

REVIEW ARTICLE

Dual oxidase: a novel therapeutic target in allergic disease

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Received 14 November 2017; Revised 17 January 2018; Accepted 22 January 2018

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NADPH oxidases (NOXs) represent a family of enzymes that mediate regulated cellular production of reactive oxygen species (ROS) and play various functional roles in physiology. Among the NOX family, the dual oxidases DUOX1 and DUOX2 are prominently expressed in epithelial cell types at mucosal surfaces and have therefore been considered to have important roles in innate host defence pathways. Recent studies have revealed important insights into the host defence mechanisms of DUOX enzymes, which control innate immune response pathways in response to either microbial or allergic triggers. In this review, we discuss the current level of understanding with respect to the biological role(s) of DUOX enzymes and the unique role of DUOX1 in mediating innate immune responses to epithelial injury and allergens and in the development of allergic disease. These novel findings highlight DUOX1 as an attractive therapeutic target, and opportunities for the development of selective inhibitor strategies will be discussed.

Abbreviations

CPZ, chlorpromazine; DPI, diphenylene iodonium; DUOX, dual oxidase; DUOXA, dual oxidase maturation factor; EGFR, EGF receptor; ER, endoplasmic reticulum; HDM, house dust mite; ILC2, type 2 innate lymphoid cell; LPO, lactoperoxidase; MPO, myeloperoxidase; NOX, NADPH oxidase; NOXA, NOX activator; PDB, protein database; PHD, peroxidase homology domain; ROS, reactive oxygen species; TK, tyrosine kinase; TLR, toll-like receptor; TPO, thyroperoxidase; TRX, thioredoxin

Introduction

The concept of oxidative stress has been widely embraced as a major factor in disease pathology and has fuelled a billion dollar industry based on antioxidant dietary supplements. However, clinical studies using antioxidant supplementation strategies have generally been unsuccessful in attenuating disease risk or progression, and antioxidant supplementation was in some cases found to even worsen pathological outcomes (Ghezzi et al., 2017). This lack of success likely relates to the flawed concept of oxidative stress as a pharmacological target. First, oxidative stress can be brought about by a range of ROS (the commonly used acronym to define this group of reactive metabolites), which can originate from external sources (e.g. environmental pollution and metabolism of xenobiotics) or be generated endogenously by various enzymatic systems, in some cases in a regulated and deliberate fashion to serve important biological functions [e.g. by activation of NADPH oxidases (NOXs)]. Therefore, generic non-selective approaches that indiscriminately suppress ROS may not have the desired outcome. A second flaw with such generic antioxidant approaches is the fact that ROS represent a diverse group of reactive metabolites that each have unique (bio)chemical properties, and it is often unclear to what extent antioxidant supplements counter the action of individual ROS species. To clarify this, it is helpful to distinguish primary from secondary ROS, with primary ROS representing the initial products of (enzymatic) O₂ reduction [i.e. superoxide anion $(\dot{O_2})$ and hydrogen peroxide $(\mathbf{H_2O_2})$ and secondary comprising reactive metabolites formed ROS by subsequent reactions of these primary ROS [e.g. with NO to form peroxynitrite (ONOO⁻), with transition metals or metalloenzymes to form hydroxyl radical (OH) or hypohalous acids, or with other biomolecules to form, for example, lipid peroxides]. The biological literature on oxidative stress has tended to focus primarily on these secondary ROS as being responsible for pathology associated with oxidative stress, whereas dysregulated production of primary ROS (O_2^{-}, H_2O_2) might be equally or even more important.

With respect to the production of primary ROS in biological systems, their main cellular source include the family of NOXs, and ROS production is often considered the sole function of NOX enzymes to mediate their biological functions (Lambeth, 2004; Bedard and Krause, 2007). These functions rely on the production of cytotoxic secondary ROS (as a host defence mechanism against infection) and also on primary ROS (mostly H₂O₂) that can control protein function via reversible oxidation of susceptible cysteine or methionine residues in a process known as redox signalling (Janssen-Heininger et al., 2008; Holmstrom and Finkel, 2014). Since the discovery of various NOX homologues about two decades ago, it has become apparent that several disease conditions are characterized by inappropriate expression or activation of NOXs. From this perspective, rather than attempting to prevent the adverse biochemistry of secondary ROS using generic approaches of antioxidants or radical scavengers, pharmacological targeting of specific NOX enzymes or other cellular sources of ROS might be more fruitful. The biology and pathology of NOX enzymes

have been summarized in several excellent recent reviews (Lambeth, 2004; Bedard and Krause, 2007; Lassegue *et al.*, 2012; Bernard *et al.*, 2014), and a number of efforts over the past decade have attempted to develop isoform-selective inhibitors of NOX family enzymes. Among these, the dual oxidases (DUOX1 and DUOX2) have been relatively ignored in such efforts, although emerging findings indicate their potential involvement in disease pathology. Therefore, this review will focus on recent advances with respect to the biology and pathology of DUOX enzymes and will discuss molecular features that may inform approaches for their selective pharmacological targeting.

Discovery and tissue expression of DUOX enzymes

The dual oxidases DUOX1 and DUOX2 are isoforms of the long-known phagocyte (now known as NOX2), but do not require any protein cofactors for activation. which is primarilv dictated by the presence of calcium-regulated EF-hand domains (a feature also shared with NOX5). In addition, the DUOX enzymes also contain a unique extracellular NH₂-terminal domain with high homology to haem peroxidases, which has earned them the name 'dual oxidase', even though the function of this peroxidase homology domain (PHD) is still somewhat unclear and may be unrelated to catalytic peroxidase activity (Meitzler and Ortiz de Montellano, 2009). Both DUOX genes share a bidirectional promoter with their corresponding DUOX maturation factors (DUOXAs) and are located in a head-to-head fashion in tandem on the long arm of chromosome 15 (De Deken et al., 2014). The DUOXAs are critical for full maturation of the DUOX proteins and coordinate their location at the plasma membrane, although immature DUOX proteins within the endoplasmic reticulum (ER) also possess catalytic activity (Morand et al., 2004; Ameziane-El-Hassani et al., 2005; Grasberger and Refetoff, 2006). Transcriptional modes of regulation of DUOX1/DUOX2 and their corresponding maturation factors are still incompletely characterized (Christophe-Hobertus and Christophe, 2010; Xu et al., 2012).

The DUOX enzymes were first identified in human and porcine thyroid tissues and were originally described as p138^{Tox} or ThOX1 and ThOX2 (Dupuy et al., 1999; De Deken et al., 2000) and were later renamed as DUOX1 and DUOX2 based on the presence of a PHD domain (Edens et al., 2001). DUOX1 and DUOX2 are also expressed in various other tissues, with significant expression of DUOX1 mRNA in lung, placenta, testis, prostate, pancreas and heart and expression of DUOX2 mRNA primarily in the colon and also in lung, kidney, liver, pancreas, prostate and testis (Edens et al., 2001). A more detailed tissue distribution of human DUOX1 and DUOX2 is illustrated in Figure 1, based on extracted RNAseq data from the genotype-tissue expression project from the Broad Institute of MIT and Harvard (www.gtexportal.org). In the thyroid, DUOX is critical for H₂O₂ production to support oxidative iodination chemistry by thyroperoxidase (TPO) to generate thyroid hormone. This function appears to be restricted primarily to DUOX2 based on identification of a number of missense mutations





Figure 1

Tissue distribution of mammalian DUOX enzymes. RNAseq data were extracted from public data deposited by the Broad Institute for the Gene Tissue Expression (GTEx v.7) project (www.gtexportal.org). EBV, Epstein–Barr virus; TPM, Transcripts Per Kilobase Million mapped reads.



in DUOX2 that result in diminished function and hypothyroidism (De Deken et al., 2014). DUOX2 is also the main isoform within the gastrointestinal (GI) tract and is expressed most prominently within the colon epithelium (El Hassani et al., 2005) at the tip of intestinal villi (Sommer and Backhed, 2015) and within rectal glands (Geiszt et al., 2003). In situ hybridization analysis of respiratory tissues has shown the presence of both DUOX1 and DUOX2 mRNA, with DUOX1 mostly expressed in the tracheal and bronchial epithelium and DUOX2 within salivary glands (Geiszt et al., 2003). Subsequent studies indicate that DUOX protein is primarily present at the apical epithelial surface in major airways (Forteza et al., 2005) and also in the alveolar epithelium, primarily in type II cells (Fischer et al., 2007). Cell-specific expression of DUOX1 in other tissues is less well characterized, but several reports have highlighted the presence of DUOX1 in epidermal keratinocytes (Hirakawa et al., 2011), urothelial cells (Donko et al., 2010) and in non-epithelial cell types such as T-cells (Kwon et al., 2010), alveolar macrophages (Rada et al., 2014b) and innate lymphoid cells (Habibovic et al., 2016).

Host defence properties of DUOX in non-mammalian organisms

Homologues of DUOX are found in almost all multicellular organisms, and DUOX enzymes therefore likely have evolved to serve fundamental functional roles, such as host defence, cell differentiation and development (Kawahara et al., 2007). Early studies in Caenorhabditis elegans indicated the presence of Ce-Duox1 (also known as BLI-3) in the hypodermis, which was found to support oxidative cross-linking of tyrosine residues to promote stabilization of the cuticular extracellular matrix (Edens et al., 2001). Similar functions for Duox in extracellular tyrosine crosslinking were also described in Drosophila melanogaster or in other arthropods, to stabilize wing cuticle structures or enhance defence against invading pathogens (Anh et al., 2011; Yang et al., 2014). Although such tyrosine crosslinking was originally attributed to its PHD domain, it also requires the involvement of a distinct haem peroxidase (Kumar et al., 2010; Yang et al., 2014; Hurd et al., 2015). More recent studies also indicate alternative functions for Ce-Duox1/BLI-3 (the single functional NOX in C. elegans) in intestinal host defence, which are related to its ability to activate intracellular signalling pathways involving p38 MAPK signalling and the Nrf (NF-E2 related factor) orthologue SKN-1, thereby augmenting resistance to invading pathogens (Hoeven et al., 2011). Similar intestinal host defence functions were also described for dDUOX, one of the two NOX homologues in D. melanogaster (Ha et al., 2005; Ha et al., 2009; Xiao et al., 2017), and Duox in zebrafish (Flores et al., 2010). Furthermore, studies in D. melanogaster have revealed both positive and negative regulatory mechanisms to control Duox expression or activation, which likely serve to assure its adequate response to pathogenic bacteria while tolerating commensal bacteria (Kim and Lee, 2014; Xiao et al., 2017).

Mammalian DUOX in the gastrointestinal tract

Similar host defence functions of DUOX were also proposed in mammalian systems (Geiszt et al., 2003), although the situation is more complex because of the presence of two distinct functional DUOX isoforms. While the two DUOX genes are highly homologous (>85%), they possess distinct differences with respect to their gene regulation (Harper et al., 2005; Linderholm et al., 2010; Raad et al., 2013) and activation mechanisms (Rigutto et al., 2009). DUOX2 expression within the GI tract is sustained by the intestinal biota, although it is not affected by commensal bacteria (Sommer and Backhed, 2015). The precise mechanisms of DUOX2 activation by pathogenic bacteria are not known but are thought to involve toll-like receptors (TLRs), intracellular NOD2 receptors and MAPK/NF-kB pathways (Lipinski et al., 2009; Sommer and Backhed, 2015). Intestinal DUOX2 is enhanced in patients with Crohn's disease and ulcerative colitis (Aviello and Knaus, 2017), and a functional role for DUOX2 in intestinal homeostasis is implicated by several reports linking inactivating DUOX2 mutations with Crohn's disease (Levine et al., 2016) or very early onset inflammatory bowel disease (Haves et al., 2015; Parlato et al., 2017). Experimental studies in mice with functional DUOX2 deficiency showed increased gastric colonization after infection with Helicobacter felis and intestinal alterations indicative of mucosal dysbiosis (Grasberger et al., 2015). In contrast to DUOX2, DUOX1 is minimally expressed in the GI tract, although DUOX1 has been detected in the stomach lining and in some gastric and colorectal epithelial cell lines (Aviello and Knaus, 2017), and virtually nothing is known regarding its potential functional role in GI biology or pathology. Although current evidence supports a functional role for DUOX2 in antimicrobial responses and in the maintenance of intestinal microbiobial homeostasis, no direct evidence exists to date to suggest that DUOX2 contributes to the pathology of inflammatory bowel disease.

Host defence functions of DUOX in the respiratory tract

Antimicrobial/antiviral host defence

Both DUOX1 and DUOX2 are expressed in the respiratory epithelium, DUOX1 being the main isoform responsible for extracellular H₂O₂ production in response to exogenous stimuli such as ATP (Forteza et al., 2005), histamine (Rada et al., 2014a) and bacterial stimuli such as LPS or flagellin (Koff et al., 2008; Boots et al., 2009; Rada and Leto, 2010). In apparent contrast, studies with differentiated airway epithelial cells indicate a prominent role for DUOX2 in basal H₂O₂ production (Gattas et al., 2009; Linderholm et al., 2010). Moskwa et al. (2007) were the first to report a role for DUOX in mammalian airway epithelial antimicrobial activity, which was attributed to DUOX2-dependent extracellular H₂O₂ production. In agreement with these findings, epithelial exposure to bacterial flagellin was found to promote interactions between TLR5 and DUOX2 to stimulate ROS production and innate immune responses (such as IL-8 and MUC5AC production) (Joo et al.,

2012). Although bacterial triggers can also activate DUOX1 (see above), studies in mice have so far failed to identify a role for DUOX1 in airway production of inflammatory cytokines or neutrophil recruitment in response to bacterial LPS (Chang *et al.*, 2015; Hristova *et al.*, 2016).

The potential importance of DUOX2 in airway antiviral responses was initially suggested by findings that DUOX2 and its maturation factor DUOXA2 are both strongly upregulated by viral infection and by **types I** (α and β) and II (y) IFNs and Th1 (type 1) cytokines (Harper *et al.*, 2005; Fink et al., 2013; Strengert et al., 2014), although viral infection can in some cases also induce DUOX1 (Grandvaux et al., 2015). DUOX2-mediated antiviral responses were found to be mediated by the induction of retinoic acidinducible gene 1 and melanoma differentiation-associated protein 5 and activation of type 1 IFN responses (Fink et al., 2013; Kim et al., 2015), which in conjunction with type 1 cytokines (**TNF-** α and **IL-1** β) induce DUOX2 to subsequently participate in antiviral pathways via IFN-β and IFN-γ (Fink et al., 2013; Grandvaux et al., 2015). The functional importance of DUOX2 in antiviral responses was demonstrated in studies with airway epithelial cells in vitro (Fink et al., 2013; Strengert et al., 2014) and in studies of influenza A infection in mice, which was augmented by intranasal inoculation with DUOX2-targeted short hairpin RNA and attenuated after administration of DUOX2 DNA (Hong et al., 2016; Kim et al., 2017). Collectively, even though bacterial and viral stimuli can activate both DUOX1 and DUOX2, evidence so far primarily implicates DUOX2 in antibacterial or antiviral host defence, and no reports exist to date to suggest a role for DUOX1.

Role in epithelial wound responses

In addition to being endowed with elaborate defence mechanisms against rapidly replicating microorganisms (bacteria, viruses, etc.), vertebrates have also evolved defence mechanisms against physical trauma or epithelial injury caused by invasion of helminths or other metazoan parasites. Parasites do not complete their life cycle within the host, and activation of cytotoxic (type 1) defence mechanisms to kill these organisms would be ineffective and too dangerous to the host. Instead, host defence against these pathogens involves type 2 immune response pathways that have evolved to promote expulsion by, for example, mucus production as well as activation of regenerative pathways to repair breaches in epithelial barrier integrity, thereby enhancing tolerance to parasite infection (Gause et al., 2013). Among the first reports addressing a host defence function of airway epithelial DUOX1 are findings highlighting its role in controlling the expression of the mucin gene MUC5AC in response to various triggers (Shao and Nadel, 2005; Li et al., 2013; Habibovic et al., 2016), thus indicating a role for DUOX1 in promoting mucociliary clearance. Moreover, studies with cultured airway epithelial cells also demonstrated a contribution of DUOX1 to epithelial wound responses to physical or chemical injury, by promoting intrinsic cell dynamics (Wesley et al., 2007; Hristova et al., 2014) and expression of various wound response genes such as MMP-9 and IL-8 (CXCL8) (Koff et al., 2008; Sham et al., 2013). Similar DUOX1mediated wound responses were also observed in an in vivo model of lung epithelial injury in mice (Gorissen et al., 2013), and analogous DUOX-mediated epidermal wound



healing was also demonstrated in zebrafish-based models of tail fin injury (Niethammer *et al.*, 2009; Razzell *et al.*, 2013), thus highlighting a highly conserved role for DUOX1 in epithelial wound responses (van der Vliet and Janssen-Heininger, 2014). The mechanisms by which DUOX1 is activated in these contexts are not fully understood but likely involve the participation of damage-associated molecular patterns such as the purine metabolite ATP, which activates epithelial DUOX1 through stimulation of **purine nucleotide P2Y receptors** at the epithelial surface (Wesley *et al.*, 2007; Hristova *et al.*, 2016).

Production of epithelial alarmins

Cytokines of the IL-1 family are central mediators of innate immunity, and some of these (e.g. the interleukins IL-1 α and IL-33) are expressed constitutively within epithelial cells or other structural cell types within their nuclei or cytoplasm, allowing them to be released rapidly upon cell stimulation or injury, to serve as 'alarmins' by acting as extracellular cytokines that alert the immune system to induce appropriate responses (Cayrol and Girard, 2014). With respect to IL-33, a major epithelial alarmin, its release causes the induction of type 2 cytokines (e.g. IL-5 and IL-13) and growth factors (e.g. **amphiregulin** or **TGF**β) within various effector cells, including locally resident type 2 innate lymphoid cells (ILC2s), and such IL-33-mediated activation of ILC2mediated type 2 responses is critical in host defence against parasitic infection (Molofsky et al., 2015). Recent studies highlighted the importance of Ca²⁺-dependent signalling pathways induced by mechanical triggers or danger signals such as ATP in epithelial secretion of IL-33, and our group recently demonstrated a critical role for activation of DUOX1 (but not DUOX2) in IL-33 secretion by non-classical pathways (Hristova et al., 2016). These findings would imply a specific host defence role for DUOX1 against infections by hookworms or other parasites, since lung epithelial and vascular injury due to worm penetration represent important features of hookworm infection (Bouchery et al., 2015), but such a role for DUOX1 has not yet been demonstrated. Consistent with such a role for DUOX1 in type 2 immunity are findings that airway epithelial DUOX1 expression is enhanced in the presence of type 2 cytokines such as IL-13 (Harper et al., 2005; Hristova et al., 2016), thereby enhancing its functional role in the context of prolonged or repeated insults. Curiously, studies in thyrocytes and intestinal epithelial cells indicate that type 2 cytokines induce DUOX2 rather than DUOX1 (Raad et al., 2013) and may, therefore, suggest a similar role for DUOX2 in intestinal defence against hookworm infection (Monticelli et al., 2015).

DUOX in other epithelia and non-epithelial cell types

DUOX1 represents the predominant NOX isoform in human keratinocytes, the major epidermal cell type (>90%) and has been linked with Ca^{2+} -dependent keratinocyte differentiation (Choi *et al.*, 2014). DUOX1 may also be involved in innate cutaneous host defence to infectious triggers or in epidermal wound responses, based on findings in non-mammalian organisms (Niethammer *et al.*, 2009; Juarez



et al., 2011; van der Hoeven *et al.*, 2015), although DUOX1 in oral and skin epithelia does not appear to be essential for induction of defensins in response to *Acinetobacter baumannii*, a Gram-negative pathogen that threatens healthcare delivery systems (Feng *et al.*, 2014). DUOX1 is also prominently expressed in urothelial cells, with a potentially similar host defence function in the bladder (Donko *et al.*, 2010). Finally, evidence is emerging for the presence of DUOX1 in non-epithelial lineages, such as T and B lymphocytes (Singh *et al.*, 2005; Kwon *et al.*, 2010), macrophages (Rada *et al.*, 2014b) and innate lymphoid cells (Habibovic *et al.*, 2016), with it being involved in T-cell or B-cell receptor signalling and having potential roles in macrophage or ILC polarization, thus indicating broader host defence functions of DUOX1.

Specific roles for DUOX1 and DUOX2 in distinct innate immune response pathways?

Epithelial barriers in vertebrates are critical in providing adequate defence against common external challenges and form a critical sentinel function to alert the immune system to coordinate appropriate immune responses to these diverse challenges (Gallo and Hooper, 2012; Holtzman et al., 2014; Lambrecht and Hammad, 2017). The presence of both DUOX1 and DUOX2 within epithelial lineages, particularly at epithelial surfaces, ideally positions them to serve critical roles in mucosal host defence and regulating appropriate immune responses. In contrast to non-vertebrates, which rely solely on innate immune responses that involve recognition of microorganisms by non-rearranging receptors and rapid response mechanisms in which their single functional DUOX gene may participate, vertebrate species also evolved with an adaptive immune system to coexist with innate immune pathways, allowing for greater variability in antigen recognition and development of memory, but also enhancing the potential for autoimmunity, allergy or allograft rejection (Janeway and Medzhitov, 2002; Hoffmann, 2003). Since vertebrate species typically contain two highly homologous DUOX genes and DUOXAs, likely as a result of gene duplication events during evolution of vertebrates from early deuterostome ancestors (Kawahara et al., 2007), we propose that DUOX1 and DUOX2 may have evolved to acquire unique roles in these specific arms of the innate immune response. Indeed, while DUOX2 appears to participate primarily in antimicrobial/antiviral responses associated with TLR activation and production of interferons and type 1 cytokines, DUOX1 is primarily involved in the activation of type 2 immune responses induced by epithelia-damaging events, such as parasite infection, protease allergens and toxins. (Figure 2). Observations of isoform-specific modes of regulation with respect to gene regulation and activation of DUOX1 and DUOX2 (Harper et al., 2005; Rigutto et al., 2009) are consistent with such unique roles in specific aspects of epithelial-derived host defence initiated by distinct receptor-mediated pathways (e.g. TLRs vs. P2Y receptors and proteinase-activated receptors). Coordinated activation of either response pathway typically serves to restore tissue homeostasis, but inappropriate activation may result in autoimmunity or metabolic disease or in allergic disease and fibrosis respectively (Figure 2). Because of the considerable cross-talk and communication between individual cell types involved in these immune responses (Rivera *et al.*, 2016), it is likely that DUOX1 and DUOX2 are both engaged in most cases and their relative contributions may differ depending on the type of pathogen or injury. In some cases, such DUOX-specific events may be antagonistic, as illustrated by the potential suppression of DUOX1 by viral infection or IFN (Grandvaux *et al.*, 2015), but may also be cooperative as highlighted by a recent study indicating that DUOX2 can mediate pannexin-mediated ATP release in response to hypotonic stress (Krick *et al.*, 2016), thereby also resulting in activation of DUOX1.

Mechanisms of DUOX-mediated host defence: from oxidant-mediated killing to redox-dependent cell signalling

Analogous to the proposed antimicrobial functions of phagocyte NOX (NOX2) in conjunction with haem peroxidases such as myeloperoxidase (MPO) in neutrophils (Winterbourn et al., 2016), DUOX1/DUOX2 are thought to exert their host defence function by generating H₂O₂ and inducing lactoperoxidase (LPO)-catalysed oxidation of thiocyanate (SCN⁻) or iodide (I⁻) within the airway lumen, to form secondary oxidants such as hypothiocyanous acid (HOSCH) and hypoidous acid (HOI), which serve to kill or repel bacteria (De Deken et al., 2014) and minimize virus infectivity (Grandvaux et al., 2015). In addition, such oxidative host defence mechanisms may also be augmented by NOX-dependent proton secretion, which compensates for charge transfer and local pH changes due to NOX activation and leads to NOX2-dependent acidification of phagosomes in phagocytic cells or DUOX1-dependent acidification of the airway lumen (Fischer, 2009; Segal, 2016), in both cases enhancing the activity of locally secreted peroxidases to generate antimicrobial oxidants (Winterbourn et al., 2016).

In addition to these extracellular oxidative host defence mechanisms, DUOX-derived H_2O_2 is also capable of inducing cellular responses by autocrine or paracrine mechanisms via redox-dependent regulation of cell signalling pathways, by reversible oxidation of functional cysteine residues. A proteomic screen revealed that DUOX1 activation induces cysteine oxidation within a number of cellular targets, including cytoskeletal proteins, oxidoreductase enzymes and proteins involved in cell metabolism (Hristova et al., 2014). Reversible cysteine oxidation also has a major impact on tyrosine kinase (TK) signalling, either by inactivation of protein tyrosine phosphatases or by activation of protein TKs (Heppner et al., 2016). Indeed, DUOX1-dependent airway epithelial wound responses as well as IL-33 secretion were found to be mediated by activation of the non-receptor TK Src and the EGF receptor (EGFR), in part by direct oxidation of cysteine residues within these kinases (Sham et al., 2013; Heppner et al., 2016; Hristova et al., 2016). Such DUOX1-dependent protein cysteine oxidation may involve a direct interaction of

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Figure 2

Schematic illustration of proposed roles of DUOX1 and DUOX2 in shaping innate type 2 and type 1 immune responses. DUOX2 is activated primarily by bacterial and viral triggers through TLR-mediated signalling and is associated with increased production of interferons and type 1 cytokines. In contrast, DUOX1 is activated primarily by non-microbial stimuli that induce tissue injury, involving activation of type 2 purine receptors (P2YR) or protease-activated receptors (PAR), leading to activation of type 2 alarmins and type 2 cytokine production. Effector cells such as neutrophils and macrophages are activated differently (e.g. N1 vs. N2 and M1 vs. M2 polarization), leading to a tailored response for efficient defence against these pathogens and restoration of homeostasis (grey arrows). Harmful inflammation due to overstimulation of either DUOX2- or DUOX1mediated innate immune pathways may result in autoimmune disease or allergic disorders respectively (red arrows). DAMPs, damage-associated molecular patterns; DC, dendritic cell; ILC1/2, type 1/2 innate lymphoid cell; NK cells, natural killer cells.

DUOX1 with its target protein, in the case of, for example, Src (Sham *et al.*, 2013), but may also involve more indirect mechanisms, for example, secondary activation of other NOX enzymes (Heppner *et al.*, 2016). DUOX2-dependent antiviral responses have been linked with activation of NF- κ B (Joo *et al.*, 2012) and **ADAM17** sheddases (Yu *et al.*, 2011), factors that are both subject to redox regulation (Janssen-Heininger *et al.*, 2008; Sham *et al.*, 2013), although it is unclear whether these enzymes are direct targets of DUOX2-derived H₂O₂.

One important area of controversy with respect to DUOX-mediated redox signalling and host defence relates to its subcellular localization. For example, while DUOX1 is thought to be present primarily at the airway epithelial surface, DUOX-dependent extracellular H_2O_2 production is marginal in murine airway epithelial cells compared with, for example, human epithelia (Moskwa *et al.*, 2007; Hristova *et al.*, 2014), which would suggest that DUOX does not contribute significantly to mucosal LPO-dependent antimicrobial killing mechanisms in mice.

However, comparative analysis of redox signalling in human and murine epithelial cells showed qualitatively and quantitatively similar protein cysteine oxidation in response to activation of DUOX1, which was largely insensitive to extracellular catalase (Wesley et al., 2007; Heppner et al., 2016). This suggests that DUOX1-dependent redox signalling originates primarily from activation of intracellularly localized DUOX1 (e.g. at ER membranes) or occurs after DUOX1 internalization in redox signalling complexes (redoxosomes). Another issue with respect to the proposed involvement of DUOX or other NOX isozymes in cellular redox signalling is the fact that NOX-derived ROS are generated extracellularly or within phagosomes/endosomes and are thus segregated from their putative cytoplasmic redox-sensitive targets by a lipid membrane. The recent discovery of **aquaporins** as selective channels for H_2O_2 resolves this issue, and aquaporin-dependent transmembrane H₂O₂ transfer likely helps confine the oxidative potential of H₂O₂ to assure specificity in redox signalling (Bertolotti et al., 2016; Thiagarajah et al., 2017).



DUOX in disease pathology

Up until recently, a function for DUOX1/DUOX2 in pathology has largely remained elusive, with the exception of somatic mutations within DUOX2 that have been associated with hypothyroidism (van der Vliet, 2011; Bernard *et al.*, 2014). Recent studies over the past few years have, however, highlighted important contributions of DUOX1/DUOX2 to chronic diseases such as cancer and allergic disease and provide a strong rationale for development of selective therapeutic strategies to inhibit these enzymes. The next sections will summarize the current evidence implicating DUOX1 and DUOX2 in disease pathology.

Acute inflammation/infection

Based on the proposed roles of DUOX1/DUOX2 in mucosal host defence by providing extracellular H₂O₂ to support LPO-mediated production of HOSCN, it has been speculated that genetic diseases associated with increased lung injury and infection, such as cystic fibrosis, may be related to defects in this host defence system. Indeed, defects in the cystic fibrosis transmembrane conductance regulator gene that cause cystic fibrosis have been associated with impaired transepithelial SCN⁻ transport, thus resulting in reduced DUOX-LPO-dependent mucosal host defence (Conner et al., 2007; Moskwa et al., 2007), although they do not appear to significantly affect DUOX1/DUOX2 expression (Pongnimitprasert et al., 2012; van der Vliet et al., unpubl. data). Conversely, minimal evidence exists to date to support a contribution of DUOX1/DUOX2 to acute lung injury or pneumonia, and studies in mouse model systems have not demonstrated a role for DUOX1/DUOX2 in LPS-induced innate cytokine responses or neutrophilia (Chang et al., 2015; Hristova et al., 2016). However, one recent study indicated a role for DUOX2 in alveolar type II cells in mediating acute lung injury in response to hyperoxia (Kim et al., 2014).

Cancer

NOX enzymes are often dysregulated in various cancers (Little et al., 2017). Overexpression of DUOX2/DUOXA2 during ulcerative colitis is thought to be responsible for oxidative DNA damage as a predisposing factor for development of colon cancer (MacFie et al., 2014). Indeed, DUOX2 is often overexpressed in cancers of the alimentary tract, including colorectal cancers, and may contribute to cancer progression (Wu et al., 2013; Qi et al., 2016), suggesting that pharmacological inhibitors with selectivity towards DUOX2 may have clinical utility in anticancer treatment (Lu et al., 2017). Recent studies also indicated a potential contribution of DUOX1 in promoting oxidative DNA damage and genomic instability in the thyroid in response to ionizing radiation, as a potentially important contributing feature to thyroid cancer (Ameziane-El-Hassani et al., 2015). In apparent contrast, several other reports indicate that DUOX1 is frequently suppressed in epithelial cancers by epigenetic mechanisms and may be associated with poor prognosis, as was reviewed recently (Little et al., 2016; 2017).

Allergic airway disease

Based on findings linking DUOX1 with type 2 immune responses and the ability of type 2 cytokines to induce DUOX1, it has been speculated that DUOX1 is commonly elevated in allergic disease (Figure 2). Indeed, enhanced expression of DUOX1 and, to a lesser extent, DUOX2 has been observed in the nasal mucosa of patients with chronic sinusitis (Cho et al., 2013), and increases in DUOX1 mRNA and protein were also observed in cultured nasal or bronchial epithelial cells from subjects with allergic asthma (Hristova et al., 2016; Wan et al., 2016) and in animal models of allergic airway inflammation (Habibovic et al., 2016). Other studies also report increases in DUOX2 in fresh bronchial epithelial cells from patients with severe asthma (Voraphani et al., 2014) and in mice during allergic inflammation induced by cockroach allergens (Nadeem et al., 2015). The functional importance of DUOX2 was suggested in a model of house dust mite (HDM)-induced allergic rhinitis and allergic asthma, which indicated translocation of TLR2/TLR4 to the cell surface in response to HDM-derived β -glucans and LPS and TLR-dependent activation of DUOX2 as critical mediators for innate immune responses to HDM activation (Rvu et al., 2013). although the significance of these pathways for mucus hyperplasia and airway hyperresponsiveness, two clinically relevant features of allergic asthma, was not assessed. Studies using a genetic mouse model of DUOX deficiency, induced by deletion of both Duoxa genes, demonstrated the importance of DUOX in mucus metaplasia, airway hyperresponsiveness and neutrophilic inflammation in an ovalbumin-induced model of allergic inflammation (Chang et al., 2013), although these latter studies did not address the relative contribution of DUOX1 and DUOX2. Our group recently demonstrated a role for DUOX1 in HDMinduced allergic inflammation, using DUOX1-deficient mice and siRNA targeting approaches, which revealed the critical importance of DUOX1 in HDM-induced type 2 inflammatory responses, as well as mucus metaplasia, subepithelial remodelling and airway hyperresponsiveness to methacholine (Habibovic et al., 2016). Moreover, DUOX1 was found to mediate neutrophilic rather than eosinophilic inflammation in these studies, which may be particularly relevant for severe asthma endotypes that are typically dominated by neutrophilic inflammation and are resistant to current therapies (Svenningsen and Nair, 2017). More importantly, these clinically relevant aspects of allergic inflammation could be reversed by siRNA-mediated inhibition of DUOX1 after establishing allergic disease in this model (Habibovic et al., 2016), indicating the therapeutic potential of inhibiting DUOX1 in the context of allergic asthma. The involvement of DUOX1 in allergic airway inflammation and mucus hyperplasia was linked to increased activation of Src and EGFR within the airway (Habibovic et al., 2016). Both TKs have been recognized as important mediators of asthma pathology (Vallath et al., 2014), but currently available inhibitors of these kinases have not been used in the treatment of asthma due to undesirable side effects. Selective inhibition of DUOX1 might thus be an attractive alternative strategy for treating severe allergic asthma. It should be noted that other NOX isoforms expressed in airway epithelial cells (e.g. NOX4) may also contribute to asthma pathology (van der Vliet, 2011; Wan et al., 2016).

Skin pathologies

Exaggerated immune responses to allergic stimuli are typically due to atopy, characterized by high IgE that can impact on allergic disease at different anatomical sites. The natural history of atopic diseases often involves initial manifestation of atopic dermatitis, which is then followed by food allergy, allergic rhinitis and/or allergic asthma, in a process referred to as the atopic march (Han et al., 2017). Since DUOX1 is present in epidermal keratinocytes and induced by type 2 cytokines (Hirakawa et al., 2011), it may also play a role in the development of atopic dermatitis with similar involvement of type 2 inflammation by epithelial-derived IL-33 and ILC2s (Savinko et al., 2012; Salimi et al., 2013), although this has not yet been tested directly. Interestingly, some proinflammatory responses to HDM-mediated stimulation of keratinocytes, as a model of atopic dermatitis, were linked to DUOX2 rather than DUOX1 (Ko et al., 2015). DUOX1 has been reported to be enhanced in dermal tissues from patients with psoriasis and lichen planus, autoimmune-type disorders associated with abnormal growth in the epidermal layer of the skin (Candel et al., 2014). These skin disorders are typically associated with enhanced Th1 and Th17 responses and with pro-inflammatory cytokines such as TNF- α . Paradoxically, several studies have shown that anti-TNF treatment can also lead to new-onset psoriasis or lichen planus, and studies in zebrafish keratinocytes demonstrated that silencing of TNF-α or its receptor **TNFR2** resulted in induction of DUOX and DUOX-dependent pro-inflammatory cytokine production, suggesting a role for DUOX in psoriasis development (Candel et al., 2014).

Remaining questions

While our understanding of the biology of DUOX enzymes has grown dramatically, controversies still remain with respect to the individual contributions of DUOX1 and DUOX2. One issue with findings implicating DUOX2 is that they are largely based on mouse models with genetic DUOX2 deficiency, which have severe congenital hypothyroidism and require continuous L-thyroxine treatment for normal development. Such approaches might alter the metabolome or microbiome in these animals and thus affect outcomes in models of complex disease. The involvement of specific DUOX isoforms has also been difficult to assess due to the lack of isoform-specific antibodies and the fact that both isoforms are often expressed simultaneously. Although DUOX1 and DUOX2 may be associated with distinct immune pathways (Figure 2), both isoforms may participate in complex chronic diseases such as allergic asthma. Asthma is not a singular disease but is composed of different endotypes that may be related to diversity in genetic background, exposure history and the presence of bacterial or viral infections, which could have variable impacts on DUOX2. Moreover, intricate communications exist between different cells of the immune system, including negative regulatory mechanisms to ensure appropriate immune responses (Rivera et al., 2016). Disruptions in such regulatory mechanisms in association with Western lifestyles are thought to favour pathologies characterized by exaggerated type 2 immune responses (de Kouchkovsky et al., 2017; Lambrecht and Hammad, 2017). Emerging evidence indicating the presence of DUOX



in various immune cells types would further highlight complex roles for DUOX in pathologies associated with chronic inflammation or dysregulated immune processes. Nevertheless, the growing evidence implicating DUOX in disease pathology, particularly in the context of allergic diseases that are rapidly increasing in Westernized societies, provides a strong rationale for the development of DUOXselective inhibitors that could be used in their therapeutic management.

The search for NOX-selective inhibitors

Current status of development of NOX inhibitors

The growing appreciation of specific role(s) of individual NOX enzymes in various biological and pathological contexts has spurred various efforts to develop isoform-specific inhibitors of NOX enzymes (Drummond et al., 2011; Gatto et al., 2013; Altenhofer et al., 2015; Cifuentes-Pagano et al., 2015; Teixeira et al., 2017). Unfortunately, the relative lack of high-resolution structural information of NOX enzymes (either in active or inactive states) has hampered rational structure-based design of isoform-selective inhibitors, and the development of NOX-selective inhibitors has relied mostly on high-throughput screens of molecular libraries. While such approaches have had some success, the molecular mechanisms of actions are often unknown. Many putative NOX inhibitors appear to act by interfering with the binding of NADPH or flavin adenine dinucleotide (FAD) to the enzyme or their electron transfer properties, but given the widespread use of these co-factors in many flavoenzymes, it is difficult to achieve selectivity for NOX. Indeed, diphenylene iodonium (DPI), one of the earliest described NOX inhibitors, was demonstrated to interact with flavins by forming covalent adducts (O'Donnell et al., 1993) and thus inhibits all NOX isoforms with similar potency (Altenhofer et al., 2015). A recent evaluation of 36 analogues of DPI identified some nitro-substituted analogues with some apparent selectivity towards NOX5 and DUOX2 compared with other NOX isoforms (Lu et al., 2017), suggesting that it may be feasible to develop isoform-selective inhibitors based on flavin-targeted compounds such as DPI. Continued structural insights based on new crystallographic data (Magnani et al., 2017) may help guide such efforts. Several other NOX inhibitors with some selectivity have been identified from high-throughput screens of molecular libraries on cell models in which different NOX enzymes were ectopically expressed (Gianni et al., 2010; Altenhofer et al., 2015; Hirano et al., 2015; Joo et al., 2016), and two recently developed NOX2-selective inhibitors were found to act by competitive inhibition of NADPH binding based on detailed mechanistic studies and molecular docking studies (Hirano et al., 2015; Joo et al., 2016). However, inhibitory actions of putative NOX inhibitors may also involve indirect mechanisms rather than selective targeting of the NOX protein, and technical issues with the assay methodology to assess NOX activity have in some cases led to false positives (Maghzal et al., 2012; Seredenina et al., 2015). Therefore, reliable identification of NOX-selective inhibitors requires the use of multiple assay methodologies to assess



NOX activity (e.g. O_2 consumption, NADPH utilization and analysis of ROS products using several probes). Among the various efforts to date to develop NOX-selective inhibitors, one such effort launched by Genkyotex based on screening 136 000 compounds, including various pyrazolopyridine diones, has yielded GKT831 as an orally bioavailable NOX1/NOX4-selective inhibitor which represents the only NOX-selective inhibitor to date that has progressed into clinical trials. Although a recently completed phase 2 study in patients with type 2 diabetes with diabetic nephropathy unfortunately did not reach its primary clinical endpoint (Labiotech.eu. 2015-09-10), other clinical studies have been initiated to address efficacy in primary biliary cholangitis (Labiotech.eu. 2017-05-03).

Do current NOX inhibitors also inhibit DUOX?

Common to almost all of the drug screening efforts so far is that they did typically not address efficacy against DUOX1 or DUOX2 (Lu et al., 2017). This is likely due to the absence (until recently) of experimental data demonstrating a role for DUOX1/DUOX2 in disease and perhaps also related to concerns that the development of DUOX2-selective inhibitors would be undesirable because of their negative impact on thyroid hormone synthesis. However, most small molecule NOX inhibitors developed to date have structural similarities with NADPH or FAD and would thus be expected to also inhibit DUOX enzymes. Indeed, the classic NOX inhibitor DPI was also found to potently inhibit DUOX (Wesley et al., 2007; Lu et al., 2017), and the recently developed NOX1/NOX4-selective inhibitor GKT831 was also reported to inhibit DUOX (Strengert et al., 2014). We recently surveyed several putative NOX inhibitors for their ability to inhibit DUOX1, and found that apocynin and VAS2870, two putative NOX inhibitors with poorly defined inhibitory mechanisms (Altenhofer et al., 2015), were rather ineffective and displayed low potency compared with DPI. In contrast, the phenothiazine compound ML171 (2-acetyl-phenothiazine), originally identified in a drug screen as a NOX inhibitor with relative selectivity against NOX1 (Gianni et al., 2010), displayed strong inhibition against ATP-mediated H₂O₂ production as well as DUOX1-dependent IL-33 secretion (Habibovic et al., 2016). Phenothiazines represent a family of heterocyclic compounds that are recognized as a class of 'privileged structures' with versatile binding properties that exhibit a number of desirable drug-like characteristics and have had a long history of drug development with various indications, as antimalarials (late 19th century), anthelminthics and antibiotics (mid-20th century), antihistaminics (1940s), and sedatives and antipsychotics (1950s) (Ohlow and Moosmann, 2011). Their mechanisms of action are highly diverse and include antihistaminergic, antidopaminergic and antiserotonergic effects, as well as more recently identified effects on dynamin and clathrinendocytotic pathways (Daniel et al., 2015). Recent studies also indicated that phenothiazine-based compounds can exert direct inhibitory actions against NOX2 and other NOX isoforms, with some isoform specificity (Seredenina et al., 2015). One important consideration is that phenothiazines in which their B ring nitrogen atom is unsubstituted, such as the putative NOX1 inhibitor ML171 (Figure 3), also possess strong radical-trapping properties and thus have more generic antioxidant properties, and N-unsubstituted phenothiazines such as ML171 were found to be inactive as direct inhibitors of NOX1-NOX5 (Seredenina et al., 2015). In contrast, N-substituted phenothiazine compounds such as the antipsychotic drug chlorpromazine (CPZ) lack such radical-scavenging properties (Figure 3) and may act as direct NOX inhibitors. Indeed, our studies indicate that CPZ and other N-unsubstituted phenothiazines can effectively inhibit DUOX1-dependent H₂O₂ production, with potency comparable with ML171 (van der Vliet et al., unpubl. data). Together with observations of NOX-selective actions of other phenothiazines (Gianni et al., 2010; Seredenina et al., 2015), these findings suggest opportunities for development of DUOX1selective inhibitors based on phenothiazine scaffolds. In fact, previous uses of phenothiazine-based compounds such as CPZ or structurally similar compounds for the treatment of allergic disease (Baum et al., 1957) might have been related in part to their ability to inhibit DUOX1.

Towards development of DUOX-selective inhibitors

Since the DUOX enzymes contain several structural features that are distinct from other NOX isozymes, the successful development of DUOX1-selective inhibitors most likely relies on targeting unique structural determinants of DUOX1 that are absent or variant in the other isoforms. Unfortunately, minimal structural information of NOX enzymes is available from crystallographic data, which only exist for the NADPH-binding domain of human NOX2 [protein database (PDB) ID: 3A1F] and the transmembrane domain (PDB ID: 500T) and dehydrogenase domain (PDB ID: 500X) of NOX5 from Cylindrospermum stagnale (Magnani et al., 2017), and can be used to gain structural insights into other NOX isoforms by homology modelling. No structural data exist for their more unique PDH domains and their EF-hand-binding domain regions. However, several recent studies have highlighted potentially unique molecular features within these and other domains within DUOX that could be



Figure 3

Structures of 2-acetyl-phenothiazine (ML171) and CPZ and their reactivity with ROS by radical-trapping mechanisms.

exploited for rationalized development of targeted inhibitors (Figure 4), which will be discussed in the next sections.

PHD domains

The N-terminal extracellular PHDs within the DUOX enzymes are so named because of their homology with mammalian haem peroxidases, but the mammalian DUOXs lack various residues within these PHD domains that are critical for haem binding and peroxidase activity, and their function most likely relates to their critical role in DUOX maturation, as these domains contain several N-glycosylation sites (Morand et al., 2004; De Deken et al., 2014). Alternatively, the PHD domains may also be crucial for appropriate interactions of DUOX with their partnering haem peroxidases, such as with TPO within the thyroid (Fortunato et al., 2010). The functional importance of the DUOX2 PHD is illustrated by the fact that several mutations within this domain are associated with hypothyroidism (Grasberger, 2010). Another critical area where DUOX PHD domains differ from mammalian peroxidases concerns their cysteine residues. Whereas mammalian haem peroxidases contain a conserved set of structurally important disulfide bonds (six in MPO and seven in LPO), human DUOX enzymes only contain six cysteine residues within their PHD, and sequence alignment indicates that none of them correspond to conserved cysteines within mammalian peroxidases that are important for structural stability (Meitzler et al., 2013). Five of these cysteines

 $(Cys^{118}, Cys^{345}, Cys^{364}, Cys^{564} and Cys^{579} in DUOX1; Cys^{124}, Cys^{351}, Cys^{370}, Cys^{568} and Cys^{582} in DUOX2) are con$ served between both isoforms and also across organisms (Meitzler et al., 2013), and mutation studies indicated that four of these (Cys³⁵¹, Cys³⁷⁰, Cys⁵⁶⁸ and Cys⁵⁸² within DUOX2) are important for DUOX maturation and emergence from the ER (Morand et al., 2004). Homology modelling studies with bovine LPO suggested that these four cysteines are solvent exposed, and subsequent mutation studies suggested their involvement in intermolecular disulfide bonding with other DUOX monomers or with their DUOXAs (Meitzler et al., 2013). More recent studies indicated that Cys^{568} and Cys^{582} within the DUOX2 PHD domain engage in intermolecular disulfide linking with DUOXA2 and that another conserved PHD cysteine (Cys¹²⁴) likely engages in intramolecular cross-linking with Cys¹¹⁶² located in one of the extracellular loops in the transmembrane region of DUOX2 (Carre et al., 2015), which might also apply to homologous cysteines in DUOX1 (Figure 4). A potential function for the other two PHD cysteines (Cys³⁵¹ and Cys³⁷⁰) was suggested by studies demonstrating that overexpression of TPO enhanced DUOX2mediated H₂O₂ production in HEK293 cells, which was not observed with DUOX2 mutants lacking Cys³⁵¹ or Cys³⁷⁰ (Fortunato et al., 2010). These studies imply that DUOX2generated H₂O₂ inhibits DUOX2 activity in a negative feedback fashion, which was prevented by enhancing H₂O₂



Figure 4

Schematic illustration of DUOX1 protein and potentially unique features for potential drug targeting. Topographical model of the DUOX1 protein highlighting specific amino acid residues that are involved in regulating DUOX1 activity or interactions with other regulatory proteins, and may represent druggable targets. Details are clarified in the text. Note that many of these amino acids are also conserved in DUOX2.



metabolism by TPO. The importance of the corresponding cysteines in DUOX1 (Cys³⁴⁵ and Cys³⁶⁴) is not presently known, but based on their solvent exposure and homology modelling studies (Figure 5A), they likely have a similar function.

EF-hand domains

DUOX proteins do not require additional co-factors, and their activation relies primarily on their Ca²⁺-binding EFhand domains. A yeast two-hybrid screen of the EF-hand fragment of DUOX1 has identified the thioredoxin (TRX)-related protein EF-hand binding protein 1 (EFP1) as a potential partner for DUOX1 (Wang et al., 2005). EFP1, also known as TXNDC11, has shared reductase activities with other TRX-related proteins and has recently been implicated in ER-localized degradation of glycoproteins (Timms et al., 2016) and may thus be involved in the folding process of DUOX1. The cytoplasmic region (containing the EF-hand binding regions) of DUOX1 (aa618-aa1044) possesses a number of cysteine residues. some of which are also present in DUOX2 but others being isoform specific. While nothing is known with respect to the functional importance of these cysteines, their thiol-disulfide status may conceivably be regulated by TXDNC11 (which may apply particularly to the region between aa951 and aa988, which contains four cysteines in relative close proximity), to alter local protein structure and/or binding of regulatory factors such as protein kinases (see next paragraph). Intriguingly, a genome-wide screen in horses has identified associations of a single nucleotide polymorphism in the TXNDC11 gene with heaves, an equine recurrent airway obstruction in horses with asthma-like features (Schnider *et al.*, 2017), which might point to a role for TXNDC11 in regulating DUOX1 maturation or activation.

Other unique features of DUOX

Although very little is known regarding other posttranslational modifications in DUOX regulation, observations of divergent activation of DUOX1 and DUOX2 by different signalling pathways has spurred analysis of phosphorvlation sites in DUOX1 and DUOX2, which identified Ser⁹⁵⁵, Thr¹⁰⁰⁷ and Ser¹²¹⁷ within DUOX1 as direct phosphorylation targets, of which Ser⁹⁵⁵ (located adjacent to the EF-hand binding regions) was found to be critical for DUOX1 activation by PKA (Rigutto et al., 2009). Studies by Knaus and coworkers indicated that DUOX activation by Ca²⁺-activating triggers was associated with dissociation of NOX activator 1 (NOXA1, a homologue of p67phox or NCF2) from the DUOX protein (Pacquelet et al., 2008). Mutation and deletion studies indicated that NOXA1 interacts with the C-terminal region in DUOX1 to suppress basal oxidase activity, and this in part involves interactions of a PXXP motif (residues 1497-1500 in



Figure 5

Location of functionally relevant cysteines within NOX/DUOX. (A) SWISS model of DUOX1 PHD based on homology mapping with the crystal structure of LPO (PDB ID 3BXI), revealing the solvent exposure of C345 and C364, which are present in their reduced state in the mature enzyme. (B) Sequence alignment of amino acids adjacent to a conserved cysteine within the C-terminal region of csNOX5(C668), AtRBOHD(C890), HsNOX2(C537) and HsDUOX1(1520). (C) Visualization of C668 in proximity to FAD with the dehydrogenase domain of csNOX5 (PDB ID: 500X). The close proximity suggests that covalent cysteine modifications likely disrupt FAD binding or its electron transfer properties.

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DUOX1) with the Src homology 3 domain within NOXA1 (Pacquelet et al., 2008). The C-terminal region of DUOX1 also contains various cysteines that may be involved in regulating activity, and recent studies in Arabidopsis demonstrated the ability of NO to suppress activation of its NOX homologue AtRBOHD via S-nitrosylation at a single residue, Cys⁸⁹⁰, within the C-terminal cvsteine region (Yun *et al.*, 2011). Sequence alignment indicates that this cysteine is conserved in mammalian NOX2 and also in DUOX proteins (Cys¹⁵²⁰ in DUOX1) (Figure 5B), suggesting the potential general importance of such reversible cysteine modifications for mammalian NOXs. Mapping of this cysteine within the crystal structure of csNOX5 (PDB ID: 500X) indicates its close proximity to FAD (Figure 5C), which would suggest a potential general function of this Cys in NOX activity, perhaps by participating in electron transfer between NADPH and FAD. Intriguingly, a recent study implicates a homologous cysteine within NOX4, as well as an adjacent cysteine, in regulating electron transfer (Nisimoto et al., 2018).

Thiol-reactive compounds inhibit DUOX1

The previous sections highlight the presence of several cysteines within DUOX and other NOX enzymes that appear to be non-essential for catalytic activity but may be involved in regulating NOX/DUOX location or activity. Hence, pharmacological approaches that selectively target these cysteines may enable the development of useful and potentially isoform-specific inhibitors. Targeting of noncatalytic cysteines by covalently bonded or irreversible inhibitors is increasingly recognized as an attractive strategy in drug design, since covalent inhibitors may have increased biochemical efficiency compared with noncovalent inhibitors, due to non-equilibrium binding. reduced sensitivity to pharmacokinetic parameters (e.g. clearance) and increased duration of action dependent on the biological lifespan of the targeted protein (Singh et al., 2011). Recent studies by our group indicated that several thiol-reactive electrophiles can potently inhibit innate allergen-induced responses in airway epithelial cells in vitro as well as in vivo, and these inhibitory effects were mediated (in part) by covalent modification of DUOX1 and inhibition of DUOX1 activity (Danyal et al., 2016). Soft electrophiles have attracted much recent interest because of their presence in certain health-promoting food groups (e.g. curcumin and sulforaphane) and their welldocumented anti-inflammatory properties, which are typically attributed to their ability to target important protein cysteine residues in, for example, NF-кВ or Keap1/nuclear factor (erythroid-derived 2)-like 2 (Nrf2), might also involve direct targeting of alternative proteins such as DUOX1 (Danyal et al., 2016). The identity of the DUOX1 cysteines targeted by these electrophiles is yet to be established, but these studies offer the exciting prospect that selective targeting of specific functionally important cysteines within DUOX1 may lead to inhibition of DUOX1, and could be exploited for the development of DUOX-selective inhibitors to treat allergic disorders such as asthma, allergic rhinitis, atopic dermatitis and conjunctivitis.

Concluding remarks and future perspectives

In this review, we summarized the current knowledge with respect to the importance of DUOX enzymes in innate host defence mechanisms and their potential contribution to disease pathology that is associated with dysregulated immune pathways. In contrast to ongoing efforts to develop inhibitors targeting other NOX isoforms, the importance of DUOX as a therapeutic target has so far not been considered. However, recent evidence highlights the importance of DUOX1 in the context of allergic disease, the incidence of which is rapidly increasing in Westernized societies due to the relative elimination of helminth infections, alterations in microbiome diversity and increased success in treating chronic infectious diseases, and provides a strong rationale for efforts to develop DUOX1-selective inhibitors. Since the DUOX enzymes are quite distinct from other NOX isoforms, it should be possible to design selective inhibitors based on known unique functional or structural features of DUOX, even in the absence of crystal structure data to aid in rational drug design. It will be more challenging to develop inhibitors that distinguish between DUOX1 and DUOX2, because of their high homology, and the best opportunity for developing such specific inhibitors will likely be based on targeting unique and variant regulatory features within their intracellular EF-handcontaining domains. Alternatively, unwanted inhibition of DUOX2 and its negative consequences for thyroid function could be minimized by developing local administration strategies, for example, in the form of inhalers or ointments. High-throughput drug screening efforts may be useful but typically rely on ectopic expression systems and generally do not monitor critical functional outcomes associated with NOX/DUOX activation. Continued efforts to obtain structural data of DUOX enzymes and the development of improved genetically engineered models to evaluate specific aspects of DUOX biology will facilitate new rationalized strategies for DUOX-specific targeting approaches and testing in relevant preclinical models.

Nomenclature of targets and ligands

Key protein targets and ligands in this article are hyperlinked to corresponding entries in http://www.guidetopharmacology. org, the common portal for data from the IUPHAR/BPS Guide to PHARMACOLOGY (Harding *et al.*, 2018), and are permanently archived in the Concise Guide to PHARMACOLOGY (Alexander *et al.*, 2017a,b,c,d).

Acknowledgements

A.V.D.V. gratefully acknowledges research support by grants from NHLBI (R01 HL085646 and HL138708) and NIA (R21 AG055325). D.E.H. acknowledges previous support from an NRSA Fellowship from NIH (F32 HL129706). A.V.D.V. would also like to thank David Seward for help with generating Figure 1 and Nathalie Grandvaux, Miklos Geiszt, Xavier de Deken and Ulla Knaus for frequent informal discussions with respect to the biology of DUOX enzymes.



Conflict of interest

The authors are co-inventors on a US patent application no. 15/299848, entitled Covalent Inhibitors of Dual Oxidase 1.

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