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The dual roles of NRF2 in tumor prevention and progression: possible implications in cancer treatment

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Abstract

The Cap'N'Collar (CNC) family serves as cellular sensors of oxidative and electrophilic stresses and shares structural similarities including basic leucine zipper (bZIP) and CNC domains. They form heterodimers with small MAF proteins to regulate antioxidant and phase II enzymes through antioxidant response element (ARE)-mediated transactivation. Among the CNC family members, NRF2 is required for systemic protection against redox-mediated injury and carcinogenesis. On the other hand, NRF2 is activated by oncogenic pathways, metabolism, and hypoxia. Constitutive NRF2 activation is observed in a variety of human cancers and it is highly correlated with tumor progression and aggressiveness. In this review, we will discuss how NRF2 plays dual roles in cancer prevention and progression depending on the cellular context and environment. Therefore, a better understanding of NRF2 will be necessary to exploit this complex network of balancing antioxidant pathways to inhibit tumor progression.

Keywords

Oxidative stress; NRF2; CNC family; antioxidant response element; ARE; small MAF; cancer

Introduction

In response to intrinsic and extrinsic stimuli, cells activate various adaptive mechanisms to promote reactive oxygen species (ROS) detoxification. The Cap'N'Collar (CNC) family proteins are transcription factors, which contain basic leucine zipper (bZIP) and CNC domains. By regulating various antioxidative genes and phase II detoxifying enzymes, which is required for metabolic detoxification of xenobiotics, they play a pivotal role in the cellular response to oxidative or electrophilic stresses [1–3]. The CNC family consists of Nuclear factor erythroid-derived 2 (NF-E2), NF-E2-related-1 [Nrf1 or NF-E2-like 1 (NFE2L1)], NRF2 (NFE2L2), NRF3 (NFE2L3), and distantly related Broad complex–Tramtrack–Bric-a-brac (BTB) and CNC homology 1 (BACH1) and BACH2. Functionally,

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the CNC transcription factors form heterodimers with small MAF proteins [4]. These heterodimers regulate genes containing the antioxidant response element (ARE) or the MAF recognition element (MARE) such as heme oxygenase 1 (*HO-1*), NADP(H):quinone oxidoreductase 1 (*NQO-1*), glutamylcysteine ligase (*GCL*), peroxiredoxin (*PRDX*), and superoxide dismutase (*SOD*), which are involved in detoxification and drug metabolism [5–7]. The ARE core sequence, 5'-RGTGA(C/G)NNNGC-3', acts as a *cis*-acting enhancer and shows significant homology to the MARE enhancer, 5'-TGCTGAG(C)TCAGCA-3' [8]. Interestingly, many studies demonstrate that among CNC members, NRF2 is heavily involved in the regulation of antioxidant genes [9–13]. In various cell lines, NRF2 expression increases ARE activity about four to six times higher than NRF1, NRF3, and NF-E2. Knocking out *Nfe2l2* in mouse fibroblast further supports that NRF2 regulates ARE-dependent genes such as GCL and HO-1. On the other hand, BACH1 and BACH2 play a repressive role by competing with NF-E2 and NRF2 [14–19]. Thus, here we review how NRF2 contributes to various physiological and pathological conditions.

Structure of Nrf2 and its stabilization under antioxidant stresses

NRF2 is a soluble protein primarily localized to the cytoplasm. It is highly conserved across species and contains seven functional Nrf2-ECH homology (NEH) domains (Figure 1) [20]. The Neh1 domain possesses the CNC-bZIP domain that is responsible for heterodimerization and ARE binding. Neh2, located in the N-terminus, is the main regulatory domain of NRF2, containing seven lysine residues for ubiquitination, and DLG (Asp-Leu-Gly) and ETGE (Glu-Thr-Gly-Glu) motifs for Kelch-like erythroid cell-derived protein with CNC homology (ECH)-associated protein 1 (KEAP1) binding. Although Neh3, Neh4, and Neh5 act as activation domains by interacting with the transcriptional coactivators [21, 22], Neh6 regulates KEAP1-independent NRF2 stability by recruiting an ubiquitin ligase complex [23]. The Neh7 domain has recently been identified to interact with retinoic X receptor alpha (RXR α), a repressor of NRF2 [24].

Under basal conditions, NRF2 is anchored in the cytoplasm through a direct interaction with the KEAP1 protein that leads to ubiquitination and proteasomal degradation [20]. KEAP1 contains three functional domains, a BTB domain, an intervening region (IVR), and a double glycine repeat (DGR) or a Kelch motif, which contains six copies of the conserved kelch repeat (two adjacent glycine residues and a tyrosine/tryptophan pairs separated by 7 residues) that form β -propeller structure (Figure 1). The BTB domain is required for KEAP1 homodimerization and the interaction with Cul3, which regulates KEAP1 through ubiquitination and proteasomal degradation. The Kelch/DGR domain includes six kelch repeats that mediate binding between KEAP1 and the Neh2 domain of NRF2. Twenty-seven cysteines within the IVR domain residues that act as active stress sensors in human Keap1 [25]. Among these, Cys151, Cys257, Cys273, Cys288, and Cys297 are known to be highly reactive towards oxidative and electrophilic stresses [25, 26]. In response to stresses, these cysteine residues become oxidized and form disulfide bonds or covalent adducts. The cysteine modifications cause a conformational change in KEAP1 to prevent NRF2 ubiquitination [27]. Free NRF2 then translocates into the nucleus, heterodimerizes with small MAFs, and binds to antioxidant genes containing the ARE domain.

Role of NRF2 in development and systemic defense mechanisms

Nfe2l2 knockout mice are viable and fertile, indicating that *Nfe2l2* is dispensable for mouse development [28]. On the other hand, *Keap1* knockout mice die postnatally due to malnutrition resulting from abnormal hyperkeratosis of the esophagus and forestomach [29]. In these mice, expression of *Nfe2l2* as well as phase II enzymes targeted by *Nfe2l2* such as *Nqo1*, *Gcl*, and *Prdx1* is significantly increased, showing that NRF2 is constitutively activated. The lethality of *Keap1* knockout mice can be rescued with deletion of *Nfe2l2* as well as reduced expression of phase II enzymes. These results indicate that *Keap1* is an upstream repressor of *Nfe2l2*, and *Nfe2l2-Keap1* homeostasis is essential for cellular defense against oxidative stress.

Although there are no significant developmental deficits, dysregulation of ARE-dependent genes causes *Nfe2l2* knockout mice to be highly susceptible to oxidative stress and xenobiotic toxicity (Table 1). *Nfe2l2* knockout mice are more susceptible to hyperoxia due to increased oxidative lung injury and inflammation. Significantly lower expression of antioxidant and phase II enzymes in these mice suggests that *Nfe2l2* contributes to the protection against oxidative lung injury [30, 31]. Likewise, although phase II enzymes are highly induced by phenolic antioxidants, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), and N-acetyl-4-aminophenol (APAP, acetaminophen), their induction is largely inhibited in *Nfe2l2* knockout mice, resulting in increased tissue toxicity and high mortality [32–34]. NRF2 also plays a radioprotective role since thoracic irradiation decreases survival of *Nfe2l2* knockout mice when compared with *Nfe2l2* WT mice [35]. These results reflect the critical role of NRF2 in coordinating the antioxidant response.

Tumor suppressive roles of NRF2

Enhanced susceptibility to chemical carcinogens is also observed in *Nfe2l2* knockout mice [36, 37]. After benzo[a]pyrene (B[a]P) or N-tirosobutyl (4-hydroxybutyl) amine (BBN) exposure, *Nfe2l2* knockout mice develop gastric neoplasia or urinary bladder carcinoma at significantly higher rates [36, 37]. In these studies cancer chemopreventive actions of 4-methyl-5-[2-pyrazinyl]-1,2-dithiole-3-thione (oltipraz) are less effective in *Nfe2l2* knockout mice because the induction of phase 2 detoxifying enzymes is significantly reduced. Treatment of 7,12-dimethylbenz(a)anthracene (DMBA), 12-O-tetradecanoylphorbol-13-acetate (TPA), or azoxymethane/dextran sulfate sodium (DSS) also enhances incidence of skin, colorectal, or mammary tumors in *Nfe2l2* knockout mice, indicating NRF2 plays a critical role in protecting against carcinogenesis [38–40].

In addition to preventing primary tumor growth, *Nfe2l2* has a protective function against tumor metastasis [41]. After intravenous injection of Lewis lung carcinoma (3LL) cell lines, *Nfe2l2* knockout mice show a significantly increased number of metastatic nodules in the lung. On the other hand, *Keap1* conditional knockout mice using the Cre-Lox system exhibit a significantly decreased number of lung metastasis after injection of 3LL cells. These results indicate that although *Nfe2l2* is dispensable during embryonic development, it is required for systemic protection against carcinogenesis and metastasis.

Oncogenic roles of NRF2

Although knockout mouse studies indicate that loss of *Nfe2l2* reduces cellular protection against oxidative stress and carcinogenesis, prolonged activation of the NRF2 protein is correlated with cancer progression in several cases. Increased NRF2 expression has been extensively studied in patients with head and neck cancer [42–44], lung cancer [45–50], gall bladder cancer [51, 52], epithelial ovarian cancer [53], osteosarcoma [54], breast cancer [55], bladder cancer [56], colorectal cancer [57], gastric cancer [58], glioblastoma [59, 60], and pancreatic cancer [61]. In these patients, Nrf2 expression is significantly correlated with increased proliferation and treatment resistance to radiation, cisplatin, and 5-fluorouracil (5-FU), seemingly through the induction of antioxidant genes [44, 45, 48, 53, 55, 58]. Patient survival and multivariate analysis further demonstrate that NRF2 is a poor prognostic factor in cancer patients (Table 2).

Although loss-of-function mutations in *KEAP1* contribute to constitutive activation of NRF2 in tumors [45, 51, 53], oncogenes and oncogenic signaling pathways are also involved in increased NRF2 expression (Figure 2). Mouse embryonic fibroblasts (MEF) and NIH3T3 fibroblasts transduced with oncogenic alleles of *K-Ras*, *B-Raf*, and *Myc* (*K-Ras*^{G12D}, *B-Raf*^{V619E} (corresponding to human *B-Raf*^{V600E}), and *Myc*^{ERT2}) increase *Nfe2l2* transcription and simultaneously, decrease ROS production [62]. In the *K-Ras* mutant mouse model of pancreatic cancer and *B-Raf*^{V619E} expressing mouse lung adenoma, NQO1 expression is increased, whereas DNA oxidation, stained by 7,8-dihydro-8-oxo-2'-deoxyguanosine (8-oxo-dGuo) is decreased. *Nfe2l2* deletion in these mice results in reduced cell proliferation and tumor burden as well as elevated DNA oxidation. Therefore, Nrf2 activation, which is mediated by oncogenic signaling, contributes to tumor growth and progression through ROS detoxification.

In addition, a number of other oncogenic protein kinases also contribute to enhanced NRF2 stability. Protein kinase C (PKC) phosphorylates NRF2 on Ser 40 and induces its dissociation from KEAP1 [63, 64]. Similarly, PKR-like ER kinase (PERK), which is essential for ER stress, also phosphorylates NRF2 and inhibits its binding to Keap1 [65]. PERK-mediated NRF2 activation promotes cell survival in response to ER stress. Inhibition of MAP kinases and PI3K blocks NRF2 nuclear translocation and ARE-mediated gene transcription [66–69]. Since oncogenic *K-RAS* signaling activates PI3K and PKC regulates the MEK-ERK pathway in cancer, there may be crosstalk between a variety of signaling pathways to regulate NRF2 [70, 71]. However, the direct roles of these oncogenic pathways in regulating NRF2-induced redox responses and tumor progression remain unclear.

The role of NRF2 in metabolism

Metabolic switches are one hallmark of cancer [72]. In addition to its role in antioxidative responses for cancer cell protection, microarray and ChIP-sequencing analysis further show that NRF2 regulates cell proliferation and survival by activating metabolic enzymes involved in pentose phosphatase pathways (PPPs) [73–75]. PPP prevents oxidative stress by generating NADPH. NRF2 mediates upregulation of metabolic genes such as glucose-6-phosphate dehydrogenase (G6PD), phosphogluconate dehydrogenase (PGD), transketolase

(TKT), transaldolase 1 (TALDO1), malic enzyme 1 (ME1), and isocitrate dehydrogenase 1 (IDH1), suggesting that Nrf2 regulates the PPP and NADPH production pathways. Mechanistically Nrf2-mediated changes in these metabolic genes alter glucose and glutamine metabolism to promote cancer cell proliferation. Fumarate accumulation due to fumarate hydratase (FH)-deficiency results in hereditary leiomyomatosis renal cell carcinoma (HLRCC) and type-2 papillary renal carcinoma (pRCC) [76]. A recent study also shows that fumarate, a metabolite of the Krebs cycle, activates NRF2 through the succination of cysteine residues of KEAP1 [77]. Elevated NRF2 expression in FH deficient pRCC further indicates that NRF2-mediated metabolic alteration plays a role in the aggressive growth of cancer.

The role of NRF2 in treatment resistance

NRF2 is also involved in resistance to cancer treatment. Inhibiting NRF2 expression in tumors enhances sensitivity to ionizing radiation and chemotherapeutic drugs such as doxorubicin, cisplatin, etoposide, and 5-FU [51, 78–83]. Doxorubicin, cisplatin, and ionizing radiation increase glutathione synthesis (GSH) levels and NRF2 activation [84, 85]. Levels of cellular GSH, which is catalyzed by GCS, are critical for detoxification of anticancer drugs [86]. Inhibition of NRF2 reverses GSH induction and radiation resistance, linking NRF2-mediated GSH induction and treatment resistance. Radiotherapy and chemotherapy induce multidrug resistance proteins (MRPs) [87, 88]. MRPs are ATP-dependent transporters that can efflux chemicals and metabolites. Thus, increased expression of MRP proteins is correlated with treatment resistance. Knockout mouse studies show that NRF2 is required for the induction of MRP1, MRP2, MRP3, and MRP4 [89–91]. In conclusion, NRF2 induces chemo- and radio-resistance while maintaining cellular homeostasis. Therefore, targeting NRF2-regulated pathways may be a good strategy to overcome resistance to cancer treatment.

Hypoxia-mediated regulation of Nrf2

Tumor hypoxia is caused by an imbalance between oxygen consumption and supply. HIF is a major regulator of hypoxic gene regulation, and HIF transactivates many downstream genes involved in crucial steps of tumor progression, including angiogenesis, glycolytic metabolism, and treatment resistance to both radiotherapy and chemotherapy [92–94]. HIF is a dimeric transcription factor comprising α and β subunits. Unlike HIF-1 β , which is constitutively expressed, HIF α is regulated by various factors including oxygen, free radicals, and oncogenic signaling pathways [95–99]. Under normal conditions, HIF α is hydroxylated by prolyl hydroxylases (PHD) [100]. Prolyl hydroxylation leads to von Hippel-Lindau (VHL)-mediated proteasomal degradation of HIF α . Under hypoxia, PHD activity is inhibited, which results in HIF α stabilization and activation. Meanwhile, hypoxia is known to increase mitochondrial ROS production, suggesting a linkage between hypoxia, HIF, and the NRF2 pathway [101]. Indeed, several studies have shown that NRF2 expression or its activation is induced by chronic or intermittent hypoxia [102, 103]. Microarray data also reveals that gain-of-function mutants of NRF2 are significantly correlated with hypoxia signatures in patients with head and neck cancer [47]. In terms of target gene regulation, NRF2 and HIF can act together or independently in regulating gene

expression such as HO-1, a common target of both NRF2 and HIF [104]. Interestingly, HO-1 can be induced in Chinese Hamster Ovary (CHO) cells even in the absence of HIF-1 activity, indicating that Nrf2 regulates HO-1 in a HIF-independent manner. On the other hand, HIF-dependent NRF2 regulation is also reported in human colorectal cancer cell lines, HCT116 and HT29 [105]. Knocking down *NFE2L2* inhibits the hypoxic induction of HIF-1 as well as a pro-angiogenic factor, vascular endothelial growth factor (VEGF). As a result, *in vivo* tumor growth and tumor angiogenesis are significantly curtailed. In this study, it is suggested that competition between NRF2 and PHD for oxygen availability activates the HIF-VEGF pathway. In patients with glioblastoma, expression of NRF2 and HIF-1 is correlated, further indicating these two proteins may cooperate or interrelate for cancer progression [59]. Thus, NRF2 may be a valuable target for repression of HIF-mediated tumor growth and angiogenesis (Figure 3).

Modulation of NRF2 signaling: NRF2 activators

Given the fact that NRF2 plays a role in disease prevention, NRF2 is an attractive target for activation. Dimethyl fumarate (DMF or Tecfidera) is a methyl ester of fumaric acid (FA), which alkylates Cys151 of KEAP1, inhibits NRF2-KEAP1 binding, and hence, stabilizes NRF2 [106]. DMF treatment reduces inflammatory responses and promotes neuroprotection. Currently DMF is approved by the FDA to treat patients with relapsing multiple sclerosis (MS). Other NRF2 activators are also being investigated in clinical trials for a variety of diseases [107, 108]. Sulforaphane (SFN) is an isothiocyanate that is naturally present in cruciferous vegetables such as broccoli and cabbage. SFN forms a covalent adduct with cysteine residues with KEAP1 at cysteine residues including Cys151 and enhances NRF2 activation [109]. Promising preclinical studies demonstrate that SFN prevents mice from forming carcinogen-induced mammary tumors, colonic crypt foci, gastric cancer, and lung cancer [110–113]. Similarly, SFN inhibited prostate cancer progression and pulmonary metastasis from TRAMP transgenic mice harboring an adenocarcinoma of the mouse prostate [114]. *In vitro*, SFN mediates cell cycle arrest, apoptosis, and inhibition of endothelial cell proliferation and migration, suggesting its potential as an anti-cancer molecule [115–117]. SFN treatment is currently being investigated in clinical trials as an NRF2 activator in patients with breast, prostate, pancreatic, and colon cancers [118–121].

The synthetic triterpenoids, 2-cyano-3,12-dioxooleana-1,9(11)-dien-28-oic acid (CDDO) and its derivative, bardoxolone methyl (CDDO-me) are known for their anti-inflammatory and anti-tumor effects [122]. The interaction between CDDO and the BTB domain of KEAP1 inhibits binding to NRF2 and leads to NRF2 activation [123]. However, phase III clinical trials in patients with chronic kidney disease were terminated prematurely due to patients having severe chronic renal disease and adverse cardiovascular effects, indicating that a detailed understanding of NRF2 activation in tissues needs to be gained before the clinical use of the NRF2 activator [124].

Modulation of NRF2 signaling: NRF2 inhibitors

In contrast to NRF2 activators, NRF2 inhibitors block tumor progression. Brusatol, a plant extract from *Brucea javanica*, reduces ARE-dependent gene expression by enhancing

degradation of NRF2 [125]. Brusatol inhibits *in vivo* tumor growth while enhancing chemosensitivity, indicating its beneficial effect as a combinatorial therapy. Luteolin, a flavonoid that also exists in plants and vegetables, blocks subcutaneous lung tumor cell growth and proliferation in mice while increasing cytotoxicity of cisplatin treatment [126, 127]. Ascorbic acid and *all-trans*-retinoic acid (ATRA), other natural compounds, suppress NRF2 activation by interfering with nuclear localization of Nrf2 or its binding to ARE [128, 129]. Specifically, ATRA, a metabolite of vitamin A, inhibits NRF2 by activating RA receptor α (RAR α). RAR α directly interacts with NRF2 and prevents its binding to ARE [128]. However, these inhibitors are electrophiles that share non-specific off-target effects and can target cysteine residues in other proteins or enzymes [108]. Therefore, development of NRF2-targeting agents with enhanced specificity is required to improve the effectiveness of cancer treatment. Additionally, conflicting roles of NRF2 in cancer prevention and cancer progression indicate that more questions need to be addressed to determine the optimal use of NRF2 activators or inhibitors in the clinic.

The relationship between NRF2 and small MAF family proteins

Consisting of MAFF, MAFK, and MAFG, the small MAF proteins are essential binding partners of the CNC family [4, 6, 130]. Both bZip protein arrays and ChIP-sequencing analysis indicate the fact that Nrf2 forms heterodimers mainly with small MAFs [74, 131]. Specifically, ChIP-sequencing data indicates significant overlap between NRF2 and MAFG binding sites. The JUN family (JUN, JUND, and JUNB) [11, 132], FOSB [133, 134], and ATF4 [135] are also known to bind to Nrf2. However, specific roles of these complexes are still under investigation.

The original MAF protein was first described as a viral oncogene, v-Maf from musculoaponeurotic fibrosarcoma, in chickens [136]. The MAF family contains the basic DNA binding domain and the leucine zipper dimerization domain [6]. The extended homology region (EHR), which is highly conserved in MAF family members, is also required for DNA binding (Figure 1). MAF proteins can be divided into two groups: large MAFs and small MAFs. Large MAF proteins, including MAFA (L-MAF), MAFB [137], c-MAF (MAF) [138], and Neura Retinal (NRL), comprise an acidic TAD in their N-terminus. Unlike large MAFs, small Maf proteins, which are 18 kDa in size, lack a TAD. Small MAF family proteins form homodimers or heterodimers with CNC family proteins, FOS, and FOSB and binds to MARE or ARE [4].

Although small MAF proteins interact with NRF2 to activate antioxidant response genes through ARE pathways, increased expression of small MAFs in response to oxidative and electrophilic stresses indicates that they are also regulated by redox pathways [139, 140]. Interestingly, the repressive role of small MAF family proteins has also been identified when they are overexpressed. Overexpression of MAFG and MAFK inhibits the NRF2-mediated induction of NQO1, Glutathione S-transferase (GST), and GCS [86, 141]. Excessive expression of small MAF proteins may lead to formation of small MAF homodimers, which inhibit antioxidant gene transcription. Therefore, functional consequences of small MAFs are highly dependent on the quantitative balance between small MAF and its CNC partners [142–144].

Similarly to NRF2, small MAF proteins are also associated with carcinogenesis. Comparative genomic hybridization arrays reveal that DNA copy number of MAFG is amplified in lung adenocarcinoma [145]. A study of lung epithelial cells suggests that negative regulation of mir-218 increases MAFG after smoking and possibly leads to lung carcinogenesis [146]. In hepatocellular carcinoma patients with *CTNGB1* (β -catenin) mutations, MAFG is also highly expressed, indicating that MAFG might be a proto-oncogene [147]. In addition, genetic disruption of small MAF proteins has also been reported in familial pancreatic cancer and CML patients, indicating a broader oncogenic role [148, 149]. In contrast, high expression of MAFF in patients with ovarian and prostate cancer is correlated with prolonged survival, suggesting a role for MAFF in tumor suppression [150].

Small MAFs also respond to microenvironmental changes. The interaction of HIF-1 α with MAFG or MAFK has been shown by yeast two-hybrid and surface plasmon resonance [151]. In this study, MAFG and MAFK bind to the PAS-A domain of HIF-1 α . Knocking down MAFG inhibits nuclear localization of HIF-1 α and, as a result, decreases expression of erythropoietin (EPO), one of HIF-1 α 's target genes under hypoxia. On the other hand, MAFG does not affect protein levels of HIF-1 α , indicating its specific role in HIF-1 α translocation. Interestingly, overexpression of MAFG also decreases the accumulation of HIF-1 α in nuclei as well as EPO expression, suggesting that it acts as an activator and a repressor depending on its abundance. In addition to hypoxia, small MAF proteins are regulated by extracellular pH [152]. For example, acidic pH (pH 6.6) significantly increases small MAF expression as well as FOSB. Co-localization studies show that both MAFG and FOSB are expressed and interact with each other in the nucleus, and that this heterodimer can activate MMP1 by binding to an AP-1 consensus site in the MMP1 promoter.

Taken together, small MAF proteins play either repressive or activating roles in antioxidant responses and carcinogenesis and these might be due to competition between small MAF homodimers and NRF2–small MAF heterodimers for binding to ARE embedded in MARE. However, other than quantity based regulation, the factors that determine the formation of different binding complexes still need to be investigated. Overall, these results indicate that small MAF expression must be finely tuned in order to activating or repressive effects on Nrf2 and other transcription factors.

Conclusion

In response to oxidative and carcinogenic stimuli, NRF2 transactivates various genes involved in defensive and adaptive pathways to prevent normal tissue damage. As a result, NRF2 deficiency causes mutant mice to be more susceptible to oxidative challenge and carcinogen exposure. Ironically, its roles in tumor progression indicate that NRF2 should be considered as a potential therapeutic target as well. NRF2 activity is also controlled by oncogenic signaling pathways, metabolism, and cellular microenvironment. Additional studies reveal NRF2 is also involved in pathogenic pathways and physiological changes, such as angiogenesis, and metastasis. As binding partners of NRF2, small MAF proteins fulfill both positive and negative functions depending on their formation of homo- or heterodimers. Thus, whether NRF2 inhibits or activates carcinogenesis is highly context

dependent. Therefore, it is still important to determine whether NRF2 is activated or suppressed in various environments and under the influence of diverse stimuli.

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- NRF2, a Cap'N'Collar (CNC) transcription factor, plays dual roles in cancer prevention and progression depending on the cellular context and environment.
- Overexpression of NRF2 in many human cancers, is significantly involved in tumor metabolism, angiogenesis, and treatment resistance, which results in poor patient survival.
- Conflicting roles of NRF2 in cancer prevention and cancer progression remain to be challenged to determine the optimal use of NRF2 activators or inhibitors in the clinic.

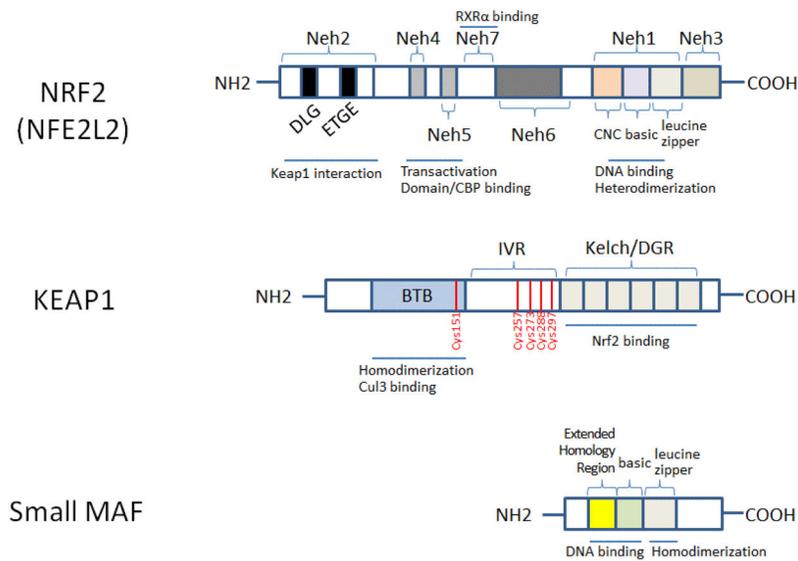


Figure 1. Structural domains of NRF2 and KEAP1

NRF2 includes the CNC-bZIP domain and functional Neh domains. The CNC-bZIP domain including Neh1 is required for DNA binding and interaction with ubiquitin conjugating enzymes. The TAD that consists of Neh5, Neh2 is involved in Keap1 binding [20]. KEAP1 contains the BTB domain for KEAP1 homodimerization and interaction with Cul3. Six kelch repeats in the Kelch/DGR domain interact with the Neh2 domain of NRF2 for binding. The IVR domain links the BTB and Kelch/DGR domains and has several critical cysteine residues for KEAP1 activation and NRF2 repression. Cysteine residues such as Cys151, Cys257, Cys273, Cys288, and Cys297 act as stress sensors to activate Keap1 and to repress NRF2 [25, 26]. Small MAF proteins utilize the highly conserved extended homology region (HER) for DNA binding [6]. The basic DNA binding domain and the leucine zipper dimerization domain are also required for their biological functions.

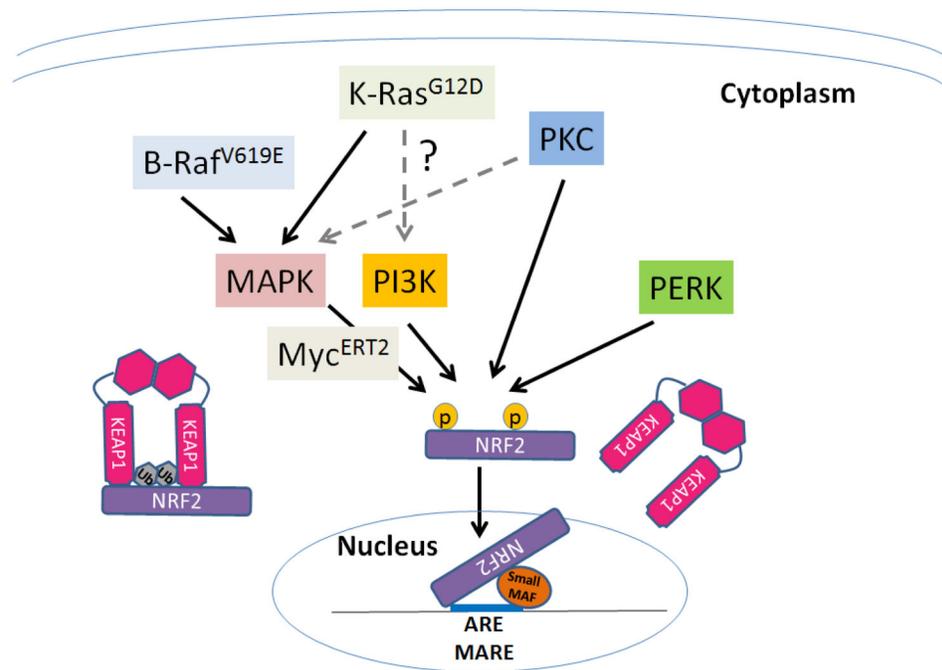


Figure 2. Oncogenic signaling pathways involved in NRF2 expression and activation
 Oncogenic mutation of *K-Ras*, *B-Raf*, and *Myc* ($K\text{-Ras}^{\text{G12D}}$, $B\text{-Raf}^{\text{V619E}}$ (corresponding to human $B\text{-Raf}^{\text{V600E}}$), and Myc^{ERT2}) increase *Nfe2l2* transcription while reducing production of free radicals and DNA oxidation which results in enhanced cell proliferation and tumor burden [62]. Protein kinase C (PKC) and PKR-like ER kinase (PERK) also phosphorylate and activate NRF2 by inhibiting its binding to KEAP1 [65]. While inhibition of MAP kinases and PI3K reduce NRF2 nuclear translocation and ARE-dependent activation, a crosstalk between various signaling pathways may be involved in regulating NRF2 [66–69].

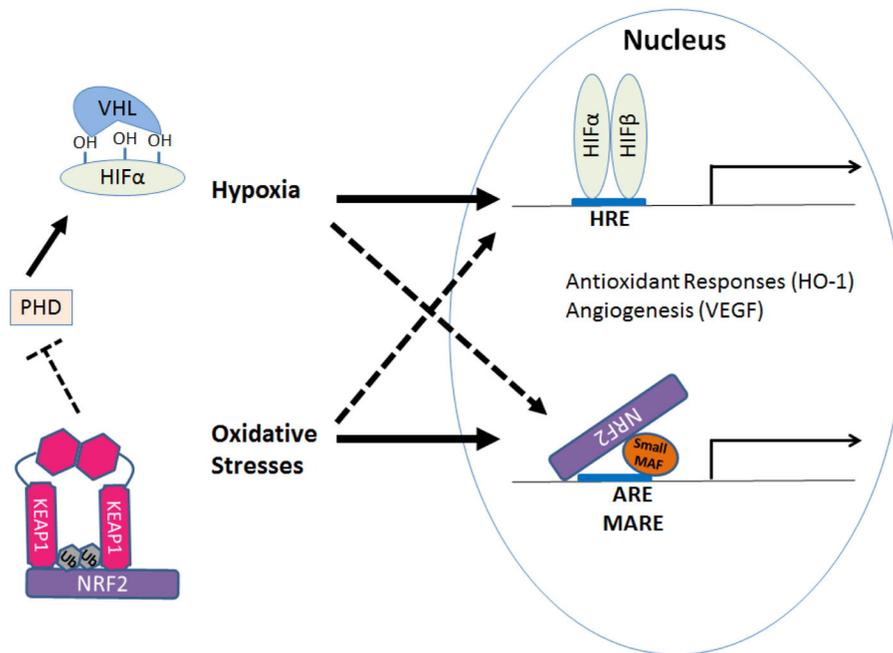


Figure 3. Activation of NRF2 and HIF under various environmental stimuli

Hypoxia inhibits prolyl hydroxylation of HIF α , which leads to its stabilization and activation as a heterodimer transcription factor with HIF β . Free radicals produced by oxidative stresses are also known to activate the HIF-pathway. NRF2, a main regulator of the antioxidative responses, has been recently recognized as a tumorigenic factor, which plays a role under hypoxia. In human colorectal cancer cells, when NRF2 is deficient, the HIF-VEGF pathway and tumor angiogenesis are inhibited, indicating that these two proteins may cooperate for tumor progression [105].

Table 1

Examples of *Nfe2l2*-mediated protection against redox-mediated injury and carcinogenesis in knockout mouse model.

	Stressors	Symptoms	Reference
<i>Nfe2l2</i> knockout mice	Hyperoxia	Acute lung injury & Inflammation	[31]
	Butylated hydroxytoluene (BHT)	Increased mortality & pulmonary injury	[33]
	N-acetyl-4-aminophenol (APAP, Acetaminophen)	Increased mortality & hepatic damage	[34]
	Radiation (16Gy)	Increased mortality	[35]
	Benzo[a]pyrene (B[a]P)	Increased gastric neoplasia	[36]
	N-nitrosobutyl (4-hydroxybutyl) amine (BBN)	Increased incidence of urinary bladder carcinoma	[37]
	7,12-dimethylbenz(<i>a</i>)anthracene (DMBA) & 12-O-tetradecanoylphorbol-13-acetate (TPA)	Increased skin tumorigenesis	[38]
	Azoxymethane/dextran sulfate sodium (DSS)	Increased incidence of colorectal tumor & inflammation	[39]
	Metroxyprogesterone acetate & DMBA	Increased progression of mammary carcinoma	[40]
	Tail vein injection of 3LL cells	Enhanced tumor lung metastasis	[41]

Table 2

NRF2 as an independent prognostic factor in cancer patients.

CNC Family	Tumor Type	Observation	Method	Other Variables for Multivariate Analysis	Reference
NRF2/Keap1	NSCLC (patients: 122)	NRF2 high/Keap1 low Poor OS, RFS	IHC	<ul style="list-style-type: none"> Age at surgery Tumor Stage Smoking 	[46]
		Increased nuclear expression Poor OS, RFS			
NRF2	HNSCC (patients: 60)	Increased mutant NRF2 signatures Poor OS	Microarray		[47]
	NSCLC (patients: 60)	Increased expression Poor OS, PFS	IHC	Not Significant	[48]
	Lung Cancer (patients: 109)	Increased NRF2 expression Poor DSS	IHC		[49]
	Lung Cancer (patients: 289)	Increased NRF2 expression Poor OS	IHC		[50]
	Gallbladder Cancer (patients: 59)	Increased expression Poor OS	IHC	Metastasis	[52]
	Epithelial Ovarian Cancer (patients: 30)	Increased NRF2 pathway Poor OS	Microarray		[53]
	Breast Cancer (patients: 452)	rs2886162 genotype AA Poor OS	SNP Genotyping	<ul style="list-style-type: none"> Nodal Status HER2 Status 	[55]
	Bladder Cancer (patients: 225)	Increased NRF2 expression Poor OS, DSS, RFS	IHC		[56]
	Gastric Cancer (patients: 186)	Increased NRF2 expression Poor OS, DFS	IHC	<ul style="list-style-type: none"> TNM stage (DFS only) 	[58]
	Glioblastoma (patients: 68)	Increased NRF2 expression Poor OS	IHC	<ul style="list-style-type: none"> HIF1α Resection Degree 	[59]
	Glioblastoma (patients: 49)	Increased NRF2 expression Poor OS	IHC		[60]
	Pancreatic Adenocarcinoma (patients: 103)	Increased nuclear expression Poor OS	IHC		[61]
	SCLC (patients: 262)	NFE2L2 Mutation Poor OS	PCR	<ul style="list-style-type: none"> Pathological Stage 	[149]
	Lung Adenocarcinoma (patients: 387)	NFE2L2 SNP Homozygous (c.617>A/A) Poor OS	SNP Genotyping		[150]

OS: Overall Survival, RFS: Recurrence Free Survival, PFS: Progression Free Survival, DSS: Disease Specific Survival; significance from Kaplan-Meier method, Highlighted in Red, OS: Overall Survival, RFS: Recurrence Free Survival, PFS: Progression Free Survival, DFS: Disease Free Survival; Independent prognostic factor using multivariate analysis, HNSCC: Head and Neck Squamous Cell Carcinoma, NSCLC: Non-Small Cell Lung Carcinoma, SCLC: Squamous Cell Lung Cancer, IHC: Immunohistochemistry, SNP: Single Nucleotide Polymorphism, TNM: Tumor Node Metastasis