

# Nitric Oxide Synthesis in the Kidney: Isoforms, Biosynthesis, and Functions in Health

By Bruce C. Kone

Nitric oxide (NO) is a gaseous free radical that serves cell signaling, cellular energetics, host defense, and inflammatory functions in virtually all cells. In the kidney and vasculature, NO plays fundamental roles in the control of systemic and intrarenal hemodynamics, the tubuloglomerular feedback response, pressure natriuresis, release of sympathetic neurotransmitters and renin, and tubular solute and water transport. NO is synthesized from L-arginine by NO synthases (NOS). Because of its high chemical reactivity and high diffusibility, NO production by each of the 3 major NOS isoforms is regulated tightly at multiple levels from gene transcription to spatial proximity near intended targets to covalent modification and allosteric regulation of the enzyme itself. Many of these regulatory mechanisms have yet to be tested in renal cells. The NOS isoforms are distributed differentially and regulated in the kidney, and there remains some controversy over the specific expression of functional protein for the NOS isoforms in specific renal cell populations. Mice with targeted deletion of each of the NOS isoforms have been generated, and these each have unique phenotypes. Studies of the renal and vascular phenotypes of these mice have yielded important insights into certain vascular diseases, ischemic acute renal failure, the tubuloglomerular feedback response, and some mechanisms of tubular fluid and electrolyte transport, but thus far have been underexploited. This review explores the collective knowledge regarding the structure, regulation, and function of the NOS isoforms gleaned from various tissues, and highlights the progress and gaps in understanding in applying this information to renal and vascular physiology.

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**N**ITRIC OXIDE (NO) is an important molecular mediator of numerous physiologic processes in virtually every organ. In the kidney, NO plays prominent roles in the homeostatic regulation and integration of glomerular, vascular, and tubular function, as well as a variety of fundamental cellular functions, including cell proliferation, transcription, and energy metabolism.<sup>1-4</sup> In the vasculature, NO functions not only as a vasodilator, but also has antithrombotic, anti-inflammatory, antiproliferative, and antioxidant properties. Although NO serves beneficial roles as a messenger and host defense molecule, excessive NO production can be cytotoxic, the result of NO's reaction with reactive oxygen and nitrogen species, leading to peroxynitrite anion, nitroxyl radical, and hydroxyl radical production, and protein tyrosine nitration.<sup>5,6</sup> Excessive NO production contributes to the pathogenesis of a variety of renal and vascular diseases characterized by inflammation and injury, including glomerulonephritis,<sup>7-9</sup> tubulointerstitial renal disease,<sup>10</sup> postischemic renal failure,<sup>11,12</sup> radiocontrast nephropathy,<sup>13</sup> obstructive nephropathy,<sup>14</sup> and renal allograft rejection.<sup>15,16</sup> Many of these diseases are the subject of reviews in this issue of the journal.

NO exerts its actions by chemical modification of targets, preferentially interacting with thiol groups, transition metals, and free radicals. In addition to its well-characterized signaling effects mediated by cyclic guanosine monophosphate

(cGMP), NO and several NO-derived species can S-nitrosylate cysteine residues in target proteins.<sup>17</sup> This redox-based posttranslational modification has been implicated in the cGMP-independent control of a broad spectrum of cellular functions, and may function in a manner akin to phosphorylation to regulate proteins.

## NO SYNTHESIS AND NOS STRUCTURE-FUNCTION RELATIONSHIPS

NO is metabolized from L-arginine by the NOS isoforms in a complex reaction requiring molecular oxygen, the reduced form of nicotinamide-adenine dinucleotide phosphate (NADPH), flavin nucleotides, tetrahydrobiopterin (BH<sub>4</sub>), a cytochrome P450-type heme moiety, and calmodulin (Fig 1).<sup>18</sup> The 3 principal NOS isoforms—neuronal NOS (nNOS), inducible NOS (iNOS), and endothelial NOS (eNOS)—are encoded by different genes and share ~55% to 60% amino acid homology (Table 1). A mitochondrial NOS also has been reported,<sup>19</sup> and it consistently was identified recently as full-

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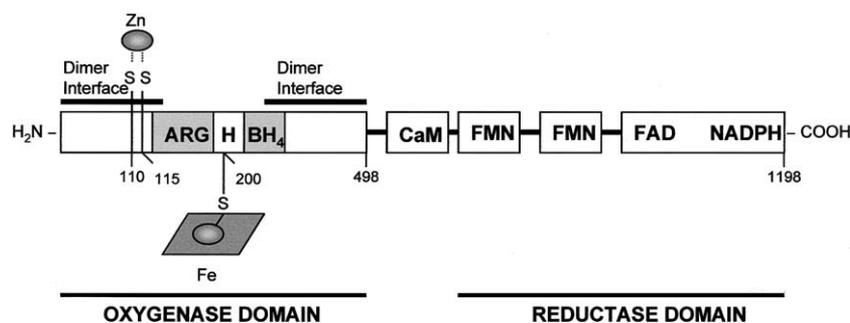
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*0270-9295/04/2404-0002\$30.00/0*

*doi:10.1016/j.semnephrol.2004.04.002*



**Fig 1. Structural organization of NOS.** Binding sites for L-arginine (ARG), CaM, calmodulin, BH<sub>4</sub>, flavin mononucleotide (FMN), flavin adenine nucleotide (FAD), and NADPH are indicated. The position of the heme iron (FE) group and the disulfide bond (ss) in the coordinating zinc-tetrathiolate center positioned at the interface of the 2 monomers. This zinc-tetrathiolate center plays a key role in stabilizing intersubunit contacts and in maintaining the integrity of the BH<sub>4</sub> binding site of iNOS are shown. Amino acids are numbered.

length nNOS with specific posttranslational modifications. nNOS and eNOS are inactive until intracellular Ca<sup>2+</sup> levels increase sufficiently to promote calmodulin binding. In contrast, iNOS binds calmodulin at resting intracellular Ca<sup>2+</sup> concentrations, and thus its activity has been viewed typically as Ca<sup>2+</sup> calmodulin independent. The genes and complementary DNAs encoding the 3 NOS isoforms have been cloned and characterized, the reaction mechanisms and crystal structures of the NOS isoforms have been solved, and mice bearing targeted deletions of each of the 3 major NOS isoforms and an nNOS/eNOS double knockout have been generated (Table 1).

All the NOS isoforms are NADPH- and calmodulin-dependent and contain consensus binding sites for flavin adenine dinucleotide (FAD), flavin mononucleotide (FMN), BH<sub>4</sub>, and a heme complex (Fig 1). They are only active as homodimers. Nonetheless, they differ to a large extent in their cellular localization, regulation, catalytic properties, and inhibitor sensitivity. Structurally, NOS enzymes are modular proteins in which the N-terminal oxygenase domain, which contains binding sites for heme, BH<sub>4</sub>, and L-arginine, is linked by a calmodulin-recognition site to a C-terminal reductase domain, which contains binding sites for FAD, FMN, and NADPH.<sup>18</sup> Electrons are donated by NADPH to the reductase domain of the enzyme and proceed via FAD and FMN redox carriers to the oxygenase domain. There they interact with the heme iron and BH<sub>4</sub> at the active site to catalyze the reaction of oxygen with L-arginine, generating citrulline and NO as products. Electron flow through the reductase domain requires the presence of bound Ca<sup>2+</sup>/calmodulin. At subsaturating

L-arginine or BH<sub>4</sub> concentrations or in the presence of certain NOS inhibitors, NOS can, under at least in vitro conditions, catalyze NADPH oxidation that is uncoupled from NO formation, forming superoxide anion.<sup>20</sup> It remains to be established whether these uncoupled reactions are biologically meaningful in vivo.

Crystal structures have been solved for truncated oxygenase domains of murine iNOS,<sup>21</sup> and for full-length human iNOS,<sup>22,23</sup> and eNOS.<sup>23</sup> Studies of iNOS and eNOS show conservation of quaternary structure, tertiary topology, and substrate and cofactor binding sites, and the importance of a coordinating zinc-tetrathiolate center,<sup>22,23</sup> in which a zinc is positioned at the interface of the 2 monomers and coordinated by 2 cysteines from each monomer. This zinc-tetrathiolate center plays a key role in stabilizing intersubunit contacts and in maintaining the integrity of the BH<sub>4</sub> binding site of iNOS. In the structure of the murine iNOS oxygenase domain (amino acid residues 66-498), Glu<sup>371</sup> is critical for substrate binding and interactions of Arg<sup>375</sup>, Trp<sup>457</sup>, Trp<sup>455</sup>, and Phe<sup>470</sup> influence tetrahydrobiopterin binding.<sup>24</sup> Site-directed mutagenesis also has shown that iNOS Cys<sup>200</sup> is essential for dimer stability,<sup>25</sup> and the regions R<sup>501</sup> to A<sup>532</sup> and I<sup>1121</sup> to L<sup>1144</sup> function as domains for calmodulin<sup>26</sup> and NADPH<sup>27</sup> binding, respectively.

Considerable functional information regarding the contributions of the individual NOS isoforms and their compensatory responses has been generated from studies of NOS isoforms knockout mice. The principal extrarenal and renal phenotypes of these mice are summarized in Table 1 and references therein.

**Table 1. Nitric Oxide Synthases**

Gene	Human Locus	Primary Tissue Distribution Under Basal Conditions	Intrarenal Protein Distribution Under Basal Conditions	Phenotype of Knockout Mice
nNOS 1439 aa	12q24.21	Neurons Skeletal muscle Macula densa segment Bronchial and tracheal epithelium	Macula densa <sup>37,185</sup> Collecting ducts <sup>38,186</sup> Renal pelvis <sup>37</sup>	<i>Renal</i> Defective proximal tubule HCO <sub>3</sub> <sup>-</sup> and fluid transport <sup>155</sup> <i>Extrarenal</i> Hypertrophy of the pyloric sphincter <sup>187</sup> Increased aggressive behavior in men <sup>188</sup> Bladder-urethral sphincter dysfunction <sup>189</sup> Relative protection from ischemic neurologic events <sup>190</sup> Accelerated neointimal formation and constrictive vascular remodeling <sup>191</sup> Impaired resetting of TGF <sup>192</sup>
iNOS 1153 aa	17q11.2-q12	Bronchial airway epithelium, alveolar macrophages Ileum Uterus Platelets	Proximal tubule (functional evidence) <sup>35</sup>	<i>Renal</i> Kidneys protected against ischemic injury <sup>193</sup> Lower fluid and bicarbonate reabsorption in proximal tubules <sup>35</sup> Protection or proximal tubules from hypoxic injury <sup>194</sup> <i>Extrarenal</i> Increased susceptibility to infection with intracellular pathogens and less susceptibility to sepsis-induced hypotension <sup>195</sup> Limited infarct-sparing effect of late phase of ischemic preconditioning <sup>196</sup> Attenuated neointima formation after perivascular arterial injury <sup>197</sup>
eNOS 1203 aa	7q35-q36	Endothelium Hippocampal CA1 neurons Cardiac myocytes	Endothelium, including afferent, efferent arterioles and vasa recta <sup>37</sup> Proximal tubules Thick ascending limbs <sup>198</sup> Collecting ducts	<i>Renal</i> Hypertension, hyperlipidemia, insulin resistance <sup>199</sup> Impaired NaCl transport in TALH <sup>198</sup> <i>Extrarenal</i> More vulnerable to cerebral and myocardial ischemia <sup>200</sup> Bicuspid aortic valves, congenital septal defects, heart failure <sup>201,202</sup> Pulmonary hypertension with chronic, mild hypoxia <sup>203</sup> Deficient growth factor-induced angiogenesis <sup>204</sup> Markedly decreased bleeding times <sup>79</sup>

All NOS isoforms potentially are subject to inhibition by endogenously produced asymmetric dimethylarginines (ADMA), which are synthesized in vivo by N-methyltransferases, a family of enzymes that methylate L-arginine residues within specific proteins. Free ADMA is released during proteolysis of methylated proteins, and it can be detected in plasma and urine. ADMA is metabo-

lized by the enzyme dimethylarginine dimethylaminohydrolase, and inhibition of dimethylarginine dimethylaminohydrolase activity results in increased ADMA levels. Plasma levels of ADMA are increased in end-stage kidney disease, and in other conditions characterized by endothelial dysfunction such as atherosclerosis, hypercholesterolemia, hypertension, and heart failure.<sup>28,29</sup>

### NET CONSTRAINTS ON NO IMPACTING FUNCTION

In considering the influence of NO on renal and vasculature function, it is important to consider the collective constraints on its ability to mediate a functional change. Controls on NOS synthesis and degradation, L-arginine uptake, NOS dimerization and association with BH<sub>4</sub>, signal transduction events, and presence of ADMA are all important factors in this regard. In addition, the sensitivity of soluble guanylyl cyclase,<sup>30</sup> and the end-product bioavailability of NO<sup>31</sup> (ie, is it bioinactivated from reaction with O<sub>2</sub><sup>-</sup> or other reactive species?) must be considered.

### LOCALIZATION OF NOS ISOFORMS IN KIDNEY

A variety of methods ranging from protein and messenger RNA (mRNA) localization methods to functional studies in isolated or in situ microperfused nephron segments have been used to identify NOS expression in the kidney. These results have been somewhat variable and not always internally consistent in terms of a correlation between the gene product identified and its function (usually judged by inhibitor sensitivity or function in knockout compared with wild-type mice). Ideally, multiple independent observers unequivocally would identify NOS isoform protein expression in specific regions of the intact kidney, and this would be correlated with functional studies of that region using NOS isoform-selective inhibitors, which are available for iNOS and nNOS, and/or knockout mice. This full set of criteria has been met infrequently (Table 1). The following examples highlight the problem. First, data generated about mRNA expression and distribution have not always been corroborated by protein expression data. For example, our laboratory<sup>32,33</sup> and others<sup>34</sup> reported basal expression of iNOS mRNA in the rat kidney, yet there has been no consistent demonstration of iNOS protein in the normal rat kidney. Although this simply may be an issue of sensitivity of the assays used for mRNA versus protein expression, it does highlight the need for caution for interpreting gene expression data. Second, there have been numerous examples of reports of NOS isoform protein expression in the kidney that have varied depending on the antibody used for the study. Finally, there have been a few functional studies that strongly have implicated the activity of

a specific NOS isoform in a specific nephron segment, which has not been shown convincingly to express protein for that isoform. For example, studies in the in situ perfused proximal tubule in iNOS knockout mice clearly have shown a role for iNOS in fluid and HCO<sub>3</sub><sup>-</sup> transport in this segment,<sup>35</sup> yet iNOS protein has not been observed consistently there.

With those caveats in mind, immunocytochemical studies have shown that all 3 isoforms of NOS are expressed in the kidney (Table 1). eNOS protein is expressed in renal vascular endothelial cells,<sup>36</sup> and nNOS protein has been found predominantly in epithelial cells of the macula densa,<sup>36,37</sup> principal cells of the collecting duct,<sup>38</sup> and renal pelvic sensory nerves.<sup>39</sup> iNOS protein is widely expressed after induction with endotoxin or proinflammatory stimuli in tubule epithelia, including the proximal tubule, thick ascending limb, and distal convoluted tubule.<sup>34</sup> Renal proximal tubules and inner medullary collecting duct cells can produce NO by means of expression of iNOS, but the true intrarenal locale of the expressed iNOS in vivo is unclear.<sup>32</sup>

### NOS GENE PRODUCTS AND THEIR REGULATION

#### nNOS

##### *Structure and Variants*

The human nNOS gene (designated *NOS1* by the Human Genome Nomenclature Committee) resides at chromosome 12q24.2 and spans over 240 kb.<sup>40</sup> nNOS is expressed basally in diverse cell types and tissues, but predominantly neurons, skeletal muscle, and the macula densa segment. Expression derived from alternative promoters of the human nNOS gene direct tissue- and cell-specific expression. A transcription cluster of exon 1 variants enriched in neuronal tissues reside in one genomic region, whereas those enriched in skeletal muscle are grouped together in another genomic region 75 kb upstream.<sup>41,42</sup> A third transcriptional cluster remote from the other 2 clusters directs Leydig cell-specific transcription.<sup>43</sup> In addition, a calcium-responsive exon 2 promoter recently has been characterized in rodent nNOS.<sup>44</sup>

The major neuronal transcript comprises 29 exons and encodes a 160-kd protein. Several splice variants also yield functional protein. An insertion between exons 16 and 17 encodes 34 additional

amino acids.<sup>45-47</sup> This variant, termed *nNOS- $\mu$* , is expressed in muscle complexed with  $\alpha$ 1-syntrophin and is co-expressed with nNOS in the pelvic plexus and bladder.<sup>45,46</sup> The testis-specific transcription cluster gives rise to an mRNA transcript comprised of 2 new 5' exons (Tex1 and Tex2) spliced to exon 4 of the full-length nNOS, and encodes a 125-kd protein that lacks the protein inhibitor of NOS binding, and the PDZ protein interaction domain implicated in membrane localization. When stably expressed in Chinese hamster ovary-K1 cells, the 125-kd protein encoded by testis-specific nNOS (TnNOS) possesses NOS enzymatic activity comparable with that of the full-length nNOS (160 kd).

### Regulation

Originally believed to be a constitutively expressed enzyme, nNOS is now known to be regulated by a variety of physiologic and pathologic stimuli. The neuronal transcriptional cluster of the human nNOS gene contains binding sites for several transcription factors, including activating protein 2 (AP-2), nuclear factor  $\kappa$  B (NF- $\kappa$ B), cAMP response element binding protein (CREB), and Ets.<sup>40</sup> Studies of nNOS promoter activity in neuronal and fibroblast cell lines revealed that Oct-2 transactivates the downstream promoter (designated 5.1),<sup>48</sup> whereas nerve growth factor induces transcription through the upstream promoter (designated 5'2).<sup>49</sup> CREB binds to 2 sites within the exon 2 5'-untranslated region (UTR) of mouse nNOS to activate transcription in cortical neurons.<sup>44</sup> Steroidogenic factor-1 also transactivates the nNOS gene through the exon 2 promoter.<sup>50</sup> The human testis transcriptional cluster also contains potential *cis*-regulatory elements,<sup>51</sup> but no functional characterization of this region has been published yet to our knowledge. nNOS also is subject to unique controls on translational efficiency. The highly structured nNOS 5'-UTRs contain *cis* RNA elements that modulate translational efficiency in vitro and in vivo.<sup>52</sup> Although nNOS expression appears to be regulated in the kidney during certain physiologic and pathophysiologic states, virtually nothing is known about the specific mechanisms involved.

Phosphorylation also may regulate nNOS. Protein kinases A, G, or C, or  $\text{Ca}^{2+}$ /calmodulin-dependent protein kinase all have been shown to phosphorylate purified nNOS and reduce its cat-

alytic activity, whereas calcineurin-mediated dephosphorylation enhances nNOS catalytic activity.<sup>53</sup> Adenosine monophosphate (AMP)-activated protein kinase increases nNOS phosphorylation in human skeletal muscle, but its effects on nNOS activity are unknown.<sup>54</sup> Protein phosphatase-2 has been shown to dephosphorylate nNOS in vitro.<sup>55</sup> Further studies are needed to clarify the role and regulation of nNOS phosphorylation in intact renal cells.

Higher-order interactions of protein complexes with nNOS regulate the spatial distribution and activity of nNOS in various cell types. As for all the NOS isoforms, calmodulin serves as an allosteric activator. The N-terminus of nNOS contains a PDZ domain that associates with multiple proteins including  $\alpha$ 1-syntrophin,<sup>56</sup> postsynaptic density proteins PSD-93 and PSD-95,<sup>57,58</sup> and the muscle isoform of phosphofructokinase, the inhibitor protein CAPON (for *carboxy-terminal PDZ* ligand of nNOS),<sup>59</sup> carboxy-terminal-binding protein,<sup>60</sup> islet cell autoantigen 512,<sup>61</sup> and  $\text{Ca}^{2+}$ -adenosine triphosphatase plasma membrane  $\text{Ca}^{2+}$  ATPases (PMCA).<sup>62</sup> nNOS also interacts with caveolin-3 in skeletal muscle, where it appears to comprise a component of the dystrophin complex.<sup>63-65</sup> An 89 amino acid light-chain dynein protein termed *PIN* (for protein inhibitor of nNOS) binds to the N-terminus of nNOS and inhibits its activity.<sup>66,67</sup> The molecular chaperone heat shock protein (hsp) 90 has been shown to complex with nNOS and to activate NO production.<sup>68</sup> Finally, bradykinin B2 receptors<sup>69</sup> and  $\alpha$ 1A-adrenergic receptors<sup>70</sup> have been shown to interact with nNOS in vitro, although the full physiologic relevance of these associations are unknown. Presumably these interactions provide a mechanism by which the activity, spatial distribution, and proximity of nNOS to regulatory proteins and intended targets is governed, which provides specificity and controls potential cytotoxicity.

### iNOS

The human iNOS gene on chromosome 17 spans 37 kb and contains 27 exons, with translation initiation encoded by exon 2.<sup>71</sup> Multiple transcription initiation sites and alternative splicing give rise to several forms of exon 1. In addition, cassette deletions give rise to multiple alternative splice variants of human iNOS.<sup>72</sup> The functions of these variants in vivo remain to be established, but one

of them, which lacks exons 8 and 9, exhibits a functional reductase domain but fails to dimerize and to produce NO when heterologously expressed in cultured cells.<sup>73</sup>

### Regulation

Multiple layers of control govern iNOS expression and activity, including changes in iNOS gene transcription; mRNA stability, translation, and degradation; substrate and cofactor binding and availability; and dimerization. Human iNOS is regulated tightly at the level of transcription, and the mechanisms of iNOS induction are cell, species, and stimulus specific. Cytokine combinations leading to iNOS induction vary between species and between cell types in the same species,<sup>74,75</sup> suggesting that tissue-specific regulation of human iNOS is important in determining its local physiologic and pathophysiologic roles. For example, the JAK/STAT pathway mediates the lipopolysaccharide plus interferon- $\gamma$ -induced iNOS expression in RAW 264.7 macrophage cells,<sup>74,75</sup> yet inhibition of the Janus-activated kinase (JAK)/signal transducers and activators of transcription (STAT) pathway enhances iNOS induction by these same stimuli in rat aortic smooth muscle cells.<sup>76</sup> Moreover, the human iNOS promoter exhibits differential responsiveness to mixtures of the same 2 cytokines in different cell lines.<sup>77</sup> In one report, different patterns of altered chromatin structure were identified in different nonrenal epithelial cell lines treated with the same combination of cytokines.<sup>78</sup> Finally, depending on the cell type studied, different regions of the 5'-flanking sequence mediate cytokine induction of the human iNOS gene.<sup>77-80</sup> All of these findings suggest that cell- and stimulus-specific control of the human iNOS promoter may be important in determining its functional roles in different tissues in humans. Very little is known, however, about the mechanisms underlying this specificity.

The bulk of analysis of iNOS gene expression, including our own, has focused on the murine gene. Structure-function studies of the murine iNOS promoter have shown that the proximal 1 kb is sufficient to confer inducibility to lipopolysaccharide and interferon- $\gamma$ .<sup>27</sup> In contrast, a large span of the 5'-flanking region (from -3.8 to -16 kb) is required for cytokine-mediated iNOS induction in humans. A limited deletion analysis of the 5'-flanking sequence of the human iNOS gene has

been performed by transfection of promoter-reporter gene constructs in cell lines from liver, lung, and colonic epithelium, but not kidney. From these limited data, the regulation of the human iNOS gene regulation appears to differ markedly from its rodent counterparts and the specific enhancers appear to be cell specific. More than 3.8 kb of the human iNOS 5'-flanking sequence is required for cytokine induction of reporter genes in both liver and colonic cell lines.<sup>75,80</sup> In DLD-1 colonic cells, sequences between -8.7 and -10.7 kb upstream from the transcription initiation site were necessary for cytokine responsiveness. In contrast, Spitsin et al<sup>79</sup> reported that sequences between -0.4 and -1.6 kb supported modest cytokine responsiveness in the A549 lung epithelial adenocarcinoma cell line, whereas Nunokawa et al<sup>81</sup> showed that 3.2 kb of the iNOS 5'-flanking sequence supported robust reporter gene expression in these same cells. Functionally important NF- $\kappa$ B-like sequences have been identified in the region of -5.2 to -6.1 kb<sup>82</sup> and -8.2 kb<sup>83</sup> in the human iNOS promoter. In addition, inducible AP-1 binding sites have been reported at -5.1 and -5.3 kb. Stat1, in response to interferon- $\gamma$ , binds to a *cis*-acting DNA element at -5.2 kb in the human iNOS promoter, and a DNA element at -5.8 kb serves as a bifunctional motif that binds either STAT1 and/or NF- $\kappa$ B in response to cytokines.<sup>84</sup> Chromatin structure analysis in A549 and AKN-1 cells showed cytokine-inducible DNase I hypersensitive sites and *in vivo* footprints in the region of -5 to -5.5 kb.<sup>78</sup> Finally, in addition to coordinating interaction of transcription factors to impact iNOS gene transcription, we recently showed that hyperacetylation, governed by limiting or facilitating interactions with histone deacetylases, diminishes cytokine induction of murine iNOS transcriptional activity, at least in part, by restricting the functional efficacy of NF- $\kappa$ B.<sup>85</sup>

Changes in mRNA stability of the iNOS gene also have been implicated in the control of iNOS gene expression. The 3'-UTR of the human iNOS mRNA contains 4 AUUUA motifs and 1 AUUUUA motif. The embryonic lethal abnormal vision-like protein HuR was found to bind with high affinity to the AU-rich elements of the iNOS 3'-UTR and to stabilize this mRNA.<sup>86</sup> In other examples, interleukin-1 $\beta$  stabilizes iNOS mRNA in pancreatic  $\beta$  cells,<sup>87</sup>  $\beta$ -adrenergic stimulation enhances interleukin-1 $\beta$  induction of iNOS in cardiac fibroblasts by stabilizing the iNOS message,<sup>88</sup>

and  $\text{BH}_4$  stabilizes the transcript in rat vascular smooth muscle cells.<sup>89</sup> In contrast, increased  $\text{Ca}^{2+}$  concentrations limited iNOS mRNA half-life in human articular chondrocytes,<sup>90</sup> and atrial natriuretic peptide (ANP) accelerated iNOS mRNA decay in macrophages.<sup>91</sup> In addition to these mechanisms, NO itself, in an autoinhibitory feedback loop mediated by cGMP, appears to destabilize its own mRNA.<sup>92</sup> Tyrosine kinases and phosphatases appear to be involved in posttranslational modification of iNOS as well, and potentially may play a role in modulating the functional activity of the enzyme.<sup>93</sup> Finally, it has been established that the proteasome is the primary degradation pathway for iNOS,<sup>94</sup> although it also has been observed that caveolin-1 complexes with iNOS and promotes iNOS proteolysis in human carcinoma cell lines.<sup>95</sup>

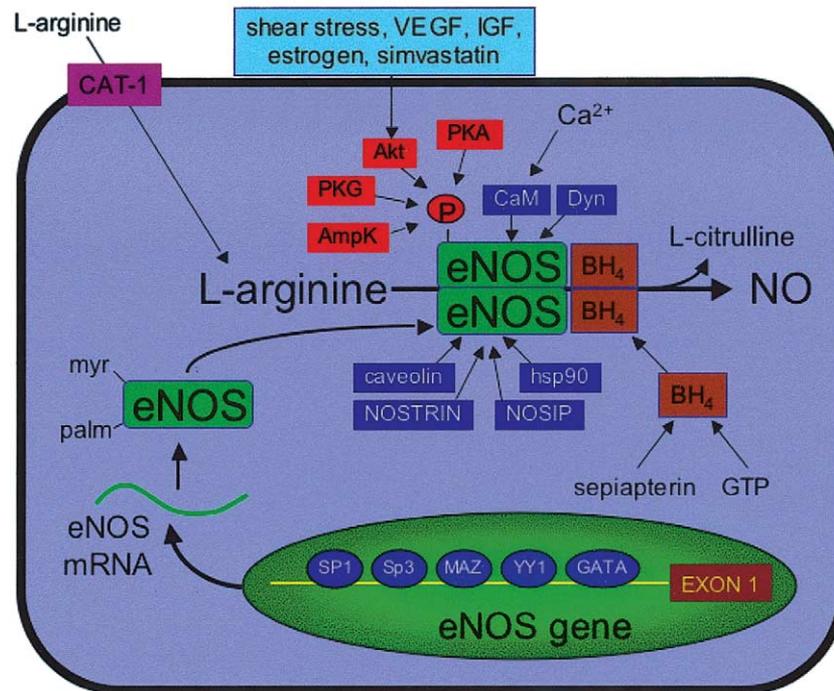
Several proteins that interact and regulate iNOS have been identified. Murine macrophages express a 110-kd protein that interacts with the N-terminus of iNOS, termed *NOS-associated protein-110 kd*, which inhibits iNOS catalytic activity by preventing dimerization.<sup>96</sup> A neural-specific cytosolic protein, kalirin, interacts with the first 70 amino acids of iNOS in yeast 2-hybrid assays and inhibits iNOS activity by preventing the formation of iNOS homodimers.<sup>97</sup> Our laboratory recently defined a regulatory interaction of iNOS with the Rac family of Rho-like guanosine triphosphatases (GTPases) that augments iNOS activity and controls its spatial distribution in activated macrophages.<sup>98</sup> Finally, iNOS, via its C-terminal final 3 amino acids, physically interacts with the apical membrane PDZ-domain protein, ezrin-radixin-moesin-binding phosphoprotein 50, in human proximal tubule epithelial cells.<sup>99</sup> This ezrin-radixin-moesin-binding phosphoprotein 50-iNOS interaction apparently serves to direct iNOS to the apical membrane and drive vectorial NO production at this surface, facilitating NO delivery to targets residing in this membrane microdomain, such as ion transporters.<sup>99</sup>

#### eNOS

The eNOS gene localizes to 7q35-36, spans approximately 21 kb of genomic DNA, contains 26 exons, and encodes an mRNA of 4,052 nucleotides.<sup>100</sup> No alternative splice variants for this isoform have been characterized yet. The gene is expressed in the endothelium of a variety of tissues, as well as in cardiac and myometrial myocytes, platelets, and in airway epithelium. Several

genetic polymorphisms of the eNOS gene have been identified and their association with human disease states as susceptibility genes, including end-stage kidney disease and hypertension, have been studied. A GT substitution in exon 7 (at position 894) in codon 298 of the human eNOS gene alters the amino acid at this residue from glutamate to aspartate.<sup>101</sup> In vitro studies have shown that this mutation results in diminished NO production compared with the wild-type gene.<sup>102</sup> The Glu298Asp variant has been reported to correlate with increased coronary spasm, myocardial infarction, and essential hypertension in various populations.<sup>103,104</sup> Noiri et al<sup>102</sup> reported that the Glu298Asp variant of eNOS is a predisposing factor in end-stage renal disease, especially end-stage renal disease secondary to diabetic nephropathy. However, the population of subjects studied was relatively small, studies of much larger groups of patients are needed.

At the transcriptional level, the eNOS promoter lacks a TATA sequence and contains a single major transcription initiation site. The promoter/enhancer region includes a CCAAT box, several half-palindrome sequences for estrogen response elements, a shear stress response element, and potential binding sites for Sp1, AP-1, cyclic adenosine monophosphate response element, GATA, nuclear factor 1,  $\gamma$ -interferon response element, and NF- $\kappa$ B. Structure-function studies indicate that basal promoter activity in transfected endothelial cells requires an upstream Sp1 binding site, a GATA site at position -230, and a PEA3 site at -26.<sup>105,106</sup> Two tightly clustered positive regulatory domains at -104/-95 and -144/-115, to which Ets family members, Sp1, variants of Sp3, MAZ, and YY1 bind, regulate human eNOS promoter activity in endothelial cells (Fig 2).<sup>107</sup> A third positive regulatory domain resides 4.9 kb upstream from the transcription start site, and binds MZF-like, AP-2, Sp-1-related, and Ets-related factors.<sup>108</sup> Finally, studies in mice transgenic for a promoter-reporter construct containing 5.2 kb of the native murine eNOS promoter showed transgene expression that was restricted to large- and medium-sized blood vessels of the heart, lung, kidney, liver, spleen, and brain. Interestingly, the renal microvasculature, with the exception of the vasa recta of the renal medulla, showed no eNOS transgene expression.<sup>109</sup>



**Fig 2.** Regulation of endothelial NOS synthesis and activity. The eNOS gene is under transcriptional control by a variety of stimuli, including estrogen and glucocorticoids. Binding of several transcription factors to positive regulatory elements in the promoter/enhancer region of the eNOS gene regulate its transcription. Once synthesized, eNOS protein undergoes myristoylation (MYR) and palmitoylation (PALM), which efficiently targets the protein to the plasma membrane caveolae. There, eNOS interacts with a variety of regulatory proteins shown in blue boxes. Under basal conditions, eNOS is tethered to caveolin and inactive. With agonist-induced increases in intracellular  $\text{Ca}^{2+}$ , calmodulin binds eNOS and displaces caveolin in a mechanism facilitated by cooperative binding of hsp90, leading to activation of eNOS activity. Binding of the GTPase dynamin-2 (DYN) to eNOS also appears to be triggered by intracellular  $\text{Ca}^{2+}$  transients and to enhance eNOS activity. eNOS traffic inducer (NOSTRIN) and eNOS interacting protein (NOSIP) serve to promote translocation and inactivation of eNOS from the caveolae. ENOS also may be activated through phosphorylation by the protein kinases AKT, protein kinase A (PKA), protein kinase G (PKG), and AMP-dependent protein kinase (AMPK). In addition, the delivery of the substrate L-arginine via CAT-1-mediated uptake and the synthesis and binding of the important cofactor  $\text{BH}_4$  are critical and regulated events for eNOS activity. See text for additional details and citations.

Shear stress, hypoxia, tumor necrosis factor- $\alpha$ , lysophosphatidylcholine, oxidized low-density lipoprotein, platelet-derived growth factor, basic fibroblast growth factor (bFGF), vascular endothelial growth factor, transforming growth factor- $\beta$ 1, oxidative stress, cyclosporine A, and angiotensin II<sup>110</sup> all have been shown to influence the level of eNOS gene expression in cultured endothelial cells. Estradiol has been shown to activate human eNOS promoter activity, in part via activation of the transcription factor Sp1, in cultured endothelial cells.<sup>111,112</sup> Similarly, a platelet-derived growth factor response element between -744 and -1,600 of the human eNOS gene appears to be important for eNOS transactivation in endothelial cells.<sup>113</sup> In contrast to these activating stimuli, glu-

corticoids have been shown to decrease GATA binding activity and thereby limit the activity of a 3.5-kb human eNOS promoter-reporter gene construct. Finally, changes in mRNA stability also affect eNOS mRNA expression in several settings. Tumor necrosis factor  $\alpha$  has been shown to destabilize eNOS mRNA,<sup>152</sup> whereas HMG-CoA reductase inhibitors, by blocking the geranylgeranylation of the GTPase Rho,<sup>114</sup> and oxidant stress,<sup>115</sup> prolong eNOS mRNA half-life.

At the posttranslational level, N-myristoylation and palmitoylation of eNOS are required for efficient eNOS targeting to caveolae of the endothelial cell membrane<sup>116,117</sup> and appear to facilitate optimal NO release (Fig 2). Similarly complex interactions with caveolins, calmodulin, and hsp90 gov-

ern eNOS activity (Fig 2). At resting intracellular calcium concentrations, eNOS is inhibited tonically through a stable interaction with caveolins.<sup>65,118-121</sup> Agonists, such as bradykinin or fluid shear stress, increase intracellular  $\text{Ca}^{2+}$  concentrations and cause calmodulin to bind and caveolin to dissociate from eNOS, resulting in an activated eNOS-calmodulin complex. Hsp90 appears to facilitate the calmodulin interaction with eNOS.<sup>122</sup> Inhibition of eNOS also occurs through interactions with membrane-proximal regions of intracellular domain 4 of several G protein-coupled receptors (the bradykinin B2, the angiotensin II AT, and the endothelin-1 endothelin B [ETB] receptors). Phosphorylation of the eNOS-interacting region of the bradykinin B2 receptor limits the binding interaction and reverses the inhibitory effect.<sup>123</sup> Other proteins, including eNOS interacting protein, a 34-kd protein that avidly binds to the carboxyl-terminal region (amino acids 366-486) of the eNOS oxygenase domain,<sup>124</sup> eNOS traffic inducer,<sup>125</sup> and the GTPase dynamin-2<sup>126</sup> apparently participate in the complex regulation of eNOS trafficking, targeting, and activity (Fig 2).

Phosphorylation plays an important role in eNOS activity (Fig 2). AMP-activated protein kinase has been shown to phosphorylate eNOS on Ser1177 in vitro and in rat heart during ischemia.<sup>127</sup> The enzyme also is phosphorylated in vitro on Ser633, Ser1177, and activated by cyclic adenosine monophosphate-dependent kinase and cGMP-dependent protein kinase II.<sup>128</sup> Bradykinin,<sup>129</sup> vascular endothelial growth factor, and shear stress trigger Akt-mediated phosphorylation of serine 1177/1179 on eNOS, leading to eNOS activation in vitro and in vivo.<sup>130-132</sup> Estrogen, through activation of phosphatidylinositol-3-OH kinase, stimulates Akt and, thereby, eNOS.<sup>133</sup> Ceramide and sphingosine-1-phosphate activate eNOS via  $\text{Ca}^{2+}$ -independent pathways.<sup>134,135</sup>

## FUNCTIONS OF NO IN THE KIDNEY AND VASCULATURE

### Effects of NO on Cellular Energetics

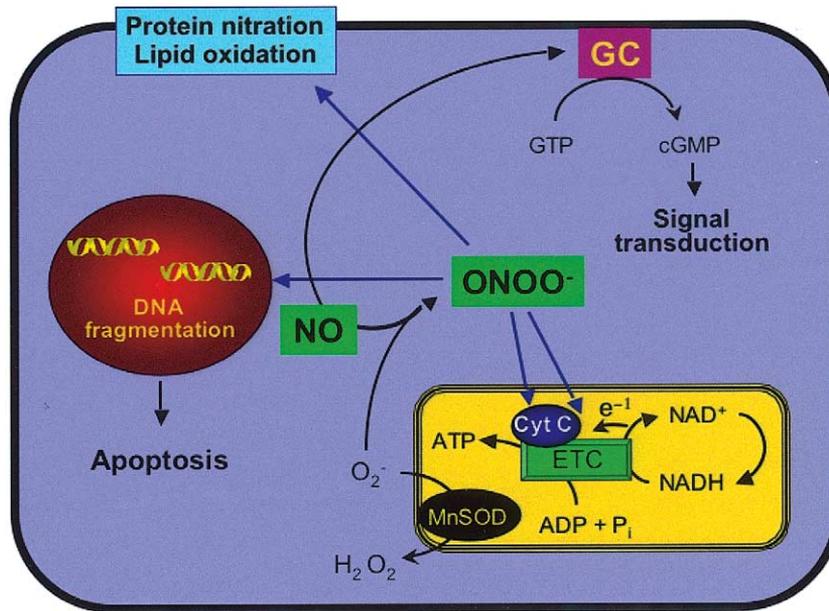
Studies in isolated mitochondria and intact cells showed that NO modulates mitochondrial  $\text{QO}_2$ , membrane potential, adenosine triphosphate production, and free radical generation (Fig 3).<sup>136-142</sup> NO potently, rapidly, and reversibly inhibits cytochrome oxidase and reduces the affinity of the

enzyme for  $\text{O}_2$ .<sup>136,143,144</sup> In addition, full-length nNOS with unique posttranslational modifications is expressed in mitochondria of various tissues, including kidney, and produces NO under physiologic conditions.<sup>145,146</sup> Collectively, these data suggest that NO might serve as a physiologic regulator of cellular respiration. Garvin and Hong<sup>147</sup> reported that nanomolar concentrations of NO could potently and reversibly inhibit respiration renal tubules and isolated mitochondria. The sensitivity to NO-mediated inhibition of respiration was comparable between outer medullary and cortical tubules. These investigators concluded that competition between NO and  $\text{O}_2$  to control respiration in the low  $\text{Po}_2$  environment of the renal outer medulla might contribute to the vulnerability of this region to hypoxia.

NO's ability to inhibit cytochrome oxidase also shifts the electron transport chain to a more reduced state, which favors superoxide anion ( $\text{O}_2^-$ ) formation at the level of complexes I<sup>148</sup> and III (Fig 3).<sup>149</sup> Depending on intracellular redox conditions, the  $\text{O}_2^-$  then can be converted by superoxide dismutase into hydrogen peroxide or react with NO to form peroxynitrite ( $\text{ONOO}^-$ ).<sup>150</sup> These highly reactive species can alter solute transport pathways,<sup>151,152</sup> nitrate proteins, damage cell membranes, cause DNA fragmentation, and promote apoptosis (Fig 3).<sup>153</sup>

### Effects of NO on Renal Solute Transport

By regulating the local renal circulation, the renal efferent and afferent nerve activity, and by direct tubular effects on fluid and electrolyte reabsorption, NO plays an important role in fluid and solute transport.<sup>154</sup> In the proximal tubule, NO has been reported to stimulate<sup>155</sup> net fluid and  $\text{HCO}_3^-$  flux, whereas only inhibitory effects of NO have been found on the  $\text{Na}^+/\text{H}^+$  exchanger<sup>156</sup> and  $\text{Na}^+$ ,  $\text{K}^+$ -adenosine triphosphatase activity<sup>157,158</sup> in this segment. Both nNOS and iNOS appear to participate in these responses. In nNOS knockout mice, both  $\text{HCO}_3^-$  absorption ( $J_{\text{HCO}_3^-}$ ) and fluid flux ( $J_v$ ) in the proximal tubule are reduced significantly, and these animals develop metabolic acidosis (Table 1).<sup>155</sup> In iNOS knockout mice,  $J_{\text{HCO}_3^-}$  and  $J_v$  were each about 35% less than their wild-type controls. Moreover, addition of the iNOS-selective inhibitor L-N6-(1-iminoethyl) lysine, reduced both  $J_v$  and  $J_{\text{HCO}_3^-}$  significantly in wild-type, but not in iNOS knockout, mice.<sup>35</sup> In



**Fig 3. Effects of NO and peroxynitrite (ONOO<sup>-</sup>) on cellular function.** Many of NO's effects are mediated through its actions on guanylate cyclase (GC), which produces the second messenger molecule cGMP that elicits vasodilation and other responses. NO also inhibits cytochrome oxidase (Cyt c) in the mitochondria, shifting the electron transport chain (ETC) to a more reduced state, which favors superoxide anion (O<sub>2</sub><sup>-</sup>) formation. Depending on intracellular redox conditions, the O<sub>2</sub><sup>-</sup> can then be converted by superoxide dismutase (MnSOD) into hydrogen peroxide or react with NO to form peroxynitrite (ONOO<sup>-</sup>). These highly reactive species can cause DNA fragmentation and apoptosis, as well as protein nitration and lipid peroxidation, which damage cells.

contrast, neither  $J_{\text{HCO}_3^-}$  nor  $J_v$  was significantly different from wild type in eNOS knockout mice.<sup>35</sup> In the aggregate, these results indicated that endogenous NO derived from both nNOS and iNOS serves to enhance fluid absorption and  $\text{HCO}_3^-$  transport, whereas eNOS does not directly modulate these parameters in the proximal tubule.

In the medullary thick ascending limb of Henle's loop (MTAL), NO inhibits net  $\text{Cl}^-$  and  $\text{HCO}_3^-$  absorption,<sup>159-161</sup> effects in part mediated by a direct inhibitory action of NO on the  $\text{Na}^+$ - $\text{K}^+$ - $2\text{Cl}^-$  cotransporter<sup>147</sup> and the  $\text{Na}^+$ / $\text{H}^+$  exchanger.<sup>159</sup> In contrast, NO stimulates the activity of apical  $\text{K}^+$  channels in this segment.<sup>162</sup> In the collecting duct, NO inhibits  $\text{Na}^+$  absorption<sup>163</sup> and vasopressin-stimulated osmotic water permeability.<sup>164</sup> In addition, Lu et al<sup>165,166</sup> showed that NO inhibits apical  $\text{Na}^+$  channels in the cortical collecting duct (CCD), and linked this mechanism to the inhibition of the basolateral small-conductance  $\text{K}^+$  channel. Moreover, NO also has been reported to inhibit the  $\text{H}^+$ -adenosine triphosphatase of intercalated cells of the collecting duct,<sup>167</sup> and to me-

diate the stimulatory effect of angiotensin II on basolateral  $\text{K}^+$ -channel activity in the CCD.<sup>168</sup>

#### Effects of NO on the Renal Microcirculation

NO is an important modulator of glomerular and renal hemodynamics.<sup>169</sup> Intrarenal NO is responsible for up to one third of the normal renal blood flow and helps to maintain the low renal vascular resistance under normal conditions. Although NOS inhibition does not interfere with the basic autoregulatory mechanism of the glomerulus, it does decrease the absolute renal blood flow.<sup>170</sup> Studies of the renal microvascular responses to NOS inhibition in animal models have shown that tonically released NO regulates both the resistances of both the afferent and efferent arterioles. As a regulator of tubular reabsorptive function, NO also serves as a major mediator of arterial pressure-induced natriuretic responses in the kidney (see later).<sup>171</sup>

NO plays a key role in regulating perfusion of the renal medulla.<sup>172-175</sup> Local infusion of NOS inhibitors into animals reduces medullary blood flow, promotes salt retention, and leads to hyper-

tension. Conversely, L-arginine infusion increases NO, enhances medullary blood flow, and abrogates hypertension in these models. High salt intake has been shown to result in increased NO concentrations and NOS expression and activity selectively in the renal medulla.<sup>172-175</sup> Conversely, Dahl salt-sensitive rats exhibit a deficiency of NOS activity that is confined to the renal medulla.<sup>176</sup> Thus, NO acts in the renal medulla to control sodium excretion during variations in salt intake and therefore helps to modulate arterial blood pressure.

#### Pressure-Natriuresis and Tubuloglomerular Feedback

Long-term control of arterial pressure is in part governed by the pressure-natriuresis mechanism, which couples increases in renal perfusion pressure to increases in renal sodium excretion. Experiments in dogs confirmed that intrarenal NO activity directly correlates with changes in arterial pressure and changes in urinary excretion rates of sodium, suggesting that acute changes in arterial pressure alter intrarenal NO production, which inhibits tubular sodium reabsorption and effects pressure natriuresis.<sup>168,171,177</sup>

NOS activity contributes to the activity of tubuloglomerular feedback (TGF), which couples tubular reabsorption to the regulation of glomerular ultrafiltration. A growing body of evidence suggests that NO produced by nNOS in the macula densa stimulates soluble guanylate cyclase, generating cGMP and activating cGMP-dependent protein kinase within the macula densa cells, which then modulate TGF responsiveness. Micropuncture studies *in vivo* have shown that NO blunts the TGF response that causes vasoconstriction of the renal afferent arteriole in response to sodium chloride reabsorption at this site, and possibly regulates renin release from the juxtaglomerular apparatus.<sup>178-181</sup> Oxidative stress produced in hypertensive rat models greatly limits NO bioactivity in the juxtaglomerular apparatus<sup>182,183</sup> (see article by Modlinger et al, in this issue). Recent studies indicate that NO produced by either eNOS or iNOS in the medullary thick ascending limb of Henle also may inhibit TGF. In the presence of the nNOS-selective inhibitor 7-nitroindazole, a nonselective NOS inhibitor significantly enhanced TGF when the macula densa was perfused orthograde via the medullary thick ascending limb of Henle, whereas the blocker had no effect on TGF when

the macula densa was perfused retrograde via the distal tubule.<sup>184</sup>

#### CONCLUSIONS AND PERSPECTIVES

The field of NO biology has advanced at a dramatic pace and has offered new tools and mechanistic insights into the regulation of NO biosynthesis, NO targets, pharmacologic and endogenous inhibitors, and biological functions mediated. Methods for detecting NO and reactive nitrogen species in biological systems are being refined, gene expression profiling is identifying target genes susceptible to regulation by NO in various cells, proteomic methods are being exploited to identify protein targets of nitration and S-nitrosylation, the phenotypes of NOS isoform knockout and compound knockout mice are being dissected in greater detail, and more pharmacologic inhibitors with greater isoform selectivity are being generated. The challenge for renal investigators is to exploit these data, reagents, methods, and animal models to address with a high degree of sophistication the impact of NO on renal health and disease, and to generate new information in renal cells that may be more broadly applicable to other cell types and tissues.

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