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Citation for published version:

Digital Object Identifier (DOI):
10.1016/j.dci.2009.04.006

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher's PDF, also known as Version of record

Published In:
Developmental and Comparative Immunology

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An ancient immunity gene duplication in *Daphnia magna*: RNA expression and sequence analysis of two nitric oxide synthase genes

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**A R T I C L E   I N F O**

Article history:
Received 30 March 2009
Accepted 27 April 2009
Available online 18 May 2009

Keywords:
Invertebrate immunity
Innate immunity
Nitric oxide synthase
*Pasteuria ramosa*
Pathogen
Parasite

**A B S T R A C T**

NO (nitric oxide) is a highly reactive free radical gas thought to play a major role in the invertebrate immune response by harming pathogens and limiting their growth. Here we report on studies of nitric oxide synthase (NOS) genes in the crustacean *Daphnia*, one of the few non–insect arthropod models used to study host–pathogen interactions. While the NOS gene is found as a single copy in other invertebrates, we found two copies (NOS1 and NOS2), which a phylogenetic reconstruction showed to be the result of an ancient duplication event. Both genes bear features commonly found in invertebrate NOS, however, the two genes differ in their rate of evolution, intraspecific polymorphism and expression level. We tested whether the more rapid evolution of NOS2 could be due to positive selection, but found the rate of amino-acid substitutions between *Daphnia* species to be compatible with a neutral model. To associate NOS or NO activity with infection, we performed infection experiments with *Daphnia magna* and one of its natural pathogens (*the bacterium Pasteuria ramosa*). In one set of experimental infections, we supplemented *D. magna* with L-arginine, the NOS substrate, or with L-NAME, a NOS antagonist, and found this to result in lower and higher infection levels, respectively, which is at least compatible with the notion that NO may aid defence against *Pasteuria*. A second experiment indicated that NOS transcription does not increase following exposure to *Pasteuria*. Thus, the function of NOS in *Daphnia* immunity remains uncertain, but the pattern of gene duplication and subsequent divergence suggests evolution via neo- or subfunctionalization.

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1. Introduction

Nitric oxide (NO) is a highly reactive free radical gas produced by the conversion of L-arginine into L-citrulline by nitric oxide synthase (NOS). Most of what is known about the biological role of NO comes from studies of vertebrates, where it has been shown to be involved in neurotransmission, inflammation and host defence (see review in [1]). With respect to host defence, the reactivity of NO with oxygen and oxygen-related reactive intermediates yields numerous species with enzymatic and DNA-damaging properties that make NO toxic to many pathogens [1–3]. Three main forms of NOS have been found in vertebrates: two constitutive forms, neuronal (eNOS or NOS1) and endothelial (eNOS or NOS3), which are expressed in almost all the cells of the body [4], and an inducible form (iNOS or NOS2, see [2,4] for a review). iNOS is expressed during inflammation or infection and increases the quantity of NO by 100–1000 times [2]. However, NO appears to be a “double-edged sword” as at high concentrations it can also damage host tissues [1,2,4,5].

Recent years have seen renewed interest in invertebrate immunity (Fig. 1, in [6]), motivated by the importance of invertebrates as vectors or intermediate hosts of human pathogens, and due to their utility as models for understanding coevolutionary processes. Understanding the role of NO in the invertebrate immune system has been part of this surge, but it is presently less well-studied than other effectors such as antimicrobial peptides or prophenoloxidase (proPO). The NOS gene has been sequenced in a range of invertebrates, including insects, molluscs and crustaceans (e.g. [7,8–11]), and in most species, a single NOS gene copy has been detected. However, in the genome of the crustacean *Daphnia pulex* two NOS genes have been described, located on different genomic scaffolds [12].

The role of NO in limiting the impact of pathogens has been demonstrated in a range of invertebrate species. For example, NO helps limit *Plasmodium berghei* development in the mosquito *Anopheles stephensi* [11], it is probably involved in killing *Schistosoma mansoni* in the snail *Biomphalaria glabrata* [13], and it is implied in *Drosophila melanogaster*’s response to parasitoids [14,15]. Additionally, NOS expression has been shown to rise
following infection in various organisms [7,8,11,13,16–20]. Our
model is the crustacean Daphnia magna, a filter-feeding cladoceran
that reproduces by cyclical parthenogenesis and is common in
freshwater ponds, and which is one of the few non-insect
arthropod models used to study host–pathogen interactions. Little
is known about the genetic basis of its immune response to
pathogens, although phenotypic responses to natural pathogens
have been thoroughly investigated. Among the numerous patho-
gens of D. magna (see review in [21]), the gram–positive bacterium
Pasteuria ramosa is an obligate endopathogen of D. magna that is
well-studied in both the laboratory and field where it naturally
infects D. magna [e.g. [22–26]]. It permits relatively easy
experimentation, and thus it has been shown that resistance to
P. ramosa depends on host and pathogen genetic background [27],
and is mediated by environmental effects [21,28–31].

To better understand the genetic and immunological basis of
resistance to pathogens in D. magna (see also [26]), here we report
on studies of Daphnia NOS genes. We took advantage of the
recently sequenced genome of a D. pulex ([http://daphnia.cgb.in-
diana.edu/][12]), in which two NOS genes have been described [12],
to acquire the full cDNA of NOS in D. magna. We also found NOS in
two copies in this species. We compared deduced NOS amino-acid
sequences in Daphnia with those of other arthropods to test
whether the Daphnia genes show signs of functional differen-
tiation, as might be predicted following a gene duplication. As some
allelic variation of NOS has been reported to be associated with
parasite infection in A. gambiae [32], we also analysed polymor-
phism of D. magna NOS cDNAs for 14 genotypes originating from
various locations in Europe, eight of which are known to differ in
their level of resistance to the pathogen P. ramosa [27]. Finally, we
quantified the relative expression levels of NOS in D. magna and
experimentally investigated the potential for NO to play a
direct role in resistance to pathogens.

2. Materials and methods

2.1. RNA isolation and cDNA sequencing of D. magna NOS

Recently, a related species to D. magna, D. pulex, was subject
to full genomic sequencing. To identify conserved regions for
designing primers for use in the polymerase chain reaction
(PCR) in D. magna, we used gene models of the two NOS cDNAs
from D. pulex [12] and 12 sequences collected from various
public libraries: (i) insects: (a) lepidopteran: Manduca sexta
(GenBank AAC61262), Bombyx mori (REFSEQ NP_001036963); (b)
dipteran: D. melanogaster (GenBank AAFF25682), A. stephensi
(GenBank AAC85717); (c) hymenopteran: Apis mellifera (REFSEQ
NP_001012980); (d) hemipteran: Rhodinus prolixus (GenBank
AA03081), Acyrthosiphon pisum (REFSEQ XP_001946209); (e)
orthoptera: Gryllus bimaculatus (DBJ BAH14964); (f) coleoptera:
Luciola cruciata (DBJ BAF3671), Tribolium castaneum (REFSEQ
XP 967195); (ii) crustaceans, decapoda: Gecarcinus lateralis
(GenBank AAT46881); (iii) chelicerata, acari: koxes scapularis
(GenBank EEOC5972). These fragments were also used to
draw an interspecific phylogeny of NOS proteins, as described
below.

Four 5-day-old Daphnia were pooled in 200 µl RNAeasy midi Kit (Qiagen),
according to the manufacturer’s instructions and further purified
with RNase-Free DNase (Promega). Two microtrols of RNA
(~200 ng/µl) was reverse-transcribed into cDNA using the
Promega Reverse Transcription System kit according to the
manufacturer’s instructions. cDNA was diluted 5-fold with H2O,
and its purity assessed [26]. Initial D. magna NOS cDNA sequences
were acquired using gene-specific degenerate primers, but to
obtain the 5’ and 3’ ends of the D. magna cDNAs, RACE-PCR was
performed with the GeneRacer™ Core kit (Invitrogen). As in D. pulex,
two homologous sequences were named and named Dmag-
NOS1 and Dmag-NOS2. The fragments were assembled using the
Genious Pro 4.0.2 software [33].

The complete D. magna cDNA data were used to refine the D.
pulex NOS1 and NOS2 gene models (Supplementary Materials S1),
for use in subsequent analyses. D. pulex and D. magna NOS protein
sequences were aligned to homologous sequences from all other
available invertebrate taxa using the ClustalW algorithm within
MacVector v7.2.3, and corrected by eye. The completed multiple
sequence alignment was used to infer a phylogeny using MrBayes
3.1.2. The mixed model option was used to choose the amino-acid
substitution model, a gamma rate distribution parameter esti-
mated from our dataset, and saving every 100th tree. Two parallel
Markov chains were run simultaneously in each of two runs. Tree
length, amino-acid model, log-likelihood score and alpha value of
the gamma distribution were examined in the program Tracer v1.3
prior to the termination of MrBayes to ensure that all parameters
had reached stationarity. Saved trees from after the burn-in were
summarised and posterior probabilities estimated. The resulting
tree was visualized with the program Treeview (v1.6.6, http://
taxonomy.zoology.gla.ac.uk/rod/rod.html).

Table 1

<table>
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<tr>
<th>Gene</th>
<th>Forward primer</th>
<th>Sequence (5’–3’)</th>
<th>Reverse primer</th>
<th>Sequence (5’–3’)</th>
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</thead>
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<tr>
<td>NOS1</td>
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<td>GCGAGACCCAGCAGCTAAGTCCT</td>
<td>SeqNOS1_R1bc</td>
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<td>ATCTCGAAGACTGAGGAGGGCCTTAC</td>
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<td></td>
<td>SeqNOS1_F4</td>
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<td>SeqNOS1_R4</td>
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<td></td>
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<td>SeqNOS1_R8</td>
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<td>SeqNOS2_R7b</td>
<td>TGGTGTGGCTTCAGCAAG</td>
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</table>
To test the prediction that the Daphnia NOS genes are evolving at a different rate compared to other invertebrate NOS genes, we first tested whether rate heterogeneity was present within the tree using the program PAML (version 3.14, [34]). The fit of two evolutionary models was subsequently tested, one that allowed the Daphnia NOS clade (containing NOS1 and NOS2) to evolve at a different rate compared to all other clades, and a second that allowed each of NOS1 and NOS2 to evolve at different rates compared to the rest of the tree. In all comparisons, as is standard in PAML analyses, a significant difference between models was tested with a likelihood ratio test.

Fig. 1. Nucleotide (above) and deduced amino-acid (below) sequence of D. magna (A) NOS1 and (B) NOS2. The nucleotide sequences are numbered from the first base at the 5' end of the transcript. The first methionine (M) is numbered on the first deduced amino-acid of the transcript and the Stop codon is also highlighted (Stop). The hydrophobic residues corresponding to Ca2+-dependent calmodulin-binding 1-5-8-14 Type A motif [43] are boxed. The polyadenylation (AATAAA) signal is black highlighted. As expected, no signal peptide was detected using the online software SignalP 3.0 in any of the protein sequences [http://www.cbs.dtu.dk/services/SignalP/, [56]].
Next, to evaluate what type of selective pressure NOS genes have experienced, the ratio of non-synonymous substitutions per non-synonymous site to synonymous substitutions per synonymous site (Dn:Ds) was calculated between Daphnia species. When Dn:Ds is >1, divergence between species is considered to be due to adaptive evolution. In addition to the full gene length comparison between D. magna and D. pulex, comparisons of two shorter fragments (549 nt from NOS1 and 660 nt from NOS2) between D. parvula (a close relative of D. pulex) with each of D. pulex and D. magna were also included.

In the NOS1 analysis, nucleotides encompassing amino-acids 1163–1346 were analysed. This region includes the NADPH ribose domain and a portion of the NADPH adenine domain as well as two interdomain regions that show low sequence homology among the taxa examined. In the NOS2 analysis, nucleotides encompassing amino-acids 621–841 were analysed. This region includes part of the BH4 domain and the camodulin domain, as well as two interdomains that show low sequence homology among the taxa examined.

2.2. Sequence polymorphism in D. magna NOS

From the complete D. magna NOS cDNA sequences, Primer3 (http://www.bioinformatics.nl/cgi-bin/primer3plus/primer3plus.cgi) was used to design nine or 10 pairs of primers to PCR amplify NOS1 and NOS2, respectively (see sequences in Table 1). All primer pairs are gene-specific and amplify overlapping/C24 500–700 bp fragments. Independent PCR were performed for each primer pair (30 cycles, 92°C for 30 s, 52°C to 56°C for 30 s and 72°C for 1 min) using the Bioline Taq DNA polymerase kit. Sequence polymorphism was studied in the same 14 Daphnia clones used in Labbé and Little [26]. Briefly, six clones (CG3, CG4, CG7, CG8, CG13, and
performed using the Roche LightCycler 1 actin for 10 s. Quantifications of NOS1 and NOS2 relative to gene-specific primers (NOS1-QF 5'-0-fragment of Dmag-NOS2 cDNAs were amplified separately using results did not differ from those obtained with actin, only the latter are reported. A 99 bp fragment of Dmag-NOS1 and a 106 bp m L of SYBR Green I Master mix (Roche). The quantification of each gene (NOS1, NOS2 and actin) was done on separate plates. Cycling conditions were as follows: 95 ºC, 5 min followed by 50 cycles of 95 ºC for 10 s, 58 ºC for 10 s and 72 ºC for 10 s. Quantifications of NOS1 and NOS2 relative to actin were performed using the Roche LightCycler® 480 software, using the maximum secondary derivative method.

2.3. NOS expression

RNA was extracted and purified from a mix of 4 crushed *Daphnia* from which cDNA was synthesized as described above (RNA concentration was ~150 ng/µl). Relative Real-Time Quantitative PCR (RT-QPCR) was implemented using the Roche LightCycler® 480. A –100 bp fragment of actin, a house-keeping reference gene, was amplified using primers from Heckmann et al. [36]. Note that a second common control gene (GAPDH) was also employed but as results did not differ from those obtained with actin, only the latter are reported. A 99 bp fragment of Dmag-NOS1 and a 106 bp fragment of Dmag-NOS2 cDNAs were amplified separately using gene-specific primers (NOS1-QF 5’/GAGCTCTCAGACAATGCCTT-3’/NOS1-QR 3’/ACGCCGCAAAATGTTTACCA’/NOS2-QF 5’/AGTGATTTTCGTGTCTGG 3’/NOS2-QR 3’/ACCCCGTGAATTACCTCCGGTAATTGCGACATT 5’, respectively). For each NOS gene and each individual, 2 µl of cDNA (1 µl for actin) and 0.5 µl of each primer (10 mM) were added to 8 µl of SYBR Green I Master mix (Roche). The quantification of each gene (NOS1, NOS2 and actin) was done on separate plates. Cycling conditions were as follows: 95 ºC, 5 min followed by 50 cycles of 95 ºC for 10 s, 58 ºC for 10 s and 72 ºC for 10 s. Quantifications of NOS1 and NOS2 relative to actin were performed using the Roche LightCycler® 480 software, using the maximum secondary derivative method.

2.4. NOS/NO and host resistance to pathogens

2.4.1. NOS expression when challenged by a pathogen

Expression of both NOS genes was further analysed in *D. magna* clone GG4 experimentally exposed to *P. ramosa*. The pathogen spores (Sp1) originated from a single, wild caught infected female and have been used to infect *Daphnia* in the laboratory for over a decade (Sp1, [27]).

Using the conserved cDNAs from the same host individuals from a previous analysis of the proPO gene [26], RT-QPCRs were implemented on each individual with both NOS1 or NOS2 specific primers as described above to compare Dmag-NOS1 and Dmag-NOS2 expression between *Daphnia* exposed or not-exposed to *P. ramosa* at six time-points following exposure. Details of the protocol can be found in Labbé and Little [26]. Briefly, after they spent 3 generations in standard conditions to equilibrate environmental effects, replicates of four 5-day-old *Daphnia* were exposed to a solution of *P. ramosa* spores or to a sham solution (18 replicates per treatment) for 2 h in 1.5 ml eppendorf tubes. After these 2 h, the *Daphnia* were placed in a new jar and reared normally. Three jars for each treatment were randomly collected 1, 2, 6, 12, 24 and 48 h after the end of the exposure treatment. Additionally, three jars were also collected at time 0, prior to exposure, as controls. For each time-point, the four *Daphnia* were transferred to one eppendorf tube with 200 µl of RNAlater™ (Ambion), and stored at –20 ºC for later extraction. Three replicates of each treatment were kept in rearing conditions until day 16, to estimate infection success. No supplement with a potential effect on NOS was added during this experiment.

The NOS gene expression data were fitted to the general linear model (GLM): log(ACTIVITY) = EXPOSURE + TIME + EXPOSURE:TIME, where EXPoSURE:TIME represents the interaction between EXPOSURE, a categorical variable with two levels (exposed/not-exposed), and TIME, a continuous variable (h). Log-transformation of the response variable ensured the normal distribution of residuals. The initial model was simplified according to Crawley [37]. Models were compared using F-tests. Analysis was performed using the R package (http://www.r-project.org/).

2.4.2. NOS substrate manipulation

To further assess whether NOS/NO might play a role in resistance to pathogens, *D. magna* were exposed to *P. ramosa* in the presence or absence of L-arginine, the substrate required for NOS activity and for which availability is likely to be limiting [11,20]. The water of the potential hosts was supplemented with L-arginine, our prediction being that increasing availability of L-arginine would limit the establishment of infection.

Six replicates of host clone GG4 were kept under controlled conditions for three generations prior to experimentation. These controlled conditions were 20 ºC, a light:dark cycle of 16:8 h, 5 x 10⁴ cells of chemostat grown algae (Scenedesmus sp) per *Daphnia* per day as food. Replicates contained 5 females from the same clutch, in a 200 ml jar of *Daphnia* medium [38]. Each generation was seeded using female newborn from the 3rd or 4th clutches. For the experiment, newborn from each of the six replicate jars were split across twelve treatments. These treatments were: no pathogen spores and *Daphnia* medium adjusted to contain 0, 1, 7.5, 15, 30 or 60 mg/ml of L-arginine (Sigma–Aldrich) per *Daphnia* day 4, each group of five *Daphnia* were transferred to a jar containing 200 ml of *Daphnia* medium (with no L-arginine) and fed 5 x 10⁶ cells of algae per *Daphnia* per day until the end of the experiment at day 30.

![Fig. 2. Bayesian phylogeny of the nitric oxide synthase (NOS) gene from available insect and crustacean sequences, numbers at the nodes are posterior probabilities. See text for the reference sequences of the various organisms. Dmag-NOS1 and Dmag-NOS2 are in bold. The scale for 0.1 amino-acid substitutions per site is indicated.](image-url)
Fig. 3. Multiple alignment for conserved motives of several arthropod NOS amino-acid sequences. See text for the reference sequences of the various organisms; for reasons of print space not all the sequences used are presented but only a representative selection of the diversity (in particular as D. pulex and D. magna are relatively close, the D. pulex sequences are not shown). Conserved amino-acid in more than 90% of the sequences are black shaded, those conserved in more than 50% of the sequences are grey shaded.

Binding sites to heme, tetragydrobiopterin (BH4), calmodulin, FMN, FAD pyrophosphate, FAD isalloxazine, flavin, NADPH ribose, NADPH adenine and NADPH are underlined.
Daphnia were transferred into fresh water three times per week. Infection status of each host was determined by eye and the presence of pathogen spores was later verified by crushing dead hosts and examining them under a microscope at 40x magnification. Results were analysed with general linear models with binomial errors in the R package. The response variable was the proportion of hosts infected. Dose of l-arginine was the categorical explanatory variable.

This experiment was repeated, but 0, 7.5 or 60 mg/ml of l-NAME were added (instead of l-arginine). This compound competes for the l-arginine binding site of NOS and inhibits the reaction, so that the addition of l-NAME is predicted to increase the probability of infection. In this experiment there were eight replicate jars per treatment and per clone and 5 Daphnia per jar. Three different clones were used, GG4, GG3 and GG15 (all were sampled in the same pond) [27]. The number of parasite transmission spores added and the other conditions were identical to the previous experiment. Analysis was performed using the R package on the proportion of hosts infected using the GLM with binomial error: proportion infected = \( \text{Dose} + \text{Clone} + \text{Dose} \times \text{Clone} \), where Dose and Clone are the categorical explanatory variables. The initial model was simplified according to Crawley [37]. Models were compared using F-tests.

3. Results and discussion

NO may be one of the most general immunity effectors [2], and yet, compared to antimicrobial peptides (AMP) or prophenoloxidase (proPO, [39,40–42]), studies of NO are limited. NO is a gas, which rapidly diffuses through the blood to reach distant tissues. NO is produced by many cells, including bacteria, fungi, and plants, and it is released as a defense mechanism against pathogens [43]. NO is also produced by many animals, including arthropods, and it is released as a defense mechanism against pathogens [44]. However, NO is not always produced in response to infection. For example, NO is produced by the body as a normal protective mechanism against parasites, but it can also be produced by the body in response to inflammation [45].

The clustering of NOS1 and NOS2 proteins in D. pulex and D. magna (Fig. 2) indicates that a NOS gene duplication predates the speciation of the two Daphnia species, which is thought to have occurred anywhere from 10mya [44] to 200mya [45]. Daphnia NOS genes are also strikingly divergent from other vertebrates, where two gene copies were used, GG4, GG3 and GG15 [all were sampled in the same pond] [27]. The number of parasite transmission spores added and the other conditions were identical to the previous experiment. Analysis was performed using the R package on the proportion of hosts infected using the GLM with binomial error: proportion infected = \( \text{Dose} + \text{Clone} + \text{Dose} \times \text{Clone} \), where Dose and Clone are the categorical explanatory variables. The initial model was simplified according to Crawley [37]. Models were compared using F-tests.

The different rates of evolution between the Daphnia NOS genes may be a result of strong positive selection, which has been frequently observed in immunity genes [46–49]. We tested if this was the case by comparing divergence at synonymous sites (which should evolve essentially neutrally) to divergence at non-synonymous sites. However, as has been previously reported, the synonymous substitution rate (Ds) between D. magna and D. pulex was high [44]. Indeed, Ds values between D. magna and D. pulex and D. magna and D. parvula indicated that the sequences were saturated for both of the NOS genes (D. magna/D. pulex: NOS1 Ds = 0.62, NOS2 Ds = 1.17, D. magna/D. parvula: NOS1 Ds = 1.03, NOS2 Ds = 0.55, all Jukes-Cantor corrected), precluding investigations into the type of selection acting in this species pair. By contrast, Ds values between D. pulex and D. parvula were suitable to evaluate Dn/Ds, and this comparison indicated that both genes are under purifying selection (NOS1 Dn/Ds = 0.14, NOS2 Dn/Ds = 0.10). However, as only a portion of each gene was sequenced, these results may not be representative of the selection pressure over the entirety of the gene sequence. Nonetheless, there is no indication that these genes are undergoing positive selection, as would be expected if one or both gene copies were involved in a coevolutionary arms race with a pathogen.

To assess intraspecific variation, we sequenced the complete cDNAs of both NOS genes from 14 different D. magna clones. For Dmag-NOS1, the standard protein is 1182 amino-acids long, but two clones (GG8 and GG15) each presented two transcripts, one encoding the standard protein and one containing a deletion of 92
nucleotides. Due to this deletion no viable protein can be translated from the usual start codon (frame shift). Alternatively, the short transcript might encode a 878 amino-acid-long protein, with an alternative start at the 306th amino-acid in the standard protein. Of 33 variable amino-acid sites within the 3546 bp Dmag-NOS1 ORF, nine contain non-synonymous mutations, among which 4 do not change the polarity of the amino-acid (Table 2A). No mutation appears to be associated with resistance as

### Table 2

cDNA sequence variation between *D. magna* clones. Each variable site is indicated with its position relative to the first nucleotide of the first methionine. (A) for NOS1 and (B) for NOS2. GC3 cDNA is used as the reference sequence, a dash (-) indicates no differences with the reference. Nucleotides R, K, M, W, S and Y correspond to heterozygote sites (IUB ambiguity codes). For non-synonymous mutations, the corresponding amino-acid changes are indicated. For NOS1, the deletion (Del.), observed for some transcripts (see text), is boxed, and nucleotide changes before that deletion are lower cased. For NOS2, a dot (.) indicates that the sequence is missing for that clone.

<table>
<thead>
<tr>
<th>Clone</th>
<th>Position</th>
<th>Amino-acid change</th>
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<tbody>
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observed by Carius et al. [27] for the four Gaazerfeld german clones ("GG" clones) or with the patterns observed in the four Scottish clones ("K" clones, T. Little, unp. data). For Dmag-NOS2, possibly due to the low expression of this gene, we obtained the full sequence for only 11 of the 14 clones. However, the sequences obtained were sufficient to gain at least some insight into the variability of Dmag-NOS2. In the 3249 bp of the ORF (1083 amino-acids), we found 65 variable sites (Table 2B), which is greater than that observed for Dmag-NOS1 ($\chi^2 = 12.10, \ p < 0.001$). Of these, 26 were non-synonymous mutations, among which 16 do not alter polarity (Table 2B). Again, no mutation in Dmag-NOS2 appears to explain the resistance variability observed among the German or Scottish clones. Overall, both NOS genes were found at relatively low constitutive levels in our Daphnia extracts: Dmag-NOS1 and Dmag-NOS2 expression levels are about half and 10% of actin expression, respectively (Fig. 4A and B, time 0). This is not surprising considering that NO is potentially toxic [1,2,4,5].

To gain a first indication if NOS and NO could be involved in resistance to pathogens in D. magna, we performed two infection experiments. In the first, we analysed expression of both NOS genes in D. magna individuals exposed to the pathogenic bacterium P. ramosa. Although these infections were successful [26], we found no statistically significant effect of exposure on the expression levels of either Dmag-NOS1 or Dmag-NOS2 (Fig. 4). This has been confirmed in recent replicates of this experiment (data not shown). Second, we simultaneously exposed hosts to P. ramosa and to a range of concentrations of L-arginine, the substrate of NOS and the limiting factor of its activity, and to two concentrations of L-NAME, which inhibits the NOS pathway. It has been shown in the mosquito A. stephensi and in the crayfish Procambrus clarkia that resistance to pathogens increased when host diet was supplemented in L-arginine [11,20], and we found a similar pattern in D. magna: the proportion of individuals infected with P. ramosa decreases with the quantity of L-arginine available (Fig. 5A), but increases with the addition of L-NAME, although this increase in only close to significance and appears to be relatively clone-dependent (Fig. 5B: GG15 does not exhibit the same trend as the other clones, which could be linked to the fact that this clone is generally more resistant to P. ramosa [27]). This observation is compatible with the hypothesis that at least one of the NOS genes functions to fight infection in D. magna, although our expression experiment indicates that this is unlikely to be attributable to increased expression levels. However, levels of NOS proteins may be different and could be examined in a further study. Alternatively the NOS RNA could be stable enough so that the translation is sufficient throughout the infection period.

Other studies have indicated that NOS expression is increased in the presence of pathogens (or LPS which mimics pathogen presence, e.g. [8,11,16,17,19,20]). The possible role of NO in the invertebrate immune response to pathogens is reinforced by evidence of pathogen adaptation to host NO production: some

Table 2 (Continued)

<table>
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<td>BelgiumD3</td>
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<td>Finnish</td>
<td>A G - - - - C G - - - A - - -</td>
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</table>

Amino-acid change

| A I K I K G S V C L S G K W V V A |
| E K E T T T S P I Y R P A M C M I P |
pathogens appear to actively move to tissues rich in NO-supportive proteins, while others induce the enzyme arginase, which competes with NOS for L-arginine substrate, thus inhibiting the host NO production [2].

In conclusion, we showed that two NOS genes are present in D. magna as the result of a relatively ancient gene duplication. The two NOS proteins differ in terms of expression level, polymorphism and divergence from the other arthropods. This could be explained by the specialization of the two proteins to different functions; NOS is implied in several disparate processes in invertebrates as well. If so, perhaps this ancient duplication is an example of neo- or subfunctionalization [50–52]. Ohno [50] first proposed that duplications provide new genetic material for evolution, as one copy may experience relaxed selective pressure. Often, new mutations will inactivate the new copy (leading to the creation of a pseudogene), but on rare occasions it could acquire a new function, i.e. neofunctionalization. Another model of evolution by duplication proposes that if a gene performs several functions (pleiotropy), a duplication may allow each daughter copy to specialize in a different subset of the original functions (subfunctionalization [53,54]; other models of evolution of duplication have been proposed, see for a review [55]). The rapid evolution of Dmag-NOS2 (see above and Fig. 2) led us to investigate whether this gene is subject to a host–pathogen arms race; however, the Dn/Ds values we observed do not support this. Further arguing against an arms race is the observation that Dmag-NOS2 has higher intraspecific variability than Dmag-NOS1 (arm-races cause selective sweeps, which diminishes polymorphism). Thus, NOS2 appears to experience relaxed selective pressure, but may be either acquiring new function or specializing on a subset of functions, potentially unrelated to immunity, while NOS1 assures that essential functions are still assumed. Whatever their mode of evolution, either or both of the NOS genes may still play a role in the immune response as indicated by our infection experiments and NO may yet have a role in resistance to P. ramosa.

Acknowledgments

We would like to thank Kirsten Ellegaard for technical assistance in the laboratory. This work was funded by a Wellcome Trust Senior Research Fellowship in Basic Biomedical Sciences to TLJ.

Appendix A. Supplementary data


References


