

REVIEW

From smoking to lung cancer: the CHRNA5/A3/B4 connection

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Nicotinic acetylcholine receptors (nAChRs) are ligand-gated ion channels that modulate key physiological processes ranging from neurotransmission to cancer signaling. These receptors are activated by the neurotransmitter, acetylcholine, and the tobacco alkaloid, nicotine. Recently, the gene cluster encoding the $\alpha 3$, $\alpha 5$ and $\beta 4$ nAChR subunits received heightened interest after a succession of linkage analyses and association studies identified multiple single-nucleotide polymorphisms in these genes that are associated with an increased risk for nicotine dependence and lung cancer. It is not clear whether the risk for lung cancer is direct or an effect of nicotine dependence, as evidence for both scenarios exist. In this study, we summarize the body of work implicating nAChRs in the pathogenesis of lung cancer, with special focus on the clustered nAChR subunits and their emerging role in this disease state.

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Introduction

Tobacco use is the leading cause of preventable mortality around the world, resulting in more than 5 million deaths per year (WHO, 2009). Approximately 600 000 of these deaths are because of second-hand smoke, with one-third of the adult population exposed to second-hand smoke globally. In the United States, overall tobacco use has been declining but approximately 46 million adults still smoked in 2008 (CDC, 2009). If current trends persist, tobacco may kill a billion people by the end of this century.

The list of diseases caused by tobacco use is expanding, according to a recent Surgeon General's report on the health effects of smoking (HHS, 2004). A causal relationship was reported between active smoking and cardiovascular diseases, respiratory diseases, reproductive disorders and several types of cancers, including

cancers of the lung, bladder, cervix, esophagus, kidney, larynx, mouth, pancreas, stomach as well as leukemia.

Cigarette smoke contains 4000 chemicals, 250 of which are known to be harmful, and at least 50 of which are carcinogens (Shields, 2002). The most potent of these carcinogens are polycyclic aromatic hydrocarbons and nicotine metabolites such as 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone (NNK) and *N*-nitrosornicotine (NNN). These nitrosamines form DNA adducts that cause mutations leading to cancer (Hecht and Hoffmann, 1988). In the following sections, we review evidence accumulated through the years (see Timeline in Figure 1) showing that nicotine, itself, promotes lung cancer through its interaction with nicotinic acetylcholine receptors (nAChRs).

Nicotinic acetylcholine receptors

nAChRs are a heterogeneous family of ligand-gated cation channels activated by the endogenous neurotransmitter acetylcholine (ACh) and exogenous chemicals such as nicotine and its metabolites. nAChRs were the first receptors to be characterized at the biochemical, biophysical, molecular and pharmacological levels and have served as prototypes for all other ligand-gated ion channels, including those activated by 5-HT₃ (5-hydroxytryptamine), GABA_A and GABA_C (γ -aminobutyric acid) and glycine (Le Novere and Changeux, 1995, Taly *et al.*, 2009). Ligand binding induces a conformational change causing the channel to open, thereby allowing the flow of Na⁺, K⁺ and Ca²⁺ ions down their electrochemical gradients. The propensity of nAChRs to flux intracellular calcium levels is important in the activation of downstream signaling cascades (Fucile, 2004).

nAChRs can be classified into two main categories: muscle or neuronal receptors. Muscle nAChRs are expressed primarily in skeletal neuromuscular junctions and are composed of the $\alpha 1$, $\beta 1$, δ and ϵ or γ subunits (McGehee and Role, 1995). In contrast, neuronal nAChRs were originally cloned from neuronal-like cell lines and brain complementary DNA libraries, hence their name, and are expressed throughout the nervous system, in which they increase neuronal excitability and facilitate synaptic transmission (McGehee and Role, 1995; Dani and Bertrand, 2007; Albuquerque *et al.*, 2009). In all, 12 neuronal nAChR subunits have been identified, namely $\alpha 2$ – $\alpha 10$ and $\beta 2$ – $\beta 4$ (Patrick *et al.*,

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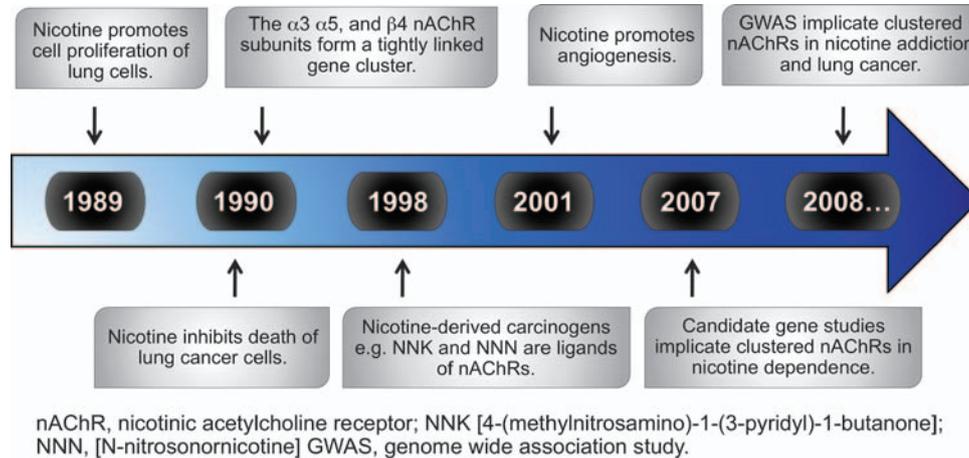


Figure 1 Timeline: key events implicating nAChRs in lung cancer etiology. GWAS, genome-wide association study; nAChR, nicotinic acetylcholine receptor; NNK, 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone; NNN, *N*-nitrososornicotine.

1993; Boyd, 1997; Gotti *et al.*, 2006). Expression of these subunits has also been observed in many other cell types, including endothelial cells, gastrointestinal tissue, glia, immune cells, keratinocytes and lung tissue (Battaglioli *et al.*, 1998; Macklin *et al.*, 1998; Maus *et al.*, 1998; Nguyen *et al.*, 2000; Arredondo *et al.*, 2001; Wang *et al.*, 2001; Kawashima and Fujii, 2003; Spindel, 2003; Gahring *et al.*, 2004; Gahring and Rogers, 2006; Wessler and Kirkpatrick, 2008).

nAChRs are integral membrane proteins composed of five subunits symmetrically arranged around a central pore (Figure 2a) (Corringer *et al.*, 2000). Each nAChR subunit consists of a large extracellular amino-terminal domain, four transmembrane domains, a cytoplasmic loop of variable length between the third and fourth transmembrane domains and a short extracellular carboxy-terminal domain (Figure 2b) (Unwin, 2005). The large extracellular domain of α -subunits contains adjacent cysteines important for ligand binding, whereas β -subunits lack these residues (Albuquerque *et al.*, 2009). Unlike other α -subunits, however, $\alpha 5$ does not contribute to ligand binding as it is missing a key tyrosine residue (Karlin, 2002). Importantly though, incorporation of the $\alpha 5$ subunit into a mature receptor does alter receptor biophysical properties such as increasing the calcium conductance (Gerzanich *et al.*, 1998).

The combination of different nAChR subunits can lead to the formation of a vast array of nAChR subtypes. The $\alpha 2$ – $\alpha 6$ subunits can form heteromeric receptors with the $\beta 2$ – $\beta 4$ subunits, whereas the $\alpha 7$ – $\alpha 9$ subunits can form homomeric receptors that are blocked by α -bungarotoxin (Couturier *et al.*, 1990; Schoepfer *et al.*, 1990; Elgoyhen *et al.*, 1994). In addition, $\alpha 9$ can form a heteromeric receptor with $\alpha 10$ (Elgoyhen *et al.*, 2001; Lustig *et al.*, 2001) and $\alpha 7$ can form a heteromeric receptor with $\beta 2$ (Liu *et al.*, 2009). Each of these receptor subtypes has distinct electrophysiological and pharmacological properties (Role and Berg, 1996; Boyd, 1997; Gerzanich *et al.*, 1997; Albuquerque *et al.*, 2009).

The functional diversity by the nAChR family offers abundant prospects for the design of novel therapeutics. Hence, nAChRs are being actively investigated as drug targets for nervous system disorders, including Alzheimer's disease, anxiety, attention deficit hyperactivity disorder, depression, epilepsy, pain, Parkinson's disease, schizophrenia, Tourette's syndrome and nicotine addiction (Lloyd and Williams, 2000; Arneric *et al.*, 2007; Romanelli *et al.*, 2007).

The $\alpha 3/\alpha 5/\beta 4$ nAChR subunit gene cluster

In recent years, a series of linkage analyses, candidate-gene association studies and genome-wide association studies have pointed to a possible role for the $\alpha 3$, $\alpha 5$ and $\beta 4$ nAChR subunits in both nicotine addiction and lung cancer (Schlaepfer *et al.*, 2008; Amos *et al.*, 2008; Berrettini *et al.*, 2008; Bierut *et al.*, 2008; Hung *et al.*, 2008; Portugal and Gould, 2008; Spitz *et al.*, 2008; Stevens *et al.*, 2008; Thorgeirsson *et al.*, 2008; Wacholder *et al.*, 2008; Weiss *et al.*, 2008; Caporaso *et al.*, 2009; Freathy *et al.*, 2009; Pillai *et al.*, 2009; Saccone *et al.*, 2009a; Sasaki *et al.*, 2010). The genes that encode the $\alpha 3$, $\alpha 5$ and $\beta 4$ nAChR subunits lie in a genomic cluster in strong linkage disequilibrium with each other (Figure 3) (Boulter *et al.*, 1990). These three genes encode a predominant nAChR subtype expressed in the peripheral nervous system (Leonard and Bertrand, 2001).

The function of the clustered subunits can be gleaned from knockout (KO) animal studies. These studies have shown that the $\alpha 3$ subunit is necessary for survival, with homozygous KO mice dying perinatally because of multiorgan dysfunction (Xu *et al.*, 1999a). $\alpha 3$ KO mice have enlarged bladders, causing bladder infection, dribbling urination and urinary stones—a phenotype resembling that of a rare human condition called megacystis-microcolon-intestinal hypoperistalsis syn-

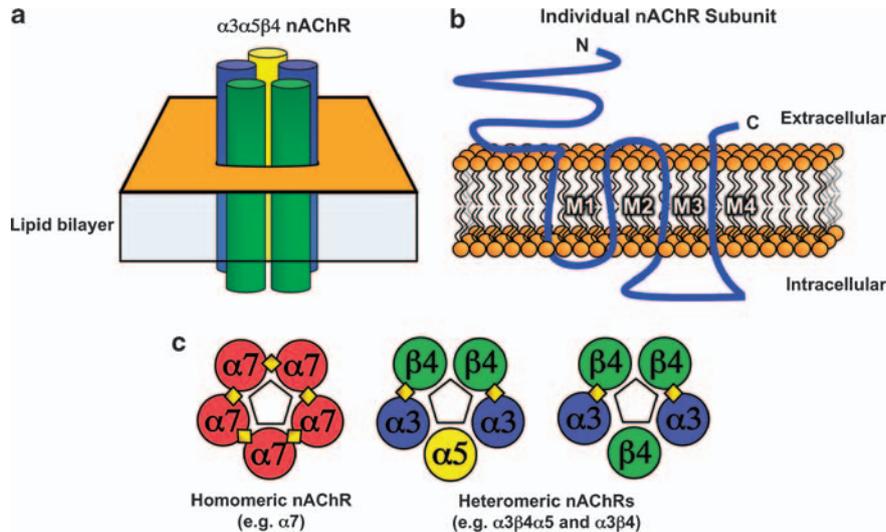


Figure 2 Structure of the nAChR. (a) Schematic representation illustrating the pentameric arrangement of subunits in an assembled nAChR. (b) Conserved domains of a nAChR subunit including the amino (N) and carboxy (C) terminals, transmembrane segments (M1–M4) and the intracellular loop. (c) Assembly of heteromeric and homomeric nAChR subtypes. Individual nAChR subunits are represented as colored circles, with diamonds representing ligand-binding sites. Pentagons in the center of each pentamer represent the pore region.

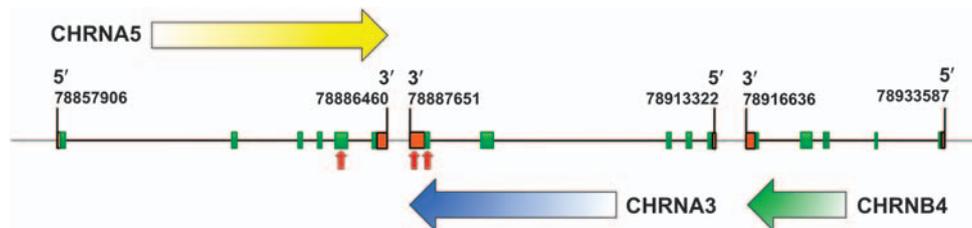


Figure 3 The human nAChR $\alpha3/\alpha5/\beta4$ gene cluster. Green boxes represent exons and orange boxes represent untranslated regions. Black lines located between green boxes represent introns whereas gray lines represent intragenic regions. The boundaries for each gene are labeled with corresponding Genbank annotations. Horizontal arrows indicate the direction of transcription. Vertical red arrows indicate SNPs associated with nicotine dependence and lung cancer.

drome. Patients with this disease also do not appear to express $\alpha3$ mRNA (Richardson *et al.*, 2001). $\alpha3$ KO mice also show extreme mydriasis and lack of pupil contraction in response to light, with loss of bladder contraction in response to nicotine (Xu *et al.*, 1999b). Furthermore, $\alpha3$ heterozygous mice are partially resistant to nicotine-induced seizures compared with wild-type littermates (Salas *et al.*, 2004a). In contrast, $\alpha5$ and $\beta4$ KO mice are both viable and lack any gross abnormalities (Xu *et al.*, 1999b; Wang *et al.*, 2002, 2003). However, $\alpha5$ and $\beta4$ KO mice do show autonomic dysfunction and are less sensitive to nicotine. Mice lacking $\alpha5$ are also more susceptible to experimentally induced inflammatory bowel disease (Orr-Urtreger *et al.*, 2005) whereas $\beta4$ KO mice show less anxiety in behavioral tests (Salas *et al.*, 2003).

The observation that the $\alpha3$, $\alpha5$ and $\beta4$ genes are co-expressed and co-regulated in many cell types in the nervous system is consistent with the hypothesis that their expression is because of coordinated transcriptional regulation. The three subunits are highly expressed in the peripheral nervous system as well as in several regions of the brain, including the brain stem, cerebellum, hippocampus, interpeduncular nucleus,

medial habenula, pineal gland and the ventral tegmental area (Quick *et al.*, 1999; Xu *et al.*, 1999a; Flora *et al.*, 2000b; Klink *et al.*, 2001; Perry *et al.*, 2002; Zoli *et al.*, 2002; Salas *et al.*, 2003; Gahring *et al.*, 2004; Salminen *et al.*, 2004; Turner and Kellar, 2005). Furthermore, mRNA levels of the three genes are coordinately upregulated during neural development and differentiation (Corriveau and Berg, 1993; Levey *et al.*, 1995; Levey and Jacob, 1996; Zhou *et al.*, 1998).

Efforts have been made to understand the regulatory mechanisms governing the expression of the clustered nAChR subunit genes. Sequencing of the individual gene promoters has revealed that each promoter lacks classical CAAT and TATA boxes (Boulter *et al.*, 1990). Instead, the promoters are GC rich and contain several binding sites for the transcription factor, Sp1. Sp1 regulates transcription of each of the clustered subunit genes through multiple binding sites in each individual promoter (Yang *et al.*, 1995; Bigger *et al.*, 1997; Campos-Caro *et al.*, 1999, 2001; Melnikova *et al.*, 2000; Terzano *et al.*, 2000; Flora *et al.*, 2000a; Melnikova and Gardner, 2001; Valor *et al.*, 2002). Chromatin immunoprecipitation experiments have confirmed Sp1 binding in the context of native chromatin

for all three promoters (Benfante *et al.*, 2007; Scofield *et al.*, 2008). It is likely that Sp1 is involved in tethering the basal transcription machinery to the TATA-less nAChR subunit gene promoters (Pugh and Tjian, 1991). In addition to the Sp1 regulation common to all three promoters, other transcription factors have been found to govern expression of the clustered genes either independently or coordinately, including achaete-scute complex homolog-1 (*ASCL1*), *Brn-3a-c*, *c-Jun*, *hnRNPK*, *PHOX2A*, *Pur α* , *Sox10*, *Sp3* and *Tst-1/Oct6/SCIP* (Yang *et al.*, 1994; Milton *et al.*, 1996; Bigger *et al.*, 1997; Du *et al.*, 1997, 1998; Liu *et al.*, 1999; Melnikova *et al.*, 2000; Benfante *et al.*, 2007; Improgo *et al.*, 2010). Two regulatory elements have also been found that direct the expression of the clustered nAChR genes in a tissue-specific manner: $\beta 4 3'$, found at the $\beta 4$ 3'-untranslated region, and *CNR4*, a conserved non-coding region located 20 kb upstream of $\beta 4$ (Xu *et al.*, 2006). Recently, we showed that a 2.3-kb fragment of the $\beta 4$ gene promoter directs spatially and developmentally regulated expression of a reporter gene *in vivo* (Bruschweiler-Li *et al.*, 2010). Whether this region also regulates expression of the $\alpha 3$ and $\alpha 5$ genes remains to be determined.

Role of nAChRs in nicotine addiction

Nicotine is one of the most widely consumed psychoactive drugs in the world and is the primary reinforcing chemical in tobacco (Stolerman and Jarvis, 1995). Nicotine addiction is initiated upon nicotine-mediated activation of nAChRs in the mesolimbic dopaminergic pathway, known as the reward circuitry of the brain (Corrigall *et al.*, 1992; Di Chiara, 2000; Dani and De Biasi, 2001). Dopaminergic neurons in this pathway originate in the ventral tegmental area and project to the nucleus accumbens (NAc) and the prefrontal cortex. Activation of nAChRs expressed in the ventral tegmental area ultimately causes an increase in the firing of dopaminergic neurons, resulting in an increase of dopamine release in the NAc (Calabresi *et al.*, 1989; Nisell *et al.*, 1994; Pontieri *et al.*, 1996; Pidoplichko *et al.*, 1997). Expression of $\alpha 4$ - and $\beta 2$ -containing receptors in the ventral tegmental area is necessary and sufficient for nicotine-mediated dopamine elevation in the NAc (Picciotto *et al.*, 1998; Marubio *et al.*, 2003; Maskos *et al.*, 2005; Pons *et al.*, 2008). $\alpha 4\beta 2^*$ nAChRs are also critical for nicotine reward/reinforcement, sensitization and tolerance (Picciotto *et al.*, 1998; Tapper *et al.*, 2004, 2007; Pons *et al.*, 2008). Elevation of dopamine levels in the NAc reinforces drug use and is critical for the onset and maintenance of nicotine dependence (Di Chiara and Imperato, 1988). Conversely, inhibiting dopamine elevation through lesions or pharmacological blockade attenuates the rewarding effects of nicotine (Corrigall and Coen, 1991).

Nicotine dependence is a consequence of both positive reinforcement and avoidance of the aversive effects of cessation (Kenny and Markou, 2001). Smoking cessa-

tion produces withdrawal symptoms, which account for the high incidence of relapse in people attempting to quit smoking (Corrigall *et al.*, 1989; Kenny and Markou, 2001). The withdrawal syndrome involves both mood-oriented (affective) and physical (somatic) symptoms (De Biasi and Salas 2008). The $\alpha 5$ - and $\beta 4$ -containing nAChRs as well as $\alpha 7$ nAChRs seem to be involved in the physical symptoms of withdrawal as somatic signs are diminished in $\alpha 5$, $\alpha 7$ and $\beta 4$ KO mice (Salas *et al.*, 2004b, 2007; Jackson *et al.*, 2008). Conversely, affective symptoms are absent in $\beta 2$ KO mice but are readily observable in $\alpha 5$ and $\alpha 7$ KO mice (Jackson *et al.*, 2008; Portugal *et al.*, 2008).

Results of the aforementioned genetic studies also support the role of the $\alpha 3$, $\alpha 5$ and $\beta 4$ subunits in nicotine dependence. In a candidate-gene study targeting 348 genes, smokers of European descent who developed nicotine dependence were compared with smokers who were not dependent (Saccone *et al.*, 2007). In this study, several single-nucleotide polymorphisms (SNPs) associated with nicotine dependence were found within the $\alpha 5/\alpha 3/\beta 4$ gene cluster. Of particular interest is the non-synonymous SNP, rs16969968, found in the fifth exon of the $\alpha 5$ gene. This polymorphism changes an aspartic acid residue into asparagine at position 398 (D398N) in the second intracellular loop of $\alpha 5$. Receptors expressing the aspartic acid variant show greater maximal response to nicotine, causing higher intracellular calcium levels (Bierut *et al.*, 2008). Individuals with one copy of the minor allele were found to have a 1.3-fold increased risk for nicotine dependence, whereas individuals with two copies of this risk variant have almost a twofold increase in risk (Saccone *et al.*, 2007). In addition, rs16969968 was found to be associated with pleasurable responses during smoking initiation among Caucasians (Sherva *et al.*, 2008).

Other SNPs highly correlated with rs16969968 also influence the risk for nicotine dependence, such as rs1051730 found in exon 5 of $\alpha 3$ and rs578776 found in the $\alpha 3$ 3'-untranslated region (Saccone *et al.*, 2007). The latter had an even stronger association with nicotine dependence. These same SNPs were associated with increased smoking intake in an independent study analyzing 219 European American families (Bierut *et al.*, 2008). Furthermore, these SNPs were associated with early-onset smoking, a phenotype associated with more severe nicotine dependence in adults (Weiss *et al.*, 2008). In addition, rs1051730 was found to be strongly associated with smoking quantity in an Icelandic population (Thorgeirsson *et al.*, 2008) and was associated with decreased likelihood of quitting during pregnancy in women of European descent (Freatly *et al.*, 2009). These studies provide compelling evidence for the role of the $\alpha 5/\alpha 3/\beta 4$ gene cluster in nicotine dependence.

Role of nAChRs in lung cancer

Smoking is the major risk factor associated with lung cancer, the leading cause of cancer-related deaths for

both men and women (ACS, 2009). Lung cancer is also the second most common form of cancer in both sexes, with an overall 5-year survival rate of 15%. The two major histopathological types of lung cancer are small cell lung carcinoma (SCLC) and non-small cell lung carcinoma (NSCLC). NSCLC can be subdivided into adenocarcinoma, squamous cell, bronchioalveolar and large cell lung carcinoma. In SCLC, >95% of patients have a history of cigarette smoking and the 5-year survival rates for these patients can reach as low as 2% (Jackman and Johnson, 2005).

Several lines of evidence indicate that nAChRs have a role in lung carcinogenesis as discussed in the following sections. nAChRs are expressed in both normal and lung cancer cells (Schuller, 1989; Maneckjee and Minna, 1990; Maus *et al.*, 1998; Wang *et al.*, 2001; Song *et al.*, 2003; Lam *et al.*, 2007; Sartelet *et al.*, 2008; Improgo *et al.*, 2010). The clustered nAChR subunits, in particular, are overexpressed in SCLC (Improgo *et al.*, 2010). This overexpression seems to be regulated by ASCL1 (Improgo *et al.*, 2010), a basic helix-loop-helix transcription factor that is also overexpressed in SCLC (Ball *et al.*, 1993). Transgenic mice that constitutively express ASCL1 and the SV40 large T antigen develop aggressive lung tumors with SCLC features (Linnoila *et al.*, 2000). Upregulation of the clustered nAChRs by ASCL1 provides a mechanism by which the effects of nicotine and other nAChR ligands are potentiated in SCLC, contributing to the aggressiveness of this type of lung cancer (Improgo *et al.*, 2010). Additional evidence for a role of the clustered nAChR genes in lung cancer comes from the recent demonstration that the $\alpha 3$ subunit gene is a frequent target of aberrant DNA hypermethylation and silencing in lung cancer (Paliwal *et al.*, 2010).

nAChRs and cell proliferation

The various ligands that activate nAChRs promote the development and progression of lung cancer through different mechanisms. First, ACh is synthesized by and acts as an autocrine growth factor for SCLC (Song *et al.*, 2003). ACh has also been shown to activate signaling pathways vital for growth and differentiation of human epithelial cells (Grando, 2008). Similarly, nicotine can induce cell proliferation in a manner reminiscent of classical growth factors activating cancer signaling pathways. Specifically, nicotine treatment has been shown to cause physical interactions between the retinoblastoma protein and the signaling kinase Raf-1, leading to downstream events such as inactivation of cyclins and cyclin-dependent kinases, dissociation of the transcription factor E2F1 from retinoblastoma protein, binding of E2F1 to proliferative promoters causing their transcription and entry into S phase (Dasgupta and Chellappan, 2006; Egleton *et al.*, 2008). In addition, nicotine treatment can increase the levels of growth factors such as brain-derived neurotrophic factor, hepatocyte growth factor, platelet-derived growth factor, transforming growth factor- α and - β , vascular

endothelial growth factor (VEGF) and VEGF-C as well as their corresponding receptors (Conti-Fine *et al.*, 2000). Moreover, nicotine activation of epidermal growth factor receptor seems to involve increases in intracellular calcium levels (Sher *et al.*, 1998). Nicotine also stimulates NSCLC cell proliferation by upregulating fibronectin expression while downregulating epithelial markers such as E-cadherin and β -catenin (Zheng *et al.*, 2007; Davis *et al.*, 2009). Nicotine-induced fibronectin expression is associated with activation of the extracellular signal-regulated kinase and the phosphoinositide 3-kinase/mammalian target of rapamycin signaling pathways and is abrogated by treatment with the $\alpha 7$ nAChR antagonist, α -bungarotoxin (Zheng *et al.*, 2007). This group also showed that nicotine induces NSCLC cell proliferation by stimulating the expression of the nuclear hormone receptor, peroxisome proliferator-activated receptor- β/δ , an effect that can be blocked by α -bungarotoxin, $\alpha 7$ nAChR short interfering RNA and phosphoinositide 3-kinase inhibitors (Sun *et al.*, 2009). Taken together, these results suggest that nicotine increases peroxisome proliferator-activated receptor- β /gene expression through $\alpha 7$ nAChR-mediated activation of phosphoinositide 3-kinase/mammalian target of rapamycin signals leading to cell proliferation (Zheng *et al.*, 2007; Sun *et al.*, 2009). Nicotine also promotes cell proliferation in other types of cancers: it promotes growth of gastric tumors by activating extracellular signal-regulated kinase and cyclooxygenase-2 and promotes growth of colon cancer through epidermal growth factor receptor, c-Src and 5-lipoxygenase-mediated signaling pathways (Shin *et al.*, 2004; Ye *et al.*, 2004).

nAChRs and apoptosis

Maneckjee and Minna (1994) first showed that low concentrations of nicotine confer resistance to apoptosis in lung cancer cells. Since then, nicotine has been shown to inhibit apoptosis induced by various stress stimuli, including ultraviolet radiation, oxidative stress and exposure to opioids, Ca^{2+} ionophores, neurotoxins and anticancer drugs (Zeidler *et al.*, 2007; Egleton *et al.*, 2008). This apoptotic inhibition seems to involve several signaling pathways. One mechanism involves phosphorylation and consequent activation of the anti-apoptotic protein, B cell lymphoma gene 2 by protein kinase C α and phospholipase C (Mai *et al.*, 2003). Consistently, nicotine inactivates the pro-apoptotic functions of Bax and Bad (Jin *et al.*, 2004; Xin and Deng, 2005). Another mechanism involves nicotine-mediated activation of Akt (also called protein kinase B), a serine-threonine kinase whose activation leads to apoptotic inhibition and tumorigenesis (Scheid and Woodgett, 2001). Nicotine exposure causes site-specific phosphorylation of Akt at Thr308 and Ser473 as well as phosphorylation of downstream Akt substrates such as mammalian target of rapamycin, FKHR, elf-4, GSK3B, tuberlin and S6K (West *et al.*, 2003). The use of

pharmacological agents suggests that this process involves $\alpha 3$ -containing nAChRs. In the same study, increased Akt activation was observed in lung cancer tissue from smokers. Further evidence implicating $\alpha 3$ in Akt signal transduction is a recent report showing that small hairpin RNA-mediated depletion of the $\alpha 3$ subunit leads to a dramatic Ca^{2+} influx in a NSCLC cell line that was followed by activation of the Akt pathway (Paliwal *et al.*, 2010). In this study, NSCLC cells, in which the $\alpha 3$ subunit was depleted, were resistant to apoptosis-inducing drugs.

nAChRs and angiogenesis

Endothelial cells express nAChRs as well as key molecules for cholinergic signaling such as choline acetyltransferase and acetylcholinesterase (Macklin *et al.*, 1998; Wang *et al.*, 2001). In these cells, ACh is thought to act in an autocrine or paracrine manner to stimulate angiogenesis (Cooke and Ghebremariam, 2008). Nicotine also functions as a pro-angiogenic agent, activating both physiological and pathological angiogenesis through the phosphatidylinositol 3-kinase and mitogen-activated protein kinase pathways (Heeschen *et al.*, 2001). Analogous to angiogenic cytokines, nicotine promotes endothelial cell migration, proliferation, survival, tube formation and nitric oxide production and can be as potent as fibroblast growth factor (Cooke and Ghebremariam, 2008). Nicotine and its metabolite, cotinine, have also been shown to upregulate the expression of VEGF in endothelial cells (Conklin *et al.*, 2002). In addition, second-hand smoke increases VEGF expression and elevates levels of circulating endothelial progenitor cells, promoting angiogenesis and tumor growth—an effect reduced by the non-selective nAChR antagonist mecamylamine (Zhu *et al.*, 2003). Even in the absence of exogenous nicotine, angiogenic processes stimulated by VEGF or fibroblast growth factor can be blocked by nAChR antagonists such as mecamylamine and hexamethonium and the $\alpha 7$ -selective antagonist α -bungarotoxin (Cooke and Ghebremariam, 2008). In lung cancer cells, nicotine also induces the expression of hypoxia-inducible factor-1 α , a transcription factor that promotes hypoxia-induced angiogenesis (Zhang *et al.*, 2007).

nAChRs and the immune system

The function of nAChRs in immunity and cancer has two aspects. The first involves the complex interplay between the inflammatory effects of irritants in cigarette smoke and the anti-inflammatory effects of nicotine (Gahring and Rogers, 2006). Chronic inflammation triggered by tobacco smoke has been shown to promote lung carcinogenesis (Takahashi *et al.*, 2010). Inflammation induced by cigarette smoke also promotes chronic obstructive pulmonary disease, a disease associated with increased lung cancer risk (Punturieri *et al.*, 2009; Grivennikov *et al.*, 2010). Chronic inflammation increases cancer risk by influencing every stage of cancer

from initiation, promotion, invasion and metastasis through induction of oncogenic mutations and genomic instability, local immunosuppression and angiogenesis (reviewed in Grivennikov *et al.*, 2010). In contrast, nicotine itself seems to suppress immune function and has been shown to be protective against inflammatory diseases such as pneumonia and ulcerative colitis (Rubin and Hanauer, 2000; Blanchet *et al.*, 2004; Shivji *et al.*, 2005). Suppression of the immune response by nicotine may affect immune surveillance, preventing the clearance of nascent tumor cells (Gahring and Rogers, 2006; Grivennikov *et al.*, 2010).

The second aspect of nAChR function in immunity and cancer involves the production of autoantibodies against nAChRs in cancer patients with paraneoplastic syndromes (Gahring and Rogers, 2006). In particular, antibodies against $\alpha 3$ nAChRs have been detected in the serum of SCLC patients who show autonomic neuropathy (Vernino *et al.*, 1998, 2000). Dysautonomia caused by these autoantibodies is characterized by symptoms such as impaired papillary light reflex, gastrointestinal dysmotility and bladder dysfunction that are reminiscent of those observed in $\alpha 3$ KO mice (Xu *et al.*, 1999a; McKeon *et al.*, 2009).

Carcinogenic nitrosamines as nAChR ligands

Nicotine-derived nitrosamines such as NNK and NNN activate nAChRs with varying affinities (Schuller and Orloff, 1998). NNK preferentially activates $\alpha 7$ nAChRs, whereas NNN has higher affinity for heteromeric nAChRs. Activation of nAChRs by these ligands promotes cell proliferation, apoptotic inhibition and angiogenesis (Schuller, 2009). NNK and NNN seem to stimulate distinct proliferative pathways in bronchial epithelial cells. NNK causes activation of the transcription factors GATA-3, nuclear factor- κ B and STAT-1, whereas NNN predominantly activates GATA-3 and STAT-1, effects that can be abolished by the nAChR antagonists α -bungarotoxin and mecamylamine, respectively (Arredondo *et al.*, 2006a). In SCLC cells, NNK promotes calcium influx, serotonin release and activation of the protein kinase C and Raf-1/mitogen-activated protein kinase pathway (Schuller, 1992; Jull *et al.*, 2001; Arredondo *et al.*, 2006b). NNK has also been shown to activate the Akt pathway *in vitro* and inhibit apoptosis (West *et al.*, 2003). In the same study, increased Akt phosphorylation was found in the lungs of NNK-treated mice. These studies suggest that carcinogenic nitrosamines can not only initiate lung cancer through their genotoxic effects, but can also promote lung cancer through nAChR-mediated mechanisms (Arredondo *et al.*, 2006a).

Risk alleles in lung cancer

Several SNPs found in the $\alpha 5/\alpha 3/\beta 4$ gene cluster seem to influence the risk for lung cancer. In a large-scale genome-wide association study involving approximately

317 000 SNPs in samples of European origin, the non-synonymous SNP, rs16969968, was found to be strongly associated with lung cancer (Hung *et al.*, 2008). This SNP was also found to increase the risk for lung adenocarcinoma in an Italian population (Falvella *et al.*, 2009). Hung *et al.* (2008) also showed that the increased risk for lung cancer was observed even in non-smokers, suggesting that the association is not simply a consequence of nicotine dependence. Another evidence for direct association is that rs16969968 did not increase the risk for other smoking-related cancers such as head and neck cancer.

The $\alpha 3$ exon 5 SNP, rs1051730, was also found to be associated with lung cancer (Hung *et al.*, 2008). Furthermore, in an independent genome-wide association study, rs1051730 was found to be associated with lung cancer and was only weakly associated with nicotine dependence (Amos *et al.*, 2008). In addition, rs1051730 was found to be associated with familial lung cancer even after adjustment for pack-years of cigarette exposure (Liu *et al.*, 2008). Another group also found rs1051730 to be associated with lung cancer and peripheral arterial disease (Thorgeirsson *et al.*, 2008). Taken together, these studies represent a strong convergence of genetic data implicating the $\alpha 3/\alpha 5/\beta 4$ gene cluster in lung cancer.

One report, however, showed that the rs1051730 SNP was associated with both nicotine dependence and lung cancer, but that there was no increased risk for lung cancer in lifetime never smokers, suggesting that the association with lung cancer was an effect of nicotine dependence (Thorgeirsson *et al.*, 2008). Reasons for the conflicting data may include differences in populations, sample sizes, phenotypes used to assess nicotine dependence and instruments used to measure phenotypes (Greenbaum and Lerer, 2009). For example, most of the studies were performed in populations of European origins, in which the frequency of the rs16969968 allele is 37%, whereas in African populations the frequency of this allele is significantly lower (Bierut *et al.*, 2008; Saccone *et al.*, 2009b).

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Conclusions and perspectives

Given the number of carcinogens found in cigarettes, it is not surprising that smoking is the major risk factor associated with lung cancer. Hence, many mechanisms leading to cancer can be envisaged. One such mechanism involves the activation of nAChRs by nicotine and its metabolites, which subsequently engage cancer signaling pathways associated with cell proliferation, apoptotic inhibition and angiogenesis. Previous studies investigating the link between nAChRs and these pathways have implicated primarily the $\alpha 7$ nAChR. The recent deluge of genetic studies, however, suggests that other subtypes should be investigated, in particular, the $\alpha 3/\alpha 5/\beta 4$ nAChR subtype. Our work showing the overexpression of the clustered nAChR genes in SCLC and their regulation by ASCL1, which has a critical role in the pathogenesis of lung cancer, provides evidence for the role of the clustered nAChR genes in this disease (Improgo *et al.*, 2010). This is further substantiated by the recent finding of aberrant DNA hypermethylation and silencing of the $\alpha 3$ subunit gene in NSCLC (Paliwal *et al.*, 2010). The use of genetic approaches to investigate the non-synonymous SNP found in $\alpha 5$ as well as other SNPs found in the cluster should be fertile areas for future investigations.

Conflict of interest

The authors declare no conflict of interest.

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