Nitro-fatty acids and cyclopentenone prostaglandins share strategies to activate the Keap1-Nrf2 system: a study using green fluorescent protein transgenic zebrafish

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doi: 10.1111/j.1365-2443.2010.01466.x
Nitro-fatty acids and cyclopentenone prostaglandins share strategies to activate the Keap1-Nrf2 system: a study using GFP transgenic zebrafish

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Running title: Nrf2 activation by nitro-fatty acids

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Total character count: 33,789
Abstract

Nitro-fatty acids are electrophilic fatty acids produced in vivo from nitrogen peroxide that have many physiological activities. We recently demonstrated that nitro-fatty acids activate the Keap1-Nrf2 system, which protects cells from damage due to electrophilic or oxidative stresses via transactivating an array of cytoprotective genes, although the molecular mechanism how they activate Nrf2 is unclear. A number of chemical compounds with different structures have been reported to activate the Keap1-Nrf2 system, which can be categorized into at least six classes based on their sensing pathways. In this study, we showed that nitro-oleic acid (OA-NO₂), one of major nitro-fatty acids, activates Nrf2 in the same manner that of a cyclopentenone prostaglandin 15-deoxy-Δ¹²,¹⁴-prostaglandin J₂ (15d-PGJ₂) using transgenic zebrafish that expresses green fluorescent protein (GFP) in response to Nrf2 activators. In transgenic embryos, GFP was induced in the whole body by treatment with OA-NO₂, 15d-PGJ₂ or diethylmaleate (DEM), but not with hydrogen peroxide (H₂O₂), when exogenous Nrf2 and Keap1 were co-overexpressed. Induction by OA-NO₂ or 15d-PGJ₂ but not DEM was observed, even when a C151S mutation was introduced in Keap1. Our results support the contention that OA-NO₂ and 15d-PGJ₂ share an analogous cysteine code as electrophiles and also have similar anti-inflammatory roles.
Introduction

The Keap1-Nrf2 system plays a central role in the cellular defense against electrophilic and oxidative stresses by orchestrating gene expression of detoxifying and antioxidant enzymes (Kobayashi & Yamamoto 2006; Kensler & Wakabayashi 2010). Nrf2 is a transcription factor that heterodimerizes with small Maf proteins and binds to the antioxidant responsive element (ARE)/electrophile responsive element (EpRE) within the regulatory region of its target genes. Keap1 is a substrate-specific adaptor protein for a Cul3-dependent E3 ubiquitin ligase complex that homodimerizes and interacts with the ETGE and DLG motifs of Nrf2. Under basal conditions, Nrf2 is maintained at low levels due to Keap1-dependent ubiquitination and proteasomal degradation. Upon exposure to electrophiles or oxidative stress, Nrf2 is stabilized and accumulates in the nucleus, where it transactivates ARE/EpRE-regulated genes.

A variety of Nrf2 activators have been reported (Kobayashi & Yamamoto 2005). Some of these activators have protective activities against carcinogenesis, neuronal damage and inflammation that can be ingested as dietary agents for the prevention and therapy of age-related diseases such as cancer, cardiovascular diseases, chronic inflammation, and neurodegenerative diseases (Calabrese et al. 2008). On the other hand, positive roles of Nrf2 in cancer tumorigenesis and chemoresistance have recently been uncovered (Hayes & McMahon 2009; Lau et al. 2008). It will be important to understand the differences between the Nrf2 activators, in particular the mechanisms of Keap1-Nrf2 activation, the activation of other systems, and which Nrf2-target genes they induce.

The new field has focused on the identification of sensor molecules that activate Nrf2. These activators have a common ability to modify sulfhydryl groups by alkylation, oxidation, or reduction. This observation suggests that cells possess a primary sensor for Nrf2 activators that is equipped with highly reactive cysteine residues. Cys-151 of mouse Keap1 is a target site for many Nrf2 activators such as DEM (Kobayashi et al. 2009; Sekhar et al. 2010). We recently found that
cyclopentenone prostaglandins, 15d-PGJ2 and prostaglandin A2 (PGA2), target residues other than Cys-151 in Keap1, perhaps Cys-273 (Kobayashi et al. 2009). Furthermore, sensor proteins for H2O2, cadmium chloride, and gold-compound auranofin were not Keap1 or Nrf2 (Kobayashi et al. 2009). The target selections of a variety of Nrf2 activators should be investigated comprehensively.

The Keap1-Nrf2 system is conserved among vertebrates, including zebrafish (Kobayashi et al. 2002; Takagi et al. 2004; Li et al. 2008). Among the known endogenous targets of zebrafish Nrf2, the pi-class glutathione S-transferase 1 gene (gstp1) showed the strongest induction in both electrophile-treated larvae and Nrf2-overexpressing embryos. The gene regulatory region of gstp1 was examined by a GFP reporter gene analysis using microinjection into zebrafish embryos, and an ARE/EpRE-like sequence located 30 bp upstream of the transcription initiation site was shown to be necessary and sufficient for the induction by Nrf2 (Suzuki et al. 2005).

In this study, we tried to generate stable transgenic zebrafish lines that express GFP in response to Nrf2 activators using a 3.5 kb gene regulatory region of gstp1 to develop a rapid and easy method for screening and classifying Nrf2 activators. Two stable transgenic lines that express GFP in the larval olfactory regions in response to Nrf2 activators were isolated. No GFP induction was detected in transgenic embryos, but strong induction in response to DEM and 15d-PGJ2, but not H2O2, was observed when both Nrf2 and Keap1 were overexpressed. Using this system, we classified a newly identified Nrf2 activator, OA-NO2, into the same category as 15d-PGJ2.
Results

**Generation of stable transgenic lines that express GFP in response to Nrf2 activators**

In transient assays, GFP expression from the p3.5gstp1GFP construct which contains a 3.5 kb promoter region of the zebrafish *gstp1* gene is strongly transactivated by Nrf2 in zebrafish embryos (Fig. 1A; Suzuki et al. 2005). Stable transgenic lines carrying this construct were isolated by genotyping F1 embryos from p3.5gstp1GFP-injected founders. Although three stable lines were isolated, none of the three lines exhibited GFP expression upon treatment with DEM, thus suggesting a position effect of the transgene (data not shown; Table S1 in Supporting Information). To circumvent this problem, a highly efficient Tol2 transposon system (Kawakami et al. 2004) was used to generate additional stable lines. A pT3.5gstp1GFP construct was made by introducing Tol2 sequences into p3.5gstp1GFP and were co-injected into zebrafish embryos with mRNA encoding Tol2-specific transposase. Injected founders (n=104) were raised and 12 transgenic lines, which showed GFP expression in F1 larvae, were isolated (Table S1 in Supporting Information). Out of 12 Tg(-3.5gstp1:GFP) lines, two lines exhibited GFP induction in response to DEM, and the rest displayed only basal GFP expression. In the larvae of these two lines (*it416a* and *it416b*), strong GFP induction was observed in the olfactory regions as for endogenous *gstp1*, while constitutive GFP expression was also detected in the lens, ears, fins, pericardium, and lateral lines (Figs. S1 and S2 in Supporting Information). We used the *it416b* line for further experiments because it exhibited stronger GFP induction than the *it416a* line.

In day 4 larvae, induction of endogenous *gstp1* expression began approximately 3 hours after DEM treatment and reached maximum expression levels around 6 to 9 hours (data not shown). GFP induction in the olfactory regions of Tg(-3.5gstp1:GFP)*it416b* larvae was first detected at 6 hours after DEM treatment and later became stronger (Fig. 1B; Movie S1 in Supporting Information). This induction was greatly reduced when *nrf2* was knocked down with the *nrf2*-specific
antisense-morpholino oligonucleotide (nrf2MO) (Kobayashi et al. 2002), suggesting that GFP induction was mediated by Nrf2 (Fig. 1C).

**Quantification of GFP induction**

To quantify the level of the GFP expression, a fluorescent intensity in the olfactory regions was measured using an imaging analyzer equipped with the BZ-8000 microscope (Keyence) (Fig. 2A). The average fluorescent intensities of DEM-induced GFP expression in the olfactory regions were measured using 3, 10, or 30 individual larvae, and all of these showed similar values (Fig. 2B). We therefore used three individuals for quantification of the GFP induction in further analyses. According to this quantification, the reduction of DEM-induced GFP expression by the nrf2-knockdown was calculated as one-third (Fig. 2C).

We first quantified the time- and dose-dependencies of DEM-induced GFP expression. GFP expression in the olfactory regions of Tg(-3.5gstp1:GFP)it416b larvae treated with various DEM concentrations was measured at 3, 6, 10 and 14 hours following treatment (Fig. 2D). GFP induction is detectable with treatment over 30 µM DEM, which is similar for detecting endogenous gstp1 induction by a real-time reverse transcription (RT)-PCR examination (Fig. 2E) or by a whole-mount *in situ* hybridization (data not shown). The onset of GFP induction (6 h) was later than that of endogenous gstp1 induction (3 h), most likely due to the time required for the accumulation of GFP protein. Altogether, these results suggest that the measurement sensitivity of DEM-induced GFP expression using the fluorescence intensities in the olfactory regions is comparable to that of endogenous gstp1 induction in the whole body using a real time RT-PCR analysis.

**Quantification of reduced GFP induction in the it567 mutant larvae**

We have screened and isolated zebrafish mutants that have defects in gstp1 induction by Nrf2
activators (Kobayashi et al. 2009). One of these mutants, it567, has reduced induction of gstp1 in response to DEM. To visualize this reduction in living larvae, we crossed it567 fish with Tg(-3.5gstp1:GFP)it416b fish. As expected, DEM-induced GFP expression in the olfactory regions of it567 homozygous larvae was significantly reduced compared to that of sibling wild-type larvae (Fig. 3; Movie S2 in Supporting Information). The result indicates that homozygous mutant larvae are easily distinguishable from wild-type siblings by monitoring GFP induction upon treatment with DEM, although we have not identified the gene responsible for the it567 mutation.

**GFP induction by a variety of Nrf2 activators**

To elucidate whether Tg(-3.5gstp1:GFP)it416b can monitor the induction by a variety of Nrf2 activators, five Nrf2-activating compounds in different classes were examined (Kobayashi et al. 2009). Day 4 larvae of Tg(-3.5gstp1:GFP)it416b fish were treated with sulforaphane, 15d-PGJ2, H2O2, auranofin or CdCl2, and the GFP expression in the olfactory regions was monitored in three individuals (Fig. 4A). GFP induction was observed in larvae treated with all tested Nrf2 activators, although it was a bit weaker upon induction with H2O2 and CdCl2. The results suggest that Tg(-3.5gstp1:GFP)it416b can be used for the analysis of Nrf2 activator sensing mechanisms and also to screen for novel and unidentified activators.

We recently classified eleven Nrf2 activators based on the requirement of these activators for an Nrf2 response (Kobayashi et al. 2009). The classification was carried out using zebrafish embryos overexpressing Nrf2 and Keap1. The embryos were treated with each Nrf2 activator and the induction of the endogenous gstp1 gene was analyzed by a whole-mount in situ hybridization or by an RT-PCR analysis. It will be time- and labor-saving if Tg(-3.5gstp1:GFP)it416b can be utilized for this analysis. To test this possibility, Nrf2 was overexpressed by an mRNA injection in embryos obtained from crossing heterozygous transgenic males and non-transgenic females and GFP expression was analyzed during gastrulation stages (Fig. S3 in Supporting Information). Robust
GFP expression was observed in the embryos injected with Nrf2 mRNA, while no GFP expression was observed in uninjected embryos.

We then generated homozygous transgenic lines to make all the injected embryos positive for GFP. Embryos obtained from homozygous transgenic males and non-transgenic females were used for the further analyses, because maternal GFP expression was observed in embryos derived from transgenic females (data not shown). When wild-type or C151S mutant Keap1 was overexpressed with Nrf2, no GFP expression was observed, indicating that Keap1 suppressed GFP inducing activity of Nrf2 (Fig. 4B). Treatment of DEM cancelled the Nrf2-suppression by wild-type Keap1 but not by C151S Keap1, while 15d-PGJ2 released Nrf2 activity from both. H2O2 treatment had no effect at all. These results suggest that Keap1 is a sensor for DEM and 15d-PGJ2, but not for H2O2, and Cys-151 is required for DEM but not 15d-PGJ2 sensing. All these results were identical as in the case of the previous analyses conducted using endogenous gstp1 induction (Kobayashi et al. 2009).

**OA-NO₂ activates Nrf2 as 15d-PGJ₂**

OA-NO₂ was next analyzed as an uncharacterized Nrf2 activator using Tg(-3.5gstp1:GFP)it416b. OA-NO₂ is a nitro-fatty acid that has been recently shown to activate Nrf2 (Freeman et al. 2008). Nitro-fatty acids are electrophilic fatty acids produced in vivo from nitrogen peroxide that have many physiological activities, such as cGMP-dependent vessel relaxation, the inhibition of the inflammatory cell function, the induction of heme oxygenase 1 expression, the inhibition of NFκB, peroxisome proliferator-activated receptor (PPAR) activation, and Nrf2 activation. GFP expression in the olfactory regions of Tg(-3.5gstp1:GFP)it416b larvae was analyzed after treatment with OA-NO₂ at 4 days post-fertilization (dpf) (Fig. 5A,B). A significant GFP induction was observed in the olfactory regions of OA-NO₂-treated larvae and was decreased upon Nrf2 knockdown after injecting nrf2MO. GFP induction was also observed with OA-NO₂ treatment of embryos.
overexpressing Nrf2 and Keap1 (Fig. 5C). Significantly, the Keap1 C151S mutation could not eliminate this induction, suggesting that Cys-151 is not a sensing site for OA-NO₂ in the Keap1-Nrf2 system. Identical results were obtained when the induction of endogenous gstp1 was analyzed by RT-PCR (Fig. 5D). We also showed that a Cys-to-Ser mutation in Cys-288, another key reactive cysteine in Keap1, had no effect on the response to OA-NO₂ (Fig. S4 in Supporting Information). It must be noted that these are same results as in the case of 15d-PGJ₂ (Kobayashi et al. 2009).

To determine the sites in Keap1 modified by OA-NO₂, mouse Keap1 protein treated with or without OA-NO₂ was digested with trypsin and analyzed by matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS). Peptide mass mapping by an MALDI-TOF MS analysis of the trypsin fragments of native mouse Keap1 made it possible to identify the peptides, thus accounting for ~80% of the protein sequence (see Table S2 in the Supporting Information). Compared with the calculated masses of the unmodified peptides, modified peptides P-1 to P-6 had an increased mass of +327.4 Da, thus corresponding to the addition of a single equivalent of OA-NO₂ (Fig. 6). The sequences and masses of the peptides were: P-1 (CHALTPR, m/z = 1124.8), P-2 (SGVGVAVTMEPCR, m/z = 1632.7), P-3 (LNSAECYYPER, m/z = 1671.7), P-4 (LSQQLCDVTLQVK, m/z = 1802.1), P-5 (SGLAGCVGGLLYAVGGR, m/z = 1976.2), and P-6 (QEEFFNLSHCQLATLISR, m/z = 2463.3), indicating that mouse Keap1 is modified by OA-NO₂ at Cys-77, Cys-226, Cys-273, Cys-368, Cys-489 and Cys-613. It should be noted that Cys-273 was included in the amino acids to which 15d-PGJ₂ and PGA₂ were shown to bind in our previous analyses (Fig. 6B; Kobayashi et al. 2009).

Another criterion of the classification is dependency to it275 gene. it275 is a zebrafish mutant which has defects in the response to some, but not all, Nrf2 activators. For example, induction of endogenous gstp1 was decreased in it275 larvae in response to 15d-PGJ₂, auranofin and CdCl₂, and was similar with wild-type larvae in response to DEM, sulforaphane and H₂O₂. gstp1 expression
was analyzed in *it275* larvae or sibling wild-type larvae with or without OA-NO$_2$ treatment at 4 dpf by an *in situ* hybridization (Fig. 7). OA-NO$_2$-dependent *gstp1* induction in gills or olfactory regions was dramatically reduced in *it275* larvae compared to wild-type larvae. The reduction was not observed in larvae treated with DEM. This result suggests that Nrf2 activation mediated by OA-NO$_2$ requires the *it275* gene, which is also similar to 15d-PGJ$_2$.

Taken together, OA-NO$_2$ was classified as a class 4 Nrf2 activator, as are 15d-PGJ$_2$ and PGA$_2$ (Kobayashi *et al.* 2009). We thus hypothesize that nitro-fatty acids and cyclopentenone prostaglandins share strategies to activate the Keap1-Nrf2 system.
Discussion

We previously demonstrated that nitrolinoleic acid (LNO₂), a nitro-fatty acid similar to OA-NO₂, also activates Nrf2 in cultured cells (Villacorta et al. 2007). The present study verifies that nitro-fatty acids are indeed effective Nrf2 activators in living animals. The covalent binding of OA-NO₂ with reactive cysteines and histidines has been demonstrated previously in a variety of proteins (Batthyany et al. 2006). It is quite possible that OA-NO₂ directly binds Keap1, most likely at Cys-273. Importantly, OA-NO₂ appears to belong to the same Nrf2 activator class as 15d-PGJ₂ as we have described herein. Strikingly the chemical structures of nitro-fatty acids (OA-NO₂ and LNO₂) and cyclopentenone prostaglandins (15d-PGJ₂ and PGA₂) are similar (Fig. 7A). We speculate that unique structures common between these compounds are essential for targeting identical sites in the Keap1 protein. Besides activating Nrf2, nitro-fatty acids can activate PPARγ as an endogenous ligand with covalent binding to Cys-285 (Schopfer et al. 2005; 2010), and can inhibit NFκB-DNA binding through direct interaction with p65 (Cui et al. 2006). Interestingly, 15d-PGJ₂ also exhibits these properties via direct binding to PPARγ at Cys-285 (Shiraki et al. 2006) and p65 of NFκB at Cys-38 (Straus et al. 2000). It is plausible that OA-NO₂ can also bind to Cys-38 of NFκB p65. We hypothesize that electrophilic signaling compounds, such as nitro-fatty acids and cyclopentenone prostaglandins, can bind to a series of key target proteins (e.g., Keap1, PPARγ and NFκB) and thereby exert their physiological functions (for example, anti-inflammatory effects) by the combined actions of their target proteins (Fig. 7B) (the cysteine code hypothesis, Kobayashi et al. 2009).

The Tg(-3.5gstp1:GFP)it416b line established in the current study can monitor electrophile-induced gene expression in vivo and will be useful for many situations, for example in gene analyses, small molecule screens, and mutant fish screens. Generation of real-time monitoring
systems of electrophile-induced Nrf2 activation has been studied for many years. Stable cell lines that can monitor Nrf2 activation were previously produced using multiple ARE/EpRE sequences as transcriptional drivers and GFP or luciferase as reporter genes (Zhu & Fahl 2001; Wang et al. 2006). The results obtained by use of these cell lines are reproducible and are more reliable than experiments relying on transient transfection. Transgenic mice which have luciferase reporter genes fused to multiple ARE/EpRE sequences were also generated (Yates et al. 2007; Fisher et al. 2007). These transgenic mice are useful since they can allow the monitoring of tissue- and developmental stage-specific profiles of Nrf2 activation. Real-time activation of Nrf2 in disease models can also be analyzed by crossing these mice with a variety of gene-disrupted mice. However, this model has shortcomings, in that administration of the substrate luciferin into mice is required, whose disposition and side-effects may affect the proper analysis of results. The use of GFP instead of luciferase will be helpful to overcome this problem: however, it is difficult to analyze GFP expression in the internal regions of a mouse. Trials to generate stable transgenic zebrafish that harbor ARE/EpRE-driven GFP reporter gene have been carried out (Carvan et al. 2000; Kusik et al. 2008) but were unsuccessful. Tg(-3.5gstp1:GFP)it416b is the first ARE/EpRE-GFP reporter line that can be used to monitor Nrf2 activation at a practical and physiologically relevant level. Our success was due to a screen of effective lines from substantial numbers of stable transgenic lines. In that sense, the use of the Tol2 transposon system was an important strategy which greatly improved the transgene integration efficiency (Kawakami 2007).

At the onset of this study, we hoped to establish transgenic lines that can analyze tissue-specific differences in GFP induction upon induction by a variety of Nrf2 activators. Unfortunately, this method did not succeed. GFP induction in gills and livers, in which endogenous gstp1 was induced (in addition to the olfactory regions), was not observed in the present lines. We supposed that cis- and trans-activating factors required for gstp1 induction differ between tissues. Indeed, cell-specific differences in the induction levels of the ARE/EpRE-reporter gene have been demonstrated using
cultured cell lines (Wang et al. 2006). Gene regulatory elements required for the expression in gills and liver other than ARE/EpRE sequences may not be included in the 3.5-kb gstp1 region. The negative and positive roles of Nrf2 in human health have both been recently demonstrated (Hayes & McMahon 2009; Lau et al. 2008). It will be important to elucidate the molecular mechanisms of the cell-specific induction of Nrf2 target genes, particularly in cancer cells. Modified bacterial artificial chromosomes for transgenesis will be useful to identify cis-activating factors for cell specificity (Yang et al. 2009).

The zebrafish is an attractive model for analyzing gene expression profiles since it has transparent embryos and larvae. Moreover, a transparent adult line, termed casper, has been recently generated (White et al. 2008). Thus, utilizing a GFP reporter will facilitate the visualization of a variety of stress responses in living animals. Indeed, cellular responses to metals, such as cadmium, copper, and arsenate, were monitored in GFP transgenic zebrafish using heat shock promoters (Blechinger et al. 2007; Wu et al. 2008; Seok et al. 2007). GFP induction by environmental estrogens and dioxin was also analyzed by GFP transgenic zebrafish using estrogen response elements + vitellogenin promoter (Chen et al. 2010) and cytochrome P4501A1 promoter (Mattingly et al. 2001), respectively, as transcriptional drivers. The zebrafish provides opportunities to accelerate the process of drug discovery (Zon & Peterson 2005). These GFP transgenic lines, including Tg(-3.5gsp1:GFP)it416b, will contribute to several aspects of the drug development process, including target identification by genetic and morpholino-oligonucleotide screens, lead discovery by small-molecule screens, and the testing of drug efficacy and toxicity. The application of Tg(-3.5gsp1:GFP)it416b to screen novel Nrf2 activators and inhibitors will be therefore be pursued in future studies.
Experimental procedures

Zebrfish

Embryos and larvae were obtained by natural mating. The wild-type strain AB and the mutant strain it567 (Kobayashi et al. 2009) were used. The stable transgenic lines Tg(-3.5gstp1:GFP)it416a and Tg(-3.5gstp1:GFP)it416b were maintained as homozygous lines. Homozygous transgenic lines were crossed with the AB strain to obtain embryos and larvae for experiments. The genotyping of transgenic lines was performed by PCR using genomic DNA as templates and the primers 5’-CCTCGTGACCACCCCTGAC-3’ and 5’-TGGCGGATCTTGAGTTCAC-3’.

The transgenic line, Tg(-3.5gstp1:GFP)it416b, can be obtained upon request under the support of Zebrafish National Bioresource Project of Japan (http://www.shigen.nig.ac.jp/zebra/index_en.html).

Chemical Treatments

For the induction studies, zebrafish were placed in culture dishes containing 100 µM DEM (Wako, Osaka, Japan), 40 µM sulforaphane (LKT laboratories, St. Paul, MN), 2.5 µM 15d-PGJ2 (Cayman Chemical, Ann Arbor, MI), 1 µM auranofin (Enzo Life Sciences, Farmingdale, NY), 1 mM H2O2 (Wako), 20 µM CdCl2 (Wako) and 1.5 or 2.5 µM OA-NO2. OA-NO2 was prepared as previously described (Baker et al. 2005).

Plasmids

pT3.5gstp1GFP was generated by replacing the Xenopus EF1α enhancer/promoter region in pT2KXIG (Kawakami et al. 2004) with a XhoI-NotI fragment of p3.5gstp1GFP (Suzuki et al. 2005). The construct was verified by DNA sequencing. Plasmids pCS2nrf2, pCS2FLmKeap1, pCS2FLmKeap1C151S, pCS2FLmKeap1C288S, pKSgstp1N, and pCS-TP were described
previously (Kobayashi et al. 2002; 2009; Kawakami et al. 2004).

Microinjection

For the overexpression of Nrf2 and Keap1 proteins, synthetic capped mRNA was generated with an SP6 mMESSAGE mMACHINE in vitro transcription kit (Ambion, Austin, TX) using linearized DNA of the pCS2 derivatives described above and injected into yolk at the one-cell stage using an IM300 microinjector (Narishige, Tokyo, Japan). For knocking-down zebrafish Nrf2 (nrf2), antisense morpholino-oligonucleotides (Gene Tools, Philomath, OR) specific for nrf2 (nrf2MO) (Kobayashi et al. 2002) were injected into yolk at the one-cell stage. For generating stable transgenic lines, 25 pg of pT3.5gstp1GFP or p3.5gstpGFP was co-injected into a blastomere of early one-cell stage embryos with 25 pg of Tol2-transposase mRNA synthesized from NotI-linearized pCS-TP as previously described (Takeuchi et al. 2010).

Expression Analysis

GFP expression during various embryonic stages was examined under a GFP2 (480 nm excitation, 510 nm barrier) filter of a MZFLIII microscope (Leica, Wetzler, Germany) equipped with a 600CL-CU digital camera (Pixera Los Galos, CA). GFP expression during larval stages was analyzed under a GFP-BP BZ filter (470 nm excitation, 535 nm emission) of a Biozero BZ-8000 microscope (Keyence, Osaka, Japan). For taking time-lapse photographs, larvae were anesthetized with 0.016% 3-aminobenzoic acid ethyl ester (Sigma-Aldrich, St. Louis, MO) and placed on a hole slide glass containing 3% methylcellulose (Sigma Aldrich) for immobilization. To quantify GFP expression, fluorescence intensity in the olfactory regions was measured by an image processing system equipped with the BZ-8000 microscope. The gene expressions of endogenous gstp1 were examined by an in situ hybridization analysis, a RT-PCR analysis, or a real-time RT-PCR analysis, as previously described (Li et al. 2008; Kobayashi et al. 2001).
MALDI-TOF MS analysis. The recombinant mouse Keap1 protein expressed by *E. coli* was incubated with or without 100 µM OA-NO2 for 60 min at 25°C in buffer containing 20 mM Tris-HCl, pH 8.5. The trypsin-digested mouse Keap1 was mixed with dithiothreitol and trifluoroacetic acid. To improve the ionization efficiency of MS, samples were purified with Zip-tip µC18 (Millipore, Bedford, MA) before MS analysis. Peptides were mixed with α-cyano-4-hydroxycinnamic acid (2.5 mg/ml) containing 50% acetonitrile and 0.1% trifluoroacetic acid and dried on stainless steel targets at room temperature. The analyses were performed using an AXIMA-TOF2 (Shimadzu, Tokyo, Japan) with a nitrogen laser. All analyses took place in the positive ion mode and the instrument was calibrated immediately prior to each series of studies.

Acknowledgements

We thank Sakura Motion Picture Co. Ltd for their assistance with the movies. We also thank T. Kinoshita, H. Niu, T. Shimokoube and Y. Terashita for help in fish maintenance, and T. Suzuki, M. Takeuchi and K. Mukaigasa for help and discussion. We also thank T. Kudoh for critical reading of the manuscript. This work was supported by Grants-in-Aid from the Japan Science and Technology Corporation (ERATO) (to M.Y.), and the Ministry of Education, Science, Sports and Culture of Japan (to M.K. and M.Y.).
References


Figure Legends

**Figure 1** DEM-induced GFP expression in *Tg(-3.5gstp1:GFP)*it416b larvae. (A) A schematic diagram of the p3.5gstp1GFP construct. Ex1 and ExII denote exon 1 and exon 2, respectively, of the *gstp1* gene. (B) Time-course of GFP expression in the olfactory regions (arrowheads) of *Tg(-3.5gstp1:GFP)*it416b larvae at 4 dpf after treatment with 100 µM DEM. The asterisks and arrows denote the constitutive GFP expression in the lens and lateral lines, respectively. Dorsal views. (C) Effects of *nrf2* knockdown on DEM-induced GFP expression. Day 4 larvae of the *Tg(-3.5gstp1:GFP)*it416b line injected with *nrf2*MO at the one-cell stage were treated with 100 µM DEM treatment for 12 hours.

**Figure 2** Quantification of DEM-induced GFP expression. (A) Fluorescence intensities in the areas enclosed by the triangles were analyzed. (B) Determination of sample numbers. The indicated numbers of *Tg(-3.5gstp1:GFP)*it416b larvae were treated with 100 µM DEM for 12 hours at 4 dpf, and the average fluorescence intensities in the olfactory regions were calculated. Error bars indicate standard deviation values. (C) The effects of *nrf2* knockdown on 100 µM DEM-induced GFP expression at 4 dpf. The average fluorescence intensities in the olfactory regions of three individual *Tg(-3.5gstp1:GFP)*it416b larvae were analyzed: larvae were injected with or without *nrf2*MO at the one-cell embryo stage. (D) Time- and dose-effects on DEM-induced GFP expression at 4 dpf. The average fluorescence intensities in the olfactory regions of three individual *Tg(-3.5gstp1:GFP)*it416b larvae were analyzed. (E) Real time RT-PCR analysis. Time- and dose-dependent effects on DEM-induced expression of endogenous *gstp1* at 4 dpf.

**Figure 3** Effect of the it567 mutation on DEM-induced GFP expression. (A) GFP expression in the it567 mutant larvae at 4 dpf. *Tg(-3.5gstp1:GFP)*it416b;it567/it567 larvae or wild-type siblings were treated with 100 µM DEM for 6 hours. Arrowheads indicate the olfactory regions. (B) Average fluorescence intensities of three individual larvae were analyzed. Error bars indicate the standard deviation values.

**Figure 4** GFP induction by a variety of Nrf2 activators. (A) GFP induction in the olfactory regions of *Tg(-3.5gstp1:GFP)*it416b larvae at 4 dpf by sulforaphane (SF), 15d-PGJ2, H2O2, auranofin (AF), and CdCl2. Ctr denotes non-treated control larvae. Error bars indicate the standard deviation values of three individual larvae. (B) GFP induction in *Tg(-3.5gstp1:GFP)*it416b embryos by DEM,
15d-PGJ$_2$ and H$_2$O$_2$. Tg(-3.5gstp1:GFP)it416b embryos co-injected with wild-type (WT) or C151S Keap1 mRNA and Nrf2 mRNA were treated with Nrf2 activators for 6 hours.

Figure 5 OA-NO$_2$ induced GFP expression in Tg(-3.5gstp1:GFP)it416b larvae and embryos. (A, B) GFP induction by 1.5 µM OA-NO$_2$ in the olfactory regions (arrowheads) of Tg(-3.5gstp1:GFP)it416b larvae at 4 dpf. The effects of Nrf2 knockdown were analyzed using nrf2MO. Error bars indicate the standard deviation values of three individual larvae. (C) OA-NO$_2$ induced GFP expression in Tg(-3.5gstp1:GFP)it416b embryos. Tg(-3.5gstp1:GFP)it416b embryos were co-injected with wild-type (WT) or C151S Keap1 mRNA and Nrf2 mRNA were treated with 2.5 µM OA-NO$_2$ for 6 hours. (D) An RT-PCR analysis of OA-NO$_2$–induced endogenous gstp1 expression. Embryos co-injected with wild-type (WT) or C151S Keap1 mRNA and Nrf2 mRNA were treated with 2.5 µM OA-NO$_2$ for 6 hours.

Figure 6 Identification of the sensor cysteines for OA-NO$_2$. (A) MS analysis of peptides from mouse Keap1 digested with trypsin following incubation with or without OA-NO$_2$. Mouse Keap1 (3 µg) was incubated at 25°C for 60 minutes in the absence (top) or presence (bottom) of 100 µM OA-NO$_2$ in a total volume of 10 µl containing 20 mM Tris-HCl (pH8.5). (B) Modification sites in mouse Keap1 for Nrf2-activating compounds was determined by MS analysis. The modification sites for 15d-PGJ$_2$ and PGA$_2$ have been analyzed previously (Kobayashi et al. 2009).

Figure 7 Effect of the it275 mutation on OA-NO$_2$-induced endogenous gstp1 expression. An in situ hybridization analysis of endogenous gstp1 expression (arrowheads) of homozygous it275 larvae and wild-type siblings treated with 1.5 µM OA-NO$_2$ or 100 µM DEM for 6 hours at 4 dpf.

Figure 8 Nitro-fatty acids and cyclopentenone prostaglandins. (A) Chemical structures of nitro-fatty acids (OA-NO$_2$ and LNO$_2$) and cyclopentenone prostaglandins (15d-PGJ$_2$ and PGA$_2$). (B) Cysteine code hypothesis. OA-NO$_2$ and 15d-PGJ$_2$ share an analogous cysteine code as nucleophilic targets and play similar anti-inflammation roles.
Supporting Information/Supplementary material

The following Supporting Information can be found in the online version of the article:

**Table S1** Generation of stable transgenic lines harboring p3.5gstp1GFP or pT3.5gstp1GFP constructs.

**Table S2** Peptides identified by MALDI-TOF MS from mouse Keap1 following treatment with OA-NO₂.

**Figure S1** DEM-induced GFP expression in stable transgenic lines.

**Figure S2** Constitutive GFP expression in *Tg(-3.5gstp1:GFP)it416b* larvae at 6 dpf.

**Figure S3** Nrf2-induced GFP expression in *Tg(-3.5gstp1:GFP)it416b* embryos.

**Figure S4** The effects of the C288S mutation in Keap1 on the OA-NO₂ response.

**Movie S1** Real-time monitoring of DEM-induced GFP expression in *Tg(-3.5gstp1:GFP)it416b* larvae.

**Movie S2** DEM-induced GFP expression in *it567* and its sibling wild-type larvae.
**Fig. 1** Tsujita et al.

(A) Diagram showing the genomic structure of the *gstp1* promoter region, including ExI, ExII, ARE/EpRE, and the p3.5gstp1GFP construct.

(B) Imaging data showing the expression of GFP in control and DEM treated groups at 0, 3, 6, 10, and 14 hours. Arrows indicate changes in GFP expression.

(C) Imaging data showing the effect of nrf2 MO injection on GFP expression in control and DEM treated groups at 6 and 14 hours. Arrowheads indicate changes in GFP expression.

* indicates significant differences.
Measurement area

Fig. 2 Tsujita et al.
Figure 3: Tsujita et al.

Panel A: Images showing olfactory expression of GFP in Sib-WT and it567 genotypes under DEM and Control conditions.

Panel B: Graph depicting olfactory expression of GFP over treatment time (h) for Sib-WT and it567 genotypes under DEM and Control conditions.
A) GFP induction in the larval olfactory regions

![Graph showing induction levels at 0, 6, and 12 hours for different treatments: SF, 15d-PGJ2, H2O2, AF, CdCl2, and Control.]

B) *it416b*/*it416b x WT*

<table>
<thead>
<tr>
<th>Nrf2</th>
<th>Keap1</th>
<th>WT</th>
<th>C151S</th>
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<tbody>
<tr>
<td>+</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>+</td>
<td>WT</td>
<td></td>
<td>C151S</td>
</tr>
</tbody>
</table>

- **DEM**
- **15d-PGJ2**
- **H2O2**
- **Control**

Fig. 4 Tsujita et al.
Fig. 5 Tsujita et al. A) OA-NO\textsubscript{2} treated

B) Fold induction

C) \textit{it416blit416b} x WT

Keap1
- WT
- C151S

Nrf2
+ +

OA-NO\textsubscript{2}

Control

D) OA-NO\textsubscript{2} Control

Keap1
- -
- -

Nrf2
+ + + +
+ + + +

gstp1

ef1\textalpha
**A**

Native mouse Keap1

![Native mouse Keap1 spectrum](image)

mouse Keap1 treated with OA-NO₂

![Mouse Keap1 treated with OA-NO₂ spectrum](image)

**B**

<table>
<thead>
<tr>
<th>Activators</th>
<th>Cysteines</th>
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<tbody>
<tr>
<td>OA-NO₂</td>
<td>77 226 [273] 368 489 613</td>
</tr>
<tr>
<td>15d-PGJ₂</td>
<td>[273] 288</td>
</tr>
<tr>
<td>PGA₂</td>
<td>[273] 297 489</td>
</tr>
</tbody>
</table>

Fig. 6 Tsujita et al.
Fig. 7 Tsujita et al.

WT-Sib

OA-NO$_2$

DEM

Control

it275

Probe: $gstp1$
A

Nitro-fatty acids

\[
\begin{align*}
\text{OA-NO}_2 & \quad \text{or} \quad \text{LNO}_2 \\
\end{align*}
\]

Cyclopentenone prostaglandins

\[
\begin{align*}
\text{15d-PGJ}_2 & \quad \text{or} \quad \text{PGA}_2 \\
\end{align*}
\]

B

\[
\begin{align*}
\text{OA-NO}_2 & \quad \text{or} \quad \text{LNO}_2 \\
\end{align*}
\]

\[
\begin{align*}
\text{15d-PGJ}_2 & \quad \text{or} \quad \text{PGA}_2 \\
\end{align*}
\]

Keap1 inhibition (C273)

NFκB p65 inhibition (C38)

PPARγ activation (C285)

Anti-inflammation

Fig. 8 Tsujita et al.