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## Inflammation in Lung Carcinogenesis: New Targets for Lung Cancer Chemoprevention and Treatment

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### Abstract

Lung carcinogenesis is a complex process involving the acquisition of genetic mutations that confer cancer development and the malignant phenotype, and is critically linked to apoptosis resistance, unregulated proliferation, invasion, metastasis, and angiogenesis. Epithelial mesenchymal transition in cancer is an unregulated process in a host environment with deregulated inflammatory response that impairs cell-mediated immunity and permits cancer progression. Given the immunosuppressive

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tumor environment, strategies to reverse these events by stimulating host immune responses are an important area of investigation. COX-2 and its downstream signaling pathways are potential targets for lung cancer chemoprevention and therapy. Clinical trials are underway to evaluate COX-2 inhibitors as adjuvants to chemotherapy in patients with lung cancer and to determine efficacy in prevention of bronchogenic carcinoma. The understanding of molecular mechanisms involved in inflammation and lung carcinogenesis provide insight for new drug development that target reversible, non-mutational events in the chemoprevention and treatment of lung cancer.

## Keywords

inflammation; lung cancer; cyclooxygenase 2; COX-2; NSCLC; chemoprevention; targeted therapy; bronchogenic carcinoma

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## 1. Introduction

Lung cancer is the leading cause of cancer-related mortality in the United States and is responsible for more deaths than prostate, colon, and breast cancers combined [1]. The overall 5-year survival rate is less than 15% for patients with lung cancer, which has remained largely unchanged for the last three decades. Understanding the molecular mechanisms involved in the pathogenesis of lung cancer can provide opportunities to develop innovative therapies for non-small cell lung cancer (NSCLC). The acquisition of genetic mutations facilitates cancer development and malignant phenotype. These mutations are critically linked to acquiring cellular properties associated with apoptosis resistance, unregulated proliferation, invasion, metastasis, and angiogenesis. Inflammation has been postulated to play a key role in lung carcinogenesis. There is a growing body of evidence to suggest that smoking induced pulmonary inflammation increases lung cancer development in smokers [2,3]. In addition, the regular use of aspirin and other non-steroidal anti-inflammatory drugs is associated with reduced risk of developing lung cancer in animal models and in smokers [3,4]. Cyclooxygenase 2 (COX-2) has been implicated in apoptosis resistance, angiogenesis, decreased host immunity, and enhanced invasion and metastasis, and thus has a critical involvement in carcinogenesis. COX-2 is one of the novel targets being studied for lung cancer therapy and chemoprevention [5,6].

## 2. COX-2

Cyclooxygenase (also referred to as prostaglandin endoperoxidase or prostaglandin G hydroperoxide synthase) is the ratelimiting enzyme for the production of eicosanoids prostaglandins (PGs) and thromboxanes (TX) from free arachidonic acid, which is released from the membrane phospholipids by phospholipase A2 [7]. Cyclooxygenase is bound to the cytosolic side of the endoplasmic reticulum and cell membrane [8]. It is a bifunctional enzyme, with fatty acid cyclooxygenase (COX) activity producing PGG2 from arachidonic acid and two O<sub>2</sub> molecules and PG hydroperoxidase (HOX) activity in which PGG2 undergoes a two-electron reduction to PGH2 [9,10]. PGH2 is converted to final products by isomerases and individual prostaglandin (PG) synthases that are often expressed in a cell type-dependent manner. Three forms of COX have now been described [11–13]. COX-1 is constitutively expressed in most cells and tissues; its activity appears to depend entirely on substrate availability. Alternatively, an inducible isoenzyme, COX-2, acts as an immediately early gene expressed in response to cytokines, growth factors, and other stimuli. All COX isoforms share the same structural features including a hydrophobic channel that allows the arachidonic acid bearing a constrained hairpin configuration to access the COX catalytic site [9,10].

Thromboxanes and prostacyclins are short-lived molecules with the half-lives on the order of seconds, whereas prostaglandins (PGs) have half-lives within the range of tens of minutes to hours [14,15]. Interacting with their cell surface G protein (heterotrimeric GTP-binding protein)-coupled receptors (GPCR), PGs serve as autocrine and paracrine mediators of "housekeeping" functions, including the regulation of renal water and sodium metabolism, stomach acid secretion, parturition, and homeostasis. It has been shown that in certain experimental settings some PGs, especially PGJ<sub>2</sub>, are able to bind nuclear receptors such as PPAR-gamma [16]. At least 9 PG receptors have been identified to date, four of which bind PGE<sub>2</sub> and two bind PGD<sub>2</sub>. There are individual receptors for PGF<sub>2</sub>-alpha, PGI<sub>2</sub> and TxA<sub>2</sub> [8]. Among other PGs, PGE<sub>2</sub> is a major COX-2 metabolite abundantly present in the cancer microenvironment, and it is an important mediator of immune regulation [17], epithelial cell growth and invasion [18] as well as epithelial survival [19].

### 3. COX-2 and Lung Cancer

Several studies have demonstrated high-level constitutive COX-2 expression in human NSCLC [20–29]. In the initial report describing COX-2 in human lung cancer, Huang et al. assessed COX-2 expression in NSCLC and normal adjacent lung tissue of resected specimens by immunohistochemistry [20]. All of the 15 tumor specimens (8 adenocarcinomas and 7 squamous cell carcinomas) showed cytoplasmic staining for COX-2 in tumor cells. In contrast, adjacent normal lung showed no COX-2 staining in the alveolar lining epithelium, but demonstrated positive cytoplasmic staining often in alveolar macrophages and occasionally in bronchiolar epithelium. Wolff et al. showed with immunohistochemistry that COX-2 was expressed in 19 of 21 adenocarcinomas and in all 11 squamous cell carcinomas studied [28]. Hida et al. reported that COX-2 overexpression was seen in approximately 70% of lung adenocarcinomas [21]. The level of staining appeared to be less in squamous cell carcinomas than in the adenocarcinomas. Hida et al. reported that COX-2 expression was documented in one-third of atypical adenomatous hyperplasias and carcinoma *in situ* which supports the role of COX-2 throughout the progression from pre-malignant lesion to the metastatic phenotype [21]. In addition, the same study demonstrated a greater proportion of lung cancer cells staining positively in lymph node metastases compared to the corresponding primary tumor [21]. In the report from Tsubochi and colleagues, there was a significant association between COX-2 expression and lymph node metastasis in patients with adenocarcinomas, but evaluation of squamous cell carcinomas did not demonstrate this relationship [22].

Other studies have corroborated and expanded on these initial findings further documenting the importance of COX-2 in lung cancer [23–27]. Khuri et al. evaluated COX-2 expression in specimens from 160 stage I NSCLC patients by *in situ* hybridization and reported that COX-2 overexpression appears to portend a shorter survival among patients with early stage NSCLC [27]. The strength of COX-2 expression was associated with both a decreased overall survival rate ( $p = 0.001$ ) and a diminished disease-free survival rate ( $p = 0.022$ ) [27]. Tsubochi et al. showed the relationship between COX-2 expression and poor prognosis in stage I adenocarcinomas [22]. Other reports have associated tumor COX-2 overexpression with poor prognosis as well independent of TNM stage in surgically resected NSCLC [27]. These reports, together with other studies documenting an increase in COX-2 expression in precursor lesions [28,29], a common polymorphism in the COX-2 gene associated with increased risk of lung cancer [30], and epidemiological studies that indicate a decreased incidence of lung cancer in patients who regularly take aspirin [31], all support the involvement of COX-2 in the pathogenesis of lung cancer.

Mounting evidence indicates that tumor COX-2 activity has a multi-faceted role in conferring the malignant and metastatic phenotype of lung cancer. Although multiple genetic alterations are necessary for lung cancer invasion and metastasis, COX-2 may be a central element in

orchestrating this process, [21–23,32] and has been implicated in apoptosis resistance [19, 33], angiogenesis [34,35], decreased host immunity [36,37], and enhanced invasion and metastasis [38,39]. These newly discovered molecular mechanisms in the pathogenesis of lung cancer provide novel opportunities for targeted therapies in NSCLC carcinogenesis [40,41]. COX-2 is one of the targets under investigation for lung cancer therapy and chemoprevention [5,6].

#### 4. COX-2 Down-Stream Signaling: Prostanoid Receptors

The prostanoid receptors are in the superfamily of G-protein coupled receptors (GPCR). PGE<sub>2</sub> exerts its multiple effects through four GPCR designated as EP1, EP2, EP3 and EP4 [11]. Studies of the receptor subtypes have shown that the EP1 receptor acts via G<sub>q</sub> protein and upon activation increases cellular Ca<sup>2+</sup> level. Studies indicate EP1 receptors can be localized not only on the cell membrane but also on the nuclear membrane [42]. The EP2 and EP4 receptor signaling is mediated by G<sub>s</sub> G-proteins and leads to activation of adenylate cyclase and elevated cAMP synthesis. In contrast, EP3 signaling through G<sub>i</sub> inhibits adenylate cyclase and cAMP synthesis [43].

The EP<sub>4</sub> receptor is critically involved in inducing the expression of COX-2 and PGE<sub>2</sub> synthase [44]. We have previously demonstrated the importance of PGE<sub>2</sub> and its signaling through the EP4 receptor in mediating NSCLC invasiveness, and shown that genetic inhibition of tumor COX-2 led to diminished matrix metalloproteinase (MMP)-2, CD44, and EP4 receptor expression and invasion [38]. These findings indicate that PGE<sub>2</sub> regulates COX-2-dependent, CD44- and MMP-2-mediated invasion in NSCLC via EP receptor signaling [38]. Yang and colleagues revealed in a murine model that tumor metastasis to the lung was significantly reduced when treated with a specific EP4 antagonist or when EP4 receptor expression was knocked down in the tumor cells using RNA interference technology [45]. In addition, the host EP4 receptors contribute to tumor metastasis and tumor growth with decreased metastasis and tumor growth in EP4 receptor knockout animals [45]. Further evidence supporting the role of prostanoid receptors in lung carcinogenesis was shown by the fibronectin mediated stimulation of human lung carcinoma cell proliferation through the PGE<sub>2</sub> receptor subtype EP4 [46]. Thus, blocking the COX-2 dependent PGE<sub>2</sub> production or activity by targeting the downstream signaling pathway of COX-2, such as EP4 receptor, may produce more profound anti-cancer effects than COX-2 inhibition alone. This could be the basis for new approaches in chemoprevention or treatment of NSCLC.

#### 5. Complicity of Host Cellular Networks in Lung Tumorigenesis

The pulmonary environment presents a unique milieu in which lung carcinogenesis proceeds in complicity with the host cellular network. The pulmonary diseases that are associated with the greatest risk for lung cancer are characterized by abundant and deregulated inflammation [47–49]. Pulmonary disorders such as chronic obstructive pulmonary disease (COPD)/emphysema and pulmonary fibrosis are characterized by profound abnormalities in inflammatory–fibrotic pathways [50–52]. For example, among the cytokines, growth factors, and mediators released in these lung diseases and the developing tumor microenvironment, IL-1 $\beta$ , PGE<sub>2</sub>, and TGF- $\beta$  have been found to have deleterious properties that simultaneously pave the way for both epithelial mesenchymal transition (EMT) and destruction of specific host cell mediated immune (CMI) responses against tumor antigens [53–56]. EMT is the developmental shift from a polarized, epithelial phenotype to a highly motile mesenchymal phenotype [57]. While this process is essential in embryogenesis and organ development, EMT is also critically involved in much adult pathology, including cancer, chronic inflammation, and fibrosis [57,58]. Although EMT is a tightly regulated process during embryonic development [59], in cancer progression, EMT is unregulated with selective elements of the

process amplified and other aspects circumvented [60]. Thus lung cancer develops in a host environment in which the deregulated inflammatory response both degrades CMI and promotes tumor progression. Investigators have attempted to reverse these events by stimulating host immune responses against tumor antigens in lung cancer.

Polymorphisms of genes coding for inflammatory pathway signaling molecules may be involved in promoting lung cancer development. Engels et al. systematically assessed lung cancer risk in relation to a large number of candidate polymorphisms in inflammation-related genes [61]. The study revealed an association of increased lung cancer risk with specific polymorphisms of IL-1A and IL-1B genes, especially among older subjects and those with a history of heavy smoking [61]. These cytokines are secreted by macrophages in response to tissue injury or infection, and are known to be critical mediators in the initiation of inflammation [61]. These findings further support the role of a deregulated inflammatory response to an environmental exposure, such as tobacco smoke, in lung carcinogenesis.

## 6. Reversal of Epithelial Mesenchymal Transition

EMT requires alterations in the cell morphology, adhesion, and migration [58]. These cellular changes result in variable expression of proteins which define EMT markers. Decreased e-cadherin level is a hallmark feature of EMT, which allows reduction in cell to cell adhesion and enhances migratory capacity [58]. We have previously shown a COX-2 dependent transcriptional regulation of e-cadherin expression and cellular aggregation in NSCLC, and a reciprocal relationship between COX-2 and e-cadherin, as well as, ZEB1 and e-cadherin [54]. COX-2 and PGE2 expression resulted in significant reduction in e-cadherin via a ZEB1 and SNAIL transcriptional factor mediated mechanism, and inhibition of COX-2 resulted in rescue of e-cadherin expression [54]. Thus, therapies targeting the COX pathway may diminish the propensity for tumor metastasis in NSCLC by blocking the PGE<sub>2</sub>-mediated induction of e-cadherin transcriptional repressors. This newly defined pathway for transcriptional regulation of e-cadherin in NSCLC has important implications for chemoprevention and treatment of NSCLC using COX-2 inhibitors in combination with other agents. For example, e-cadherin expression in NSCLC has recently been implicated as a marker of sensitivity to epidermal growth factor receptor (EGFR) tyrosine kinase inhibitors (TKI) [62]. Thus, COX-2 inhibitors enhance tumor e-cadherin expression, and may therefore augment sensitivity to EGFR TKI therapy [63].

Histone deacetylase (HDAC) inhibitors may be another strategy to increase e-cadherin and overcome EGFR inhibitor resistance in patients with lung cancer. Transcriptional repressor, ZEB1, inhibits e-cadherin expression by recruiting HDAC. Witta et. al. have shown that e-cadherin transfection into a gefitinib-resistant line increased its sensitivity to gefitinib, and pretreating resistant cell lines with an HDAC inhibitor, induced e-cadherin and EGFR [64]. This resulted in enhanced growth-inhibition and apoptosis effect of gefitinib similar to that in gefitinib-sensitive NSCLC cell lines [64]. Thus, combined HDAC inhibitor and gefitinib treatment may represent a potential strategy to overcome resistance to EGFR TKI.

Bone morphogenetic protein-7 (BMP-7), also known as osteogenic protein-1, is a member of the transforming growth factor- $\beta$  (TGF- $\beta$ ) superfamily [65–67]. It is expressed during embryonic development and plays an important role in organogenesis [65,66]. BMP-7 production is highest in the kidney, and its genetic deletion in murine studies revealed severe impairment in eye, skeletal, and kidney development [67]. In the embryonic lung, BMP-5 and BMP-7 expression has been detected in the mesenchyme and endoderm, respectively, and BMP-4 expression has been restricted to the distal epithelial cells and the adjacent mesenchyme [68]. TGF- $\beta$  is a major regulator and inducer of EMT [58]. Zeisberg et. al. have reported that BMP-7 reverses the TGF- $\beta$ 1 induced EMT by re-induction of e-cadherin through a Smad

dependent mechanism in renal tubular epithelial cells and mammary ductal epithelial cells [69]. In addition, administration of BMP-7 led to repair of severely damaged renal tubular epithelial cells and reversal of chronic renal injury [69]. These results provide evidence of the complex interaction between BMP-7 and TGF- $\beta$ 1 in the regulation of EMT, and imply a potential role of BMP-7 as a therapeutic target in reversing EMT in carcinogenesis.

## 7. Immunosuppression

It was originally hypothesized more than thirty years ago that specialized T cell subpopulations existed that functioned to suppress immune responses [70]. North and others pursued this avenue of investigation within the context of tumor immunity [71,72]. However, these early studies in the field of suppressor T cells were stymied by an inability to characterize the cellular and molecular mechanisms responsible for the observed suppressive phenomena. There has been a renewed interest in the study of T cell mediated suppression of immunity that has been accompanied by the identification regulatory T cells. Although a variety of T regulatory cells have been described [73], much attention has focused on the specific activities of those that have been referred to as “naturally occurring” CD4+CD25<sup>high</sup> T regulatory cells [74,75], and hereafter refer to these as CD4+CD25+ T reg cells. Although investigators had pursued this topic for many years, the ground-breaking studies of Sakaguchi et al. [76] have been viewed as initiating a renaissance in T reg cell research; these, as well as more recent results have led to the characterization of the CD4+CD25+ T cell population as “professional suppressor cells” [75]. These studies revealed that transfer of CD25-depleted CD4 cells to nude mice recipients resulted in the spontaneous development of autoimmune disease [76]. Reconstitution of CD4+CD25+ cells within a limited period after transfer of CD4+CD25- cells prevented the autoimmune disease in a dose-dependent fashion. These initial studies indicated that CD4+CD25+ cells contribute to the maintenance of self-tolerance by down-regulating immune response to self and non-self antigens; elimination or reduction of CD4+CD25+ cells ablated this general suppression, and thereby not only enhanced immune responses to non-self antigens, but also elicited autoimmune responses to certain self-antigens [76]. Subsequent studies have revealed that these cells are both hyporesponsive and suppressive and can act through an APC independent pathway [76–79]. The CD4+CD25+ cells were found to require TCR-dependent activation for induction of suppressor activity [77]. The thymic origin of CD4+CD25+ T reg cells has been documented [80,81]. As originally hypothesized by Shevach [82] and subsequently demonstrated by Jordan et al. [83], the derivation of T reg cells in the thymus appears to occur through a process referred to as “altered negative selection.” More recently it has been appreciated that T reg cells can differentiate from activated human PBL CD4+CD25- cells in the periphery [84,85]. Although many aspects of this peripheral T reg cell differentiation pathway have not yet been defined, it may be pivotal in limiting immune responses to human cancer.

The active immune suppression induced by the tumor has been well documented in lung cancer and other malignancies [86]. Tumor-reactive T cells have been shown to accumulate in lung cancer tissues but fail to respond [87,88]. In fact, a high proportion of NSCLC tumor-infiltrating lymphocytes (TIL) are CD4+CD25<sup>high</sup> T regulatory (T reg) cells [89]. Tumor cells may contribute to promoting immune suppression by directing surrounding inflammatory cells to release suppressive cytokines in the tumor milieu, augmenting the trafficking of suppressor cells to the tumor site, and/or promoting differentiation of effector lymphocytes to a T reg cell phenotype [32,90]. Liu et al. recently demonstrated that tumor cells could directly convert CD4+CD25- T cells to Treg cells through the production of high levels of TGF- $\beta$ , suggesting a possible mechanism through which tumor cells evade the immune system [91].

One major impediment to effective therapy is our inadequate understanding of how lung cancer cells escape immune surveillance and inhibit anti-tumor immunity [92]. In previous studies an

immune suppressive network in NSCLC that is due to over-expression of tumor COX-2 has been defined. COX-2 isoenzyme activity is significantly increased in cancerous tissues compared to their normal counterparts in several malignancies and studies document this over-expression in human lung cancer [93]. In murine lung cancer models specific genetic or pharmacological inhibition of COX-2 *in vivo* led to significant tumor regression [36]. Although COX-2 metabolites have been identified as mediators of immunosuppression, the specific molecular and cellular pathways in the COX-2-dependent immune suppressive network are now being defined. Particular attention has recently focused on defining the pathways whereby COX-2 and its metabolite PGE<sub>2</sub> inhibit immune responses in lung cancer by promoting T regulatory cell activity. PGE<sub>2</sub> promotes the CD4<sup>+</sup>CD25<sup>+</sup> T regulatory phenotype and increases the expression of the forkhead transcription factor FOXP3 that is known to program the development and function of T reg cells. This pivotal relationship is currently under investigation in the laboratory utilizing human cells *in vitro* as well as in patients with lung cancer. Based on the results of pre-clinical murine models [94] and human cells *in vitro* [37], clinical studies are now evaluating the optimal biological dose of a COX-2 inhibitor, celecoxib, to decrease FOXP3 and T regulatory function in patients with lung cancer.

Tumor progression has been associated with alteration in normal hematopoiesis. The ability of cancer to evade immune recognition and resist immune mediated injury can also be mediated by shifting the hematopoietic process to accumulation of cells of the myelo-monocytic lineage at the primary tumor site and at lymphoid organs [95,96]. Myeloid suppressor cells (MSCs) are one of these cell populations and have potent ability to inactivate CD4<sup>+</sup> and CD8<sup>+</sup> cells [95,96]. MSCs produce high levels of arginase I which depletes L-arginine and mediates inhibition of T cell function [97]. Inhibition of COX-2 blocked arginase I induction, and elicited a lymphocyte-mediated antitumor response. Furthermore, signaling through the PGE<sub>2</sub> receptor EP4, expressed in MSCs, induced arginase I [97]. These results demonstrate another pathway of prostaglandin-induced immune dysfunction, and further substantiate the potential cancer prevention and therapeutic effects of COX-2 inhibitors.

## 8. Interaction Between COX-2 and EGFR Signaling

Studies demonstrating that EGFR and COX-2 have related signaling pathways that can interact to regulate cellular proliferation, migration and invasion [98–102] have triggered interest in evaluating the combination of COX-2 and EGFR inhibition in NSCLC. Coffey, et al. [100] demonstrated that the activation of EGFR by transforming growth factor alpha stimulates COX-2 production resulting in increased release of PGE<sub>2</sub> and increased mitogenesis. They also showed that COX-2 inhibition in a human colon cancer cell line led to attenuation of TGF- $\alpha$  activity. Another study [99] evaluated the effects of PGE<sub>2</sub> on EGFR activation in a colon cancer cell line. PGE<sub>2</sub> induced increased phosphorylation of EGFR and Erk 1/2, leading to cell proliferation. Inactivation of EGFR TK with selective inhibitors resulted in decreased PGE<sub>2</sub>-related Erk activation, decreased c-fos mRNA production and decreased cell proliferation. In addition, EGFR inhibitors have been associated with a decrease in the production of angiogenic factors such as IL-8 and VEGF [103,104]. This has also been found to be a mechanism of angiogenesis inhibition by COX-2 inhibitors [105,106]. When studied in combination in a familial adenomatous polyposis (FAP) mouse model, treatment with EKB-785 (an EGFR TKI) and sulindac (a COX inhibitor) resulted in a 95–97% reduction in the incidence of colonic polyps [107]. Consistent with these findings, the co-expression of EGFR and COX-2 in human cervical cancer specimens portends a poor prognosis with increased recurrences [108]. Recently, Chen et al [109] reported that the combination of an EGFR TKI with celecoxib either additively or synergistically inhibited growth of squamous cell carcinoma of the head and neck (SCCHN), significantly induced G1 arrest and apoptosis, and suppressed capillary formation of endothelium. Furthermore, the combination showed strong reduction of EGFR, Erk1/2, and Akt phosphorylation in SCCHN cells as compared with

the single agents [109]. Importantly, we have recently found a novel mechanism of PGE<sub>2</sub>-induced EGFR TKI resistance in NSCLC mediated through an EGFR-independent activation of the MAPK/Erk signaling pathway [98]. In these investigations, we demonstrate that PGE<sub>2</sub> is able to completely overcome the growth inhibitory activity of EGFR TKIs in approximately 40% of NSCLC cell lines.

## 9. COX-2 Clinical Trials

Based on these findings, recent studies have been conducted evaluating combined inhibition of the EGFR and COX-2 pathways in patients with NSCLC. Gadgeel et al. [110] reported a Phase II study of gefitinib and celecoxib in patients with platinum refractory NSCLC. Patients received gefitinib 250 mg daily and celecoxib 400 mg twice daily. The response rate to the combination of celecoxib and gefitinib was similar to that observed with gefitinib alone. O'Byrne [111] recently reported a phase I/II trial of combination therapy with gefitinib (250 mg/day) and rofecoxib (50 mg/day) in patients with platinum-pretreated relapsed NSCLC. Gefitinib combined with rofecoxib was found to provide disease control rates equivalent to that expected with single-agent gefitinib. The lack of beneficial effect of combined EGFR TKI and COX-2 inhibitor therapy from these studies raise the question of whether higher dosage may have a critical effect on efficacy.

Reckamp et al. conducted a Phase I trial evaluating escalating doses of celecoxib (200–800 mg twice daily) in combination with a fixed dose of erlotinib (150 mg/day) in late stage NSCLC patients and established an optimal biological dose (OBD) of 600 mg twice daily, as defined by the maximal decrease in urinary prostaglandin E-M (PGE-M) [63]. This study revealed an acceptable toxicity profile with combination therapy and demonstrated a disease control rate above that expected for erlotinib alone. Based on these results, a Phase II trial is planned to assess combination therapy with celecoxib at 600 mg twice daily and erlotinib versus single agent erlotinib. The use of COX-2 inhibitors at the optimal biological dose may improve efficacy of combination therapy and may explain the lack of benefit in some trials in which a lower dose of COX-2 inhibitors were used. Also, selection of patients with high expression of COX-2 may reveal a beneficial effect of COX-2 inhibitors used in combination with targeted agents or chemotherapy in clinical trials.

Although the use of COX-2 inhibitors at the optimal biological dose may promote responses to combination therapy, there may be associated toxicities with the use of COX-2 inhibitors. Gridelli et al. [112] evaluated the addition of rofecoxib (50 mg/day) to cisplatin and gemcitabine in stage IV or IIIB NSCLC subjects. The groups receiving rofecoxib were closed early due to safety issues surrounding the higher frequency of cardiac ischemia in subjects that received Rofecoxib at 50 mg/day [112]. In a cumulative meta-analysis of 18 randomized controlled trials and 11 observational studies, Juni et al. reported on the increased risk of myocardial infarction in subjects who received rofecoxib [113]. Other reports have shown that rofecoxib exhibits a greater risk of cardiovascular toxicity as compared to celecoxib and may be dose dependent [114]. Solomon et al. found that rofecoxib was associated with a greater incidence of cardiovascular toxicity compared to celecoxib and NSAIDs, and that patients taking rofecoxib at >25 mg doses were associated with higher risk than lower doses [114]. These studies suggest that COX-2 inhibitors may have differing cardiovascular risk and dose may also determine safety profile. It is unclear if cardiac ischemia will occur at a higher risk with short-term usage of COX-2 inhibitors alone or in combination with targeted therapies or conventional chemotherapy.

Several ongoing clinical trials are evaluating COX-2 inhibitors as adjuvants to chemotherapy in patients with advanced NSCLC. Lilenbaum and colleagues reported a phase II trial of irinotecan/docetaxel or irinotecan/gemcitabine with or without celecoxib to determine if



COX-2 inhibition may enhance the efficacy of these chemotherapeutic agents [115]. Patients were randomly assigned to receive irinotecan 60 mg/m<sup>2</sup> and docetaxel 35 mg/m<sup>2</sup>, or irinotecan 100 mg/m<sup>2</sup> and gemcitabine 1,000 mg/m<sup>2</sup>, with or without celecoxib 400 mg twice daily, for four cycles [115]. The median survival was 6.31 months for patients treated with celecoxib and 8.99 months for those treated with chemotherapy alone, and the one-year survival rates were 24% and 36%, respectively [115]. COX-2 inhibition did not appear to enhance efficacy of this chemotherapeutic regimen.

Other studies are focused on the potential role of COX-2 inhibitors in chemoprevention. Mao et al. reported on the feasibility of celecoxib as a chemopreventive agent for lung cancer by administering heavy current smokers with a 6 month course of oral celecoxib and performing serial bronchoscopies with bronchoalveolar lavage and biopsy [116]. Treatment with celecoxib significantly reduced the Ki-67 labeling index in smokers by 35% ( $p = 0.016$ ), and increased the expression of nuclear survivin by 23% ( $p = 0.036$ ) without significantly changing that of cytoplasmic survivin [116]. These findings support the hypothesis that oral administration of celecoxib is capable of modulating Ki-67 labeling index in the bronchial tissue of active smokers at high risk for developing lung cancers [116]. Larger randomized, placebo-controlled clinical trials are underway to determine efficacy of COX-2 inhibitors in preventing the development of bronchogenic carcinoma [6,117].

## 10. Conclusion

Lung carcinogenesis is a complex process involving the acquisition of genetic mutations that lead to cancer development and the malignant phenotype. These mutations are critically linked to cellular changes, such as apoptosis resistance, unregulated proliferation, invasion, metastasis, and angiogenesis. Elucidation of the molecular mechanisms involved in these cellular changes provides opportunities to develop innovative therapies. COX-2 has been implicated in apoptosis resistance, angiogenesis, decreased host immunity, and enhanced invasion and metastasis, and thus has a pivotal role in carcinogenesis. COX-2 is one of the targets under investigation for lung cancer therapy and chemoprevention. Furthermore, targeting the downstream signaling pathways of COX-2 may produce more profound effects than COX-2 inhibition alone, and thus strategies to antagonize the prostanoid receptors, such as EP4, are potential candidate targets in cancer prevention and therapy.

EMT in cancer is an unregulated process in a host environment with deregulated inflammatory response that degrades CMI and that permits lung cancer progression. Understanding transcriptional regulation of key features in EMT, such as down regulation of e-cadherin, has important implications for chemoprevention and treatment of NSCLC using COX-2 inhibitors in combination with other agents. COX-2 inhibition enhances tumor E-cadherin expression, and may therefore augment sensitivity to other anti-tumor agents, such as EGFR TKI therapy. Based on these observations, several ongoing clinical trials are currently evaluating COX-2 inhibitors as adjuvants to chemotherapy in patients with advanced NSCLC and to determine efficacy of COX-2 inhibitors in prevention of bronchogenic carcinoma. In addition, the reversal of EMT has been a focus of intense investigation. As further understanding of the complex interaction between BMP-7 and TGF- $\beta$  in the regulation of EMT is acquired, strategies to enhance BMP-7 expression are potential therapeutic targets to reverse EMT in lung carcinogenesis.

Given the immunosuppressive environment in the tumor, investigators are attempting to reverse these events by stimulating host immune responses against tumor antigens in lung cancer. Both TGF- $\beta$  and PGE2 are among the mediators that promote the CD4<sup>+</sup>CD25<sup>+</sup> T regulatory phenotype and increase the expression of the forkhead transcription factor FOXP3 that is known to program the development and function of T reg cells. These pivotal

relationships are currently under investigation in the laboratory, and clinical studies are underway currently to evaluate the optimal biological dose of a COX-2 inhibitor, celecoxib, to decrease FOXP3 and T regulatory function in patients with lung cancer.

In summary, the understanding of molecular mechanisms involved in inflammation and lung carcinogenesis provide insight for new drug development that target reversible, non-mutational events in the chemoprevention and treatment of lung cancer.

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## Biographies

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