We found that, in starved cells, there were at least two highly phosphorylated PKC isoforms in *dgkd*^{-/-} cells compared with *dgkd*^{+/+} cells. Using an antibody that is specific for phospho-PKC α ^{Ser657}, we determined that it was one of the highly phosphorylated PKCs in keratinocytes (Fig. 6C). Using scanning densitometry of Western blots, we found 1.20 (± 0.04 ; $n = 5$; $P < 0.05$) times more phospho-PKC α in DGK δ -null keratinocytes compared with WT or heterozygous cells. And based on the mobility of PKC δ , which migrates farther than other PKCs, we determined that it was often phosphorylated at higher levels in *dgkd*^{-/-} fibroblast and keratinocyte lysates (Fig. 6C). In five experiments using scanning densitometry, we found 1.63 (± 0.95) times more phospho-PKC δ in DGK δ -null keratinocytes compared with WT or heterozygous cells. The changes in PKC δ were not statistically significant, likely because its phosphorylation was often, but not always, elevated in the knockout cells. To verify these observations in newborn mice, we immunoblotted newborn lung lysates and similarly found significantly increased phospho-cnPKC in *dgkd*^{-/-} mice (Fig. 6 D and E). The lung

PKCs (anti-Myc). To immunoprecipitate transfected EGFR, we incubated 250 μ g of cell lysate overnight at 4°C with anti-EGFR (Ab-13; Neomarkers, Fremont, CA) and added protein A/G plus agarose for 1 h, followed by washes as above. To immunoprecipitate endogenous EGFR, 2 mg of newborn liver or brain lysates was combined with anti-EGFR (no. E12020; Transduction Laboratories, San Jose, CA) overnight at 4°C; then, protein A/G agarose was added for 1 h, followed by washes as above.

DAG Quantity Assays. Immortalized embryo fibroblasts were starved overnight and treated with TGF α (10 ng/ml) for 15 min. Cells were washed once with PBS and harvested in methanol. Lipid extractions, DAG quantity assays, and lipid phosphate assays were performed as described in ref. 40.

Assays of TACE Activity. Primary or immortalized embryo fibroblasts were transfected with either control vector or a growth factor (TGF α , HB-EGF, amphiregulin, or betacellulin). Twenty-four hours later, the cells were starved overnight. Agonist (50 ng/ml phorbol ester, 2 units/ml thrombin, or 25 μ M lysophosphatidic acid) in fresh medium was added for 30, 60, or 120 min. The medium was collected, and debris was pelleted. The amount of growth factor in the medium and cell lysates was then determined by using sandwich ELISAs (protocols are available

on request). All agonists that were tested caused a 2- to 3-fold increase in growth factor shedding compared with nontreated controls. Results were normalized to total protein or growth factor in the lysate. Additional experiments testing the effects of overexpressing either DGK δ splice variant in HEK293, HeLa, or MCF-7 cells demonstrated no difference in growth factor release. To assay TNF α or p75 TNF receptor (TNFR) shedding, livers from newborn mice were homogenized in DMEM, and debris was allowed to settle. The remaining cell suspension (500,000 cells in 1 ml) was treated with agonist (5 μ g/ml lipopolysaccharide or 50 ng/ml phorbol ester) for 3 h at 37°C. TNF α (no. KMC3012; Biosource, Carlsbad, CA) or p75 TNFR (no. 269SKI; PharMingen, San Jose, CA) was assayed in the cell lysate or medium by using sandwich ELISAs.

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