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Synthesizing and Salvaging NAD⁺: Lessons Learned from Chlamydomonas reinhardtii

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Abstract

The essential coenzyme nicotinamide adenine dinucleotide (NAD⁺) plays important roles in metabolic reactions and cell regulation in all organisms. Bacteria, fungi, plants, and animals use different pathways to synthesize NAD⁺. Our molecular and genetic data demonstrate that in the unicellular green alga Chlamydomonas NAD⁺ is synthesized from aspartate (de novo synthesis), as in plants, or nicotinamide, as in mammals (salvage synthesis). The de novo pathway requires five different enzymes: L-aspartate oxidase (ASO), quinolinate synthetase (QS), quinolate phosphoribosyltransferase (QPT), nicotinate/nicotinamide mononucleotide adenylyltransferase (NMNAT), and NAD⁺ synthetase (NS). Sequence similarity searches, gene isolation and sequencing of mutant loci indicate that mutations in each enzyme result in a nicotinamide-requiring mutant phenotype in the previously isolated nic mutants. We rescued the mutant phenotype by the introduction of BAC DNA (nic2-1 and nic3-1) or plasmids with cloned genes (nic1-1 and nic15-1) into the mutants. NMNAT, which is also in the de novo pathway, and nicotinamide phosphoribosyltransferase (NAMPT) constitute the nicotinamide-dependent salvage pathway. A mutation in NAMPT (npt1-1) has no obvious growth defect and is not nicotinamide-dependent. However, double mutant strains with the npt1-1 mutation and any of the nic mutations are inviable. When the de novo pathway is inactive, the salvage pathway is essential to Chlamydomonas for the synthesis of NAD⁺. A homolog of the human SIRT6-like gene, SRT2, is upregulated in the NS mutant, which shows a longer vegetative life span than wild-type cells. Our results suggest that Chlamydomonas is an excellent model system to study NAD⁺ metabolism and cell longevity.

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Introduction

The coenzyme nicotinamide adenine dinucleotide (NAD⁺) is an essential enzyme. Electron transfer between NAD⁺ and its reduced form NADH are essential to cells as they are involved in glycolysis and the citric acid cycle as well as regeneration of ATP from ADP [1]. NAD⁺ is consumed in several non-redox processes in cells [2] for review. NAD⁺ is a substrate of ADP-ribose transferase, which transfers ADP-ribose from NAD⁺ to ADP-ribose receptors, which are involved in DNA damage responses, transcriptional regulation, chromosome separation and apoptosis. NAD⁺ is also the target of ADP-ribose cyclases, which produce cyclic ADP-ribose that acts in second messenger signaling pathways. NAD⁺ is a substrate of sirtuins (SIRT/Sir2, Silent Information Regulator Two), a group of NAD⁺-dependent deacetylases that remove acetyl groups from lysine residues on histones, microtubules, and other proteins. Thus, NAD⁺, via sirtuins, modulates many events.

NAD⁺ synthesis pathways are categorized into either de novo pathways, which start with the amino acid aspartate or tryptophan, or salvage pathways, which start with nicotinamide (NAM) or nicotinic acid (NA) (Figure 1). Plants and some bacteria initiate de novo synthesis from aspartate and use two enzymes, L-aspartate oxidase (ASO) and quinolinate synthetase (QS), to synthesize quinoline (QA). Fungi, animals and some bacteria synthesize QA from tryptophan via six enzymes, tryptophan 2,3-dioxygenase (TDO)/indoleamine 2,3-dioxygenase (IDO), arylformamidase (AFMID), kynurenine 3-monooxygenase (KMO), kynureninase (KYNU), and 3-hydroxyanthranilate 3,4-dioxygenase (3HAO). The three enzymes shared by both de novo pathways, quinolinate phosphoribosyltransferase (QPT); nicotinate/nicotinamide mononucleotide adenylyltransferase (NMNAT); and NAD synthetase (NS), are required for the conversion of QA to NAD⁺.

In the salvage pathways, the starting substrate is usually NA or NAM (Figure 1). Fungi, plants, and most bacteria, use NAM in a 4-step process involving nicotinamide (NAMase), nicotinate phosphoribosyltransferase (NAPRT), NMNAT, and NS to synthesize NAD⁺. In C. elegans, this is the only known pathway to synthesize NAD⁺ [3]. On the other hand, in mammals and some bacteria, NAD⁺ is synthesized via a 2-step enzymatic process and the enzymes involved are nicotinamide phosphoribosyltransferase (NMPT) and NMNAT.

The consumption of NAD⁺ by sirtuin mediated-protein deacetylation results in the production of nicotinamide. Recent studies have linked SIRT proteins to transcriptional gene silencing [4],...
Author Summary

Nicotinamide adenine dinucleotide (NAD\(^+\)) is an essential coenzyme. NAD\(^+\) is necessary for electron transfer in many metabolic reactions. NAD\(^+\) functions as a substrate for several enzymes, one of which is sirtuin, an enzyme involved in gene regulation and aging. NAD\(^+\) can be synthesized either from amino acids (de novo) or metabolites (salvage). Given the importance of NAD\(^+\), enzymes involved in NAD\(^+\) synthesis are targets for drug discovery. In the unicellular green alga *Chlamydomonas* we investigated both the *de novo* and salvage NAD\(^+\) biosynthetic pathways. Mutations in the plant-like *de novo* synthesis pathway lead to a nicotinamide-requiring phenotype. We identified an insertion mutation in the first enzyme in the mammal-like salvage pathway; it has no growth defect in cells with an active *de novo* synthesis pathway but causes lethality when the *de novo* synthesis pathway is inactive. Coupled with NAD\(^+\) biosynthesis, sirtuin is involved in NAD\(^+\) consumption. Our study links upregulation of a sirtuin gene with extended life span in the *nic13-1* mutant strain, which has a defective *de novo* synthesis pathway and suggests that *Chlamydomonas* is an excellent genetic model to study NAD\(^+\) metabolism and cell longevity.

De novo synthesis pathways

Salvage synthesis pathways

**Figure 1. The biosynthetic pathways of nicotinamide adenine dinucleotide (NAD\(^+\)).** Enzymes that are present in *Chlamydomonas* are indicated in blue and enzymes that are absent are indicated in red. Green arrows indicate steps specific to the aspartate pathway; dark purple arrows indicate steps specific to the tryptophan pathway; gray arrows indicate steps specific to the 4-step pathway; orange arrows indicate steps specific to the 2-step pathway; black arrows indicate steps that are commonly shared by multiple pathways. Abbreviations: ASO, L-Aspartate oxidase; QS, Quinolinate synthetase; QPT, Quinolinate phosphoribosyltransferase; NAMAT, Niacinate/nicotinamide mononucleotide adenylyltransferase; NS, NAD\(^+\) synthetase; TDO, Tryptophan 2,3-dioxygenase; IDO: Indoleamine 2,3-dioxygenase; AFMID, Arylformamidase; KMO, Kynurenine 3-monooxygenase; KYNU, Kynurenase; 3HAO, 3-Hydroxyanthranilate 3,4-dioxygenase; NAMase, nicotinamidase; NAPRT, nicotinate phosphoribosyltransferase; SIRT, silent information regulator two. *Chlamydomonas* genes identified in this study are indicated in parentheses. doi:10.1371/journal.pgen.1001105.g001
A group of NAM-requiring mutants (nic) was isolated by Eversole that fail to grow well on medium lacking NAM [18]. The mutations also confer sensitivity to 3-acetylpyridine (3-AP) [19]. Eight NAM-requiring strains were originally isolated and six of these mutant strains are still extant. The NIC7 locus was identified in a walk through the mating-type locus and shown to encode a homolog of QS [20,21]. We tested whether the remaining NIC loci encode the enzymes of the de novo aspartate NAD+ synthesis pathway. The nic mutant loci define six different loci and map to six different linkage groups (LG) [19]: NIC1 maps to LG XV; NIC2 maps to LG II; NIC7 maps to LG VI; NIC11 maps to LG IV; NIC13 maps to LG X; and NIC15 maps to LG XII/XIII [20, 22–25; see Materials and Methods for linkage group to chromosome translation]. In our study, phenotypic characterization and genetic crosses of NIC11 strains obtained from the Chlamydomonas Center indicate that the Nic− phenotype of these nic11 strains (sensitivity to 3-AP or a growth defect on medium lacking NAM) can no longer be scored. Therefore, only five mutant strains are used in our study and we find that they encode the five enzymes in the de novo biosynthesis of NAD+ from aspartate.

Results

Chlamydomonas Nic− mutant phenotype can be rescued by addition of NAM

Wild-type (CC-124) and five different nic mutant cells (nic1-1, nic2-1, nic7-1, nic13-1, and nic15-1) were tested for their ability to utilize intermediate substrates in different NAD+ biosynthesis pathways (Figure 2). Wild-type cells show no obvious growth defect on any of the media tested. All the nic mutant strains fail to grow on Sager and Granick rich medium without NAM (R) or R medium supplemented with 3-AP, as previously described [19]. These mutants grow well on media supplied with either NAM or NMN, two chemical substances found only in the 2-step salvage biosynthesis pathway of NAD+. Addition of NA, an intermediate substrate found in the 4-step salvage pathway showed very weak rescue of the Nic− mutant phenotype of the mutants. Addition of 3-HA, which is synthesized in the tryptophan de novo pathway could not rescue the growth defect of any nic strains. NaAD, which acts in both de novo pathways, also does not rescue the Nic− mutant phenotype. The failure to rescue may indicate a failure of Chlamydomonas to transport these metabolites into cells.

3-AP is considered to be a NA analogue, which causes NA deficiency in mice. Injecting animals with NA, NAM, or tryptophan rescues the NA deficiency [26,27]. Given that 3-AP causes cell lethality in Chlamydomonas nic mutant cells, we tested whether addition of NAM or NA could rescue the phenotype. Addition of NAM showed weak rescue of the nic7-1 and nic15-1 mutants but not the other mutants (Figure 2). Addition of NA, NMN, NaAD, or 3-HA does not rescue the lethality conferred by 3-AP in any of the mutants.

De novo biosynthesis of NAD+ in Chlamydomonas resembles the pathway used by seed plants

Katoh et al. showed that Arabidopsis synthesizes NAD+ from aspartate and all five enzymes involved in this pathway have been characterized [28,29]. We identified the Chlamydomonas homologs by sequence similarity and linked the genes to corresponding nic mutants via DNA sequencing and complementation with transgenes. The results are summarized in Table 1.

Chlamydomonas ASO gene, which contains 4 exons and encodes a 669 aa protein (Figure 3A; [15]), is ~63 kb away from the ODA12 gene [30], which maps to LG XII/XIII [31]. The Chlamydomonas nic15-1 mutant is tightly linked to MAI1 on LGXII/XIII [22].

The nic15-1 strain (See Materials and Methods) contains a single nucleotide change C_{1376}T that predicts a S459F change in the predicted protein (Figure 3A). The S_{459}F change falls in a highly conserved region among bacterial and plant ASO proteins and is likely to affect normal function of this protein (Figure S1). We performed gene complementation with either a BAC [32L22] or a plasmid containing the full-length ASO gene (pNIC15a). Both transformations produced 3-AP-resistant colonies (n = 14 for the BAC and n = 24 for the plasmid), which indicates that Nic− mutant phenotype was rescued by re-introducing the ASO gene.

The nic7-1 mutant maps to a 7.9 kb region on LG VI. Transformation of this fragment rescues the 3-AP sensitive phenotype of nic7-1 cells, but the nature of this mutant and the gene structure of NIC7 were not determined [20]. Ferris et al. proposed that NIC7 encodes QS, given the NIC7 gene product displays low similarity to bacterial QS [21]. Using RT-PCR and DNA sequencing, we found that the NIC7 gene contains 15 exons and it shares 65% identity to Arabidopsis QS. Sequencing of the NIC7 coding region reveals a L_{453}Q change in the nic7-1 mutant (Figure 3A). The amino acid L_{453} within the quinolinate synthetase domain is conserved among almost all plant QS proteins but not in bacterial proteins (Figure S2).
Table 1. List of Chlamydomonas enzymes involved in de novo NAD⁺ biosynthesis from L-aspartate.

<table>
<thead>
<tr>
<th>EC number</th>
<th>Enzyme</th>
<th>BLAST protein</th>
<th>Chromosome</th>
<th>GenBank Accession number</th>
<th>Identity/similarity</th>
<th>Mutant</th>
<th>Mutation</th>
<th>Gene rescue</th>
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<tr>
<td>1.4.3.16</td>
<td>ASO</td>
<td>NP_568304</td>
<td>12</td>
<td>XP_001698664</td>
<td>51%/65%</td>
<td>nic15-1</td>
<td>S148F</td>
<td>BAC (n = 14) Plasmid (n = 24)</td>
</tr>
<tr>
<td>2.5.1.72</td>
<td>QS</td>
<td>NP_199832</td>
<td>6</td>
<td>HM061643</td>
<td>63%/80%</td>
<td>nic7-1</td>
<td>L351P</td>
<td>BAC and Plasmid</td>
</tr>
<tr>
<td>2.4.2.19</td>
<td>QPT</td>
<td>NP_973393</td>
<td>2</td>
<td>XP_001694961</td>
<td>55%/69%</td>
<td>nic2-1</td>
<td>Frame shift at 187, stop codon at 240</td>
<td>BAC (n = 8)</td>
</tr>
<tr>
<td>2.7.7.18/2.7.7.1</td>
<td>NMNAT</td>
<td>NP_200392</td>
<td>14</td>
<td>FJ944016</td>
<td>52%/68%</td>
<td>nic1-1</td>
<td>Q345H, Q346stop</td>
<td>BAC (n = 5) Plasmid (n = 2)</td>
</tr>
<tr>
<td>6.3.5.1</td>
<td>NS</td>
<td>At1g55090</td>
<td>10</td>
<td>FJ944017</td>
<td>52%/63%</td>
<td>nic13-1</td>
<td>S740D</td>
<td>Reversion analysis</td>
</tr>
</tbody>
</table>

Results from [20].
doi:10.1371/journal.pgen.1001105.t001

CN43, a DNA marker mapped to LG II [31] is ∼212kb from the Chlamydomonas QPT gene as determined by the JGI Chlamydomonas v4.0 genome assembly. The nic2-1 mutant maps to LG II [224]; M. Miller and S. K. Dutcher, unpublished observations). RT-PCR and sequencing of the QPT coding region in the nic2-1 mutant strain reveal a single nucleotide deletion at nucleotide 559 that leads to a frameshift. The amino acid sequence changes at Gly187 and generates a premature stop codon at amino acid 240 (Figure 3A; Figure S3). The mutant protein contains all the conserved QA-binding sites (Figure S3, blue reversed triangles) but the α-β-12 helices and β-1-2 helices were observed to form α/β barrel without the conserved bar. Transformation with a BAC clone (38P5) containing a full-length QPT gene yields 8 independent 3-AP-resistant colonies.

The Chlamydomonas NMNAT gene was predicted to contain 4 exons and encode a 234 aa protein [15]. However, RT-PCR, nested PCR and DNA sequencing shows the coding region of Chlamydomonas NMNAT is composed of only 2 exons that encodes a 524 aa protein, as predicted by the GreenGenie2 algorithm [33]. Sequence alignment reveals that Chlamydomonas NMNAT contains extra glycine/proline/glutamine-rich sequences compared to NMNAT from other organisms (Figure S4). The Chlamydomonas NMNAT gene is ∼262 kb away from the IDA2 gene [34] and maps to LG XV [31], near where the NIC1 gene maps [25]. Sequencing of the NMNAT genomic DNA from a nic1-1 strain indicates two adjacent nucleotide changes A1406G, C1407T result in S140F/R, C1407T result in F1407S. These nucleotide changes are likely to generate a truncated NMNAT in the nic1-1 mutant strain. The 3-AP-sensitive nic1-1 mutant phenotype is leaky and reverts at a low frequency of ∼1 spontaneous 3-AP-resistant colony per 10⁶ cells. Therefore, a co-transformation approach was used for gene complementation. BAC DNA (10M24) or plasmid DNA (pNIC1-56) containing the full-length NMNAT gene was co-transformed with a paromomycin-resistant gene (pREP8, [35]). A subset of the paromomycin-resistant colonies (5/20 for BAC and 2/2 for plasmid transformation) showed resistance to 3-AP.

The Chlamydomonas NS homolog maps between GP220 and GP441, which are two molecular markers on LG X [31], where nic1-1 maps [25]. RT-PCR and DNA sequencing from wild-type cells indicate this gene contains 20 exons that encode an 832 aa protein. The intron between exons 2 and 3 is unusually long (∼3.5 kb) for a Chlamydomonas gene (Figure 3A). Similar to Chlamydomonas NMNAT, Chlamydomonas NS contains extra sequences not found in other organisms. This insert is rich in alanine residues (Figure S5). The coding region of NS in nic13-1 was sequenced and a triple nucleotide substitution (TCC→ATT) is predicted to produce a S740D change (Figure 3A). The S740D is highly conserved among plants, green algae, and mammals (Figure S5). Further evidence that this point mutation is responsible for the mutant phenotype is provided by reversion analysis. We reasoned that a single base change of ATT (I) to AGT (S) would generate an I740S reversion. This change would also create a β6 site (TCTCAGTA), which is not present in either wild-type or nic13-1 cells (Figure 3B). Eighteen 3-AP-resistant colonies were isolated following UV mutagenesis of nic13-1 cells. Six of them contained a β6 site as monitored by PCR and restriction digestion of the product (Figure 3B). Of these, three revertants were randomly selected for sequencing. The ATT→AGT change was confirmed in all three selected revertants. The other 12 revertants were not analyzed. Transformation of nic13-1 cells with BAC (10H24) produced two 3-AP-resistant colonies and this provides further evidence that the mutation in NS is responsible for the nic13-1 mutant phenotype.

Salvage biosynthesis of NAD⁺ in Chlamydomonas uses the pathway found in mammals

Since Chlamydomonas nic mutants can utilize both NAM and NMN (Figure 2), two metabolites found in the 2-step salvage pathway, we propose that Chlamydomonas uses this pathway to synthesize NAD⁺. The 2-step salvage pathway utilizes two enzymes, NAMPT and NMNAT. A NAMPT homolog, which is ∼30% identical to human NAMPT, was identified via sequence similarity search (Figure S6). RT-PCR and DNA sequencing indicated the Chlamydomonas NAMPT gene (NP_711240, GenBank HM061641) contains 10 exons and encodes a 543 aa protein (Figure 4A) in CC-124 wild-type cells. However, we failed to amplify the full-length NPT1 transcript (∼2.2 kb) from another wild-type strain (CC-125) (Figure 4C). Further investigation using 3’ RACE and 5’ RACE shows that an insertion in exon 2 of the NPT1 gene is present in the CC-125 strain (Figure 4A, 4B). This region was partially sequenced and the inserted DNA sequence maps to multiple places in the genome and is likely to contain one or more transposable elements. The insertion causes two truncated NPT1 transcripts in the CC-125 strain. The first one is ∼0.6 kb long and contains the endogenous NPT1 promoter and ends within ∼100 bp of the inserted DNA (Figure 4A). It is predicted to contain an open reading frame (ORF), which encodes a 127 aa protein. This predicted protein contains the first 60 aa of the conserved phosphoribosyltransferase domain, which is ∼450 aa long. The second transcript is ∼1.8 kb long and starts with
130 bp of the inserted DNA (Figure 4A). This truncated transcript contains part of exon 2 and the rest of the gene and is predicted to contain an ORF encoding a 435 aa protein. The predicted protein lacks the first 65 aa of the conserved phosphoribosyltransferase domain. Thus, we conclude that the CC-125 strain carries a defective NPT1 and we name the allele *npt1-1* (nicotinamide phosphoribosyltransferase). All the nic mutants contain a full-length NPT1 transcript (Figure 4B, 4C).

Given that CC-124 and CC-125 strains are considered to be "wild-type" strains in the *Chlamydomonas* community, we tested whether any other wild-type strains contain this insertion. The CC-124 and CC-125 strains originated from the 137c zygotic isolate by Smith in 1945 [36]. The meiotic progeny from 137c was distributed to Sager in 1953 and to Ebersold in 1955. Four of the strains we tested, CC-1690 (21gr), CC-1691 (6145c), CC-407 (C8), and CC-408 (C9), originated from the Sager 1953 branch. The other three strains, CC-503 (*cw9* 2, used for the genomic sequence by JGI), CC-620 (R3), and CC-621 (NO), as well as CC-124 and CC-125, all came from the Ebersold branch. Genomic DNA PCR was used to identify the transposon insertion event while cDNA

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**Figure 3. Chlamydomonas nic mutants carry various point mutations in NIC genes.** (A) Schematic diagrams show the gene structures of NIC1, NIC2, NIC7, NIC13, NIC15 and the positions of mutations are indicated by asterisks. Blue solid box, exon; solid line, intron; dashed line, undefined length of intron. Each magenta box below the gene structure indicates changes in nucleotide/amino acid in the mutants when compared to the wild-type strain. Changes in codon that results in amino acid changes are highlighted in black. (B) PCR and enzymatic digestion to identify *nic13-1* revertant sequence from 18 *nic13-1* UV revertants. Top, nucleotide and amino acid sequences around the mutation points in various strains. The SfcI restriction enzyme recognition site is underlined in the *nic13-1* revertant sequence. Bottom, SfcI digestion products in various strains.

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PCR indicated the presence/absence of the *NPT1* transcript. Most of the strains have an intact *NPT1* gene (CC-407, 408, 503, 620, 1690, and 1691). The CC-621 strain (upper panel, Figure 4B) has an insertion in exon 2 of *NPT1*, but the insertional sequence is not identical to the CG-125 insertion since the PCR primers that recognize the insertion in CC-125 failed in CC-621 (lower panel, Figure 4B). As expected, the CC-621 strain also does not express the full-length *NPT1* transcript (Figure 4C). In contrast to the *nic* mutant strains, the *npt1-1* mutant strains, CC-125 (*npt1-1* and CC-621 (*npt1-2*), show no obvious growth defect on rich medium or medium supplied with 3-AP (Figure 2 and data not shown).

Sequence similarity searches indicate that *Chlamydomonas* does not contain four of the six enzymes required to synthesize NAD\(^+\) from the *de novo* tryptophan pathway and it is missing a homolog of NAPRT from the 4-step salvage pathway. *Chlamydomonas* has genes for the IDO and KMO enzymes in the tryptophan pathway and has a NAMase homolog in the 4-step salvage pathway. Given the apparent incompleteness of either of these two pathways, we hypothesized that *Chlamydomonas* is unable to synthesize NAD\(^+\) via the tryptophan pathway or the 4-step salvage pathway (Figure 1).

If the hypothesis that *Chlamydomonas* contains only the *de novo* aspartate pathway and the 2-step salvage pathway is correct, then double mutant strains containing the *npt1-1* mutation as well as one of the *nic* mutations should be lethal and fail to grow on medium supplied with NAM. Otherwise, if there were additional NAD\(^+\) synthesis pathways available, then *npt1-1; nic2-1* or *npt1-1; nic15-1* double mutants should survive on NAM medium. We performed crosses between the *nic* mutants and the *npt1-1* mutant strain. Genotypes of the meiotic progeny were scored based on their viability (*nic*) or inviability (*nic*) on medium containing 3-AP, and the presence (*npt1*) or absence (*NPT1*) of the *NPT1* transposon insertion, which was tested by genomic DNA PCR. The results are summarized in Table 2. Out of 198 viable progeny generated from 4 different crosses, no *npt1; nic* double mutants were recovered on NAM medium. Because addition of NMN rescued the *nic* mutants and it is downstream of the NAMPT catalyzed step, we expected that *npt1; nic* double mutants should be viable on medium supplied with NMN. However, we found that no *npt1; nic* double mutants were isolated out of 148 viable progeny on NMN medium. One potential cause may be the hydrolysis or inefficient uptake of NMN by meiotic progeny compared to vegetative cells. Alternatively, the *NCP* message may not be expressed in meiotic progeny (Figure 2). Thus, based on the results from these genetic crosses between the *nic* mutants and the *npt1-1* mutant, we conclude that *Chlamydomonas* synthesizes NAD\(^+\) via the *de novo* aspartate pathway and the 2-step salvage pathway and it is very unlikely that there is additional NAD\(^+\) biosynthesis pathway.

Transcriptional regulation among genes involved in the NAD\(^+\) biosynthesis pathways

Previous studies on bacterial and mammalian NAD\(^+\) biosynthesis indicate that transcriptional regulation among genes involved in the pathways is common. In *Escherichia coli* and *Salmonella enterica*, expression of *nadB* (encodes ASO) and *nadA* (encodes QS) is regulated by *nadR*, which has NMNAT activity [37,38]. In mammals, the circadian expression of *NAMPT* is

**Figure 4.** *Chlamydomonas* strain CC-125 contains an insertion in the NAMPT gene. (A) Schematic diagram shows gene structure of the *Chlamydomonas* NAMPT gene. An insertion in exon 2 in the *npt1-1* mutant strain is indicted by an orange arrow. Blue solid box, exon; black solid line, intron; green solid box, 5' UTR; gray solid box, 3' UTR; magenta and red solid boxes, sequences from the putative transposon(s); hatched boxes, incomplete regions of exon 2. (B) PCR amplification of *NPT1* genomic DNA around the insertional region. Upper panel, primers spanning the insertional point can amplify the wild-type *NPT1* but not *NPT1* with an insert. Lower panel, one primer binds to the inserted sequence while the other binds to *NPT1*. Thus only *NPT1* with the specific inserted sequence can be amplified. (C) RT-PCR amplification of the whole coding region of *NPT1*. L27a, a ribosomal protein gene serves as a control [84]. Control, no DNA template was added in PCR.

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Table 2. Progeny analysis from crosses between npt1-1 and nic mutant strains.

<table>
<thead>
<tr>
<th>Genotypes of meiotic progeny analyzed from npt1-1 x nic</th>
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<th>nic2-1</th>
<th>nic13-1</th>
<th>nic15-1</th>
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<tbody>
<tr>
<td>R+NM Medium</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NIC; NPT1</td>
<td>6</td>
<td>27</td>
<td>8</td>
<td>27</td>
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<td>NIC; npt1</td>
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doi:10.1371/journal.pgen.1001105.t002

Overall, gene expression of the NIC, NPT1 and SRT2 genes shows complicate patterns. No single gene is upregulated or downregulated in all mutants and no single mutant shows clear upregulation or downregulation of all genes involved in a pathway. This result suggests that in addition to regulation at the transcription level, NAD⁺ biosynthesis may be regulated post-transcriptionally.

The link between NAD⁺ biosynthesis in Chlamydomonas and longevity

In studies of yeast, worms, and mammals, upregulation of NAD⁺-dependent histone deacetylase Sir2/SIRT1 is correlated to longevity [40,41]. In rice, RNA interference of OsSRT1 leads to DNA fragmentation and programmed cell death [42]. We wanted to test if Sir2 homologs play a similar role in algae. A sequence similarity search using SIR or SIRT proteins finds two proteins in Chlamydomonas. We named the one most to similar to yeast Sir2 protein SRT2. RT-PCR and sequencing show that the Chlamydomonas SRT2 gene contains 9 exons (Figure 6A) and encodes a 320 aa protein (GenBank HM061642). Sequence alignment (Figure S7) shows that this protein contains the NAD-dependent catalytic core domain and is closely related to human SIRT6, SIRT7, and plant SRT proteins, which are class IV SIRT proteins. The second Sir2-like gene, SRT1, is most similar to human SIRT4 [11], which is a mitochondrial protein. This gene encodes a 399 aa protein (GenBank HM161714) and belongs to the class II sirtuin family (Figure 6A and Figure S7).

Since Sir2-like proteins are involved in the enzymatic step of converting NAD⁺ to NAM, which is the substrate of NAMPT [39]. To investigate whether transcriptional regulation among the NIC genes and NPT1 exists in Chlamydomonas, we measured transcript levels of these genes in nic and npt1-1 mutants by quantitative real-time RT-PCR (qRT-PCR, Figure 5). Changes were not considered significant unless a gene is >2-fold upregulated or <2-fold downregulated when compared to its expression level in wild-type cells.

The first step in the de novo aspartate pathway, which is rate limiting in bacteria, is catalyzed by ASO, encoded by NIC15. As expected, mutations in the downstream enzymes (nic1-1, nic2-1, and nic13-1) result in reduced NIC15 transcript while the npt1-1 mutation causes a 2-fold elevation in NIC15 transcript level. The NIC7 transcript level was not affected in any of the mutants tested. NIC2 and NIC13 transcript levels are upregulated in the npt1-1 mutant and in all the nic mutants except nic2-1. The NIC1 transcript level is upregulated in the nic mutants but not in npt1. Finally, the expression level of NPT1 is only upregulated in the nic15-1 mutant strain.

Figure 5. Gene expression in wild-type, npt1-1, and nic mutant cells. Relative real-time RT-PCR was used to detect transcripts. Results represent 2 biological replicates and standard errors are indicated by error bars.
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As shown by Dutcher and Trabuco, biflagellate cells are only produced by uni3-1 cells that have undergone at least two cell divisions [43]. Aflagellate cells never produce biflagellate daughters, but a uniflagellate or biflagellate uni3-1 cell produces one aflagellate daughter cell and one biflagellate daughter cell. We suggest that the biflagellate cell is the equivalent of using the mother cell in budding yeast as a marker of generational age. Having two flagella allows a cell to swim effectively to the air-liquid interface of the medium, while an aflagellate or uniflagellate daughter cell sinks to the bottom of the culture tube. The biflagellate daughter cells can then be transferred to a new test tube and of the number of generations that the uni3-1 cells undergoes can be monitored (Figure 6C). As illustrated in Figure 6D, NIC13; uni3-1 biflagellate cells complete 38–40 cell cycles. On the other hand, nic13; uni3-1 cells complete 48–50 cell cycles. This represents a ~25% increase in reproductive capacity. We assayed a nic2-1; uni3-1 strain since it does not have increased SRT2 levels but has a synthesis defect and found that it completed 37 cell cycles like wild-type cells (data not shown). Therefore, we conclude that NAD+ biosynthesis in Chlamydomonas can affect life span and this might be achieved by alternating the expression level of Chlamydomonas SRT2.
Discussion

The essential roles of NAD⁺ in many metabolic oxidation-reduction reactions are well established. Recent studies link its function to transcriptional regulation [44], epigenetic regulation [45], longevity [2], cell death [46], neurogeneration [47], circadian clocks [48], and signal transduction [49]. Understanding its biosynthetic pathways will facilitate understanding of lifespan extension [50], disease regulation [51], drug design [52], as well as evolution [53].

Recent studies on NAD⁺ biosynthesis indicate that pathways in different organisms are more diverse than expected. The tryptophan pathway, which was thought to be eukaryotic specific, was identified in several bacteria [54]. The aspartate pathway, which was considered only prokaryotic, is present and essential to Arabidopsis thaliana [28]. An organism may contain all the enzymes required for more than one pathway, but a single pathway is predominantly used. Bacillus subtilis can synthesize NAD⁺ via aspartate or the 4-step pathway but only genes involved in the conversion from NA to NAD⁺ are indispensable [53]. Arabidopsis thaliana contains the aspartate pathway and the 4-step pathway. However, homozygous ASO and QS mutants, which specifically affect the aspartate pathway, are inviable [28]. In mammals, the enzyme NAMPT, which is the rate-limiting enzyme in the 2-step pathway, is essential even though organisms harbor all the enzymes required to synthesize NAD⁺ from tryptophan [56]. However, in D. melanogaster and C. elegans, there is only one pathway. The de novo NAD⁺ synthesis pathway is incomplete and they rely on the NAMase-dependent salvage pathway to synthesize NAD⁺ [53].

Our study indicates that Chlamydomonas can synthesize NAD⁺ via the aspartate pathway, which is found in land plants and bacteria, or the 2-step salvage pathway, which is found in mammals. This combination in Chlamydomonas makes it a great model for the study of NAD⁺ biosynthesis. Similar to Arabidopsis, Chlamydomonas contains one copy of each gene that encodes the de novo pathway enzymes and the Chlamydomonas proteins are 51%–63% identical to Arabidopsis homologs. However, unlike Arabidopsis mutants, which are lethal when homozygous [28,57], the Chlamydomonas nic mutants show conditional lethality as they are rescued by the addition of NAM or NMN to the medium. Thus, the effects of loss of function mutations, which can not be studied in Arabidopsis, can be easily analyzed in Chlamydomonas. In mammals, NAMPT is essential. It is encoded by three different genes and the proteins localize to different cellular compartments. In addition, mammal NAMPT has an extracellular form; both intracellular (iNAMPT) and extracellular (eNAMPT) forms are involved in NAD⁺ synthesis and in regulation of insulin secretion in pancreatic β cells [58]. Chlamydomonas contains only one copy of NAMPT (NPT1). The npt1-1 mutant has no growth defect but none of the nic; npt1-1 double mutants are viable (Table 2). Since Chlamydomonas cells are haploid and easy to maintain, this mutant provides an alternative for screening for NAMPT-blocking drugs. The potential drugs would have no effect on wild-type cells but would be lethal to nic cells.

In mammals 3-AP acts as an analog of nicotinic acid and inhibits the 4-step salvage pathway. In Chlamydomonas, 3-AP prevents the rescue of nic mutants by NMN and greatly suppresses the rescue by NAM. The easiest explanation for these results would be that Chlamydomonas has the 4-step salvage pathway and it is active. However, the Chlamydomonas genome has only three of the four enzymes; the genome assembly is missing the key enzyme, NAPRT. It remains a possibility that Chlamydomonas has a NAPRT gene, but it is not present in the assembled genome sequence. Two lines of evidence suggest that a functional NAPRT is not likely to be present in Chlamydomonas. First, using 40 million Illumina transcriptome reads (1.2 Gb of sequence) from three independent mRNA preparations, we find evidence for transcription of the first 45 amino acids of NAPRT using a splice aware assembly algorithm, but find no evidence for the transcription of the rest of the gene that contains all of the known active sites needed for function [59,60] (unpublished data). Given the high identity of this protein from microalgae to mammals, it is likely either that the rest of the Chlamydomonas NAPRT gene was lost or the gene is not transcribed beyond the first 135 bps of the open reading frame. Second, the genome sequence of Volvox carteri (http://genome.jgi-psf.org/Volca1/Volca1.home.html), a multicellular green alga that shared a common ancestor with Chlamydomonas around 35 million years ago [61], also lacks NAPRT. Therefore, we suggest that Chlamydomonas cells do not have a functional copy of NAPRT. It remains an open possibility whether an alternative enzyme without sequence similarity exists in Chlamydomonas.

Our study on Chlamydomonas also provides important insights into the evolution of NAD⁺ biosynthesis (Figure 7). Through sequence similarity searches, we find that Volvox contains enzymes required for the aspartate de novo pathway and the 2-step salvage pathway. Given the common ancestor, it is not surprising that both of them contain NAMPT, the enzyme that is unique to the 2-step pathway. Two unicellular green microalgae, Ostreococcus lucimarinus and Ostreococcus tauri [62,63], contain enzymes required for the aspartate de novo pathway and the 4-step salvage pathway. Ostreococcus are believed to have diverged from Chlamydomonas around 750 million years ago, ~250 million years after the separation of chlorophytes (green algae) and streptophytes (seed plants) [64]. The unicellular chaoanoflagellate Monosiga brevisalis, which is considered the progenitor to animals and separated from other metazoans more than 600 million years ago [65], has enzymes found in the tryptophan pathway and the 2-step pathway, as in animals. Chlamydomonas, which has remnants of four pathways, may suggest that an ancestral organism had multiple pathways and that most organisms have retained only a subset.

In Arabidopsis, the first three enzymes, ASO, QS, and QPT, are localized to chloroplasts. It is currently unclear where the other two proteins, NMNAT and QS, are localized. When we used Predotar [66] and TargetP [67] for Chlamydomonas protein localization prediction, ASO, QS, and NS are predicted to localize to mitochondria by both programs. NMNAT is predicted to be in the mitochondria by TargetP while Predotar gives no specific location. The localization of QPT is unspecified by either program. The actual localization of Chlamydomonas proteins will require experimental determination. If all Arabidopsis enzymes are localized to chloroplasts while all Chlamydomonas enzymes are not, it would suggest that having NAD⁺ biosynthesis in plastids happened after the separation of green algae and seed plants.

As illustrated in Figure 1, NMNAT is an essential enzyme utilized by all NAD⁺ biosynthetic pathways. We observed that NIC1 has a low basal expression level in wild-type cells compared to the other NIC genes, but is upregulated 2–6 fold in various nic mutants. This upregulation is consistent with the hypothesis that NMNAT is the key enzyme involved in all NAD⁺ biosynthetic pathways and any mutation along the pathway affects the expression of NIC1 significantly. The nonsense mutation found in nic1-1 cells presumably generates a truncated protein that must be partially functional as we would expect that a null mutant would disrupt both pathways and be lethal like the double nic; npt1-1 mutant strains. The truncated protein has the catalytic motif residue H30 but only one of two substrate binding motif residues (W98 and not R224) [68,69].
Figure 7. NAD$^+$ biosynthesis in Chlamydomonas reveals evolutionary aspects. Evolutionary distances between different organisms are indicated on the left. Branch lengths are not to scale. Chlamydomonas reinhardtii and Volvox carteri are indicated in bold letters. Filled dots indicate the presence of a trait in organisms and open dots indicate absence. Traits found in photosynthetic organisms are indicated in green and traits associated primarily with the animal lineage are indicated in magenta. The distinct traits of NAD$^+$ biosynthesis in Chlamydomonas and Volvox are highlighted in the orange box. 2-step, 2-step salvage pathway of NAD$^+$ biosynthesis; 4-step, 4-step salvage pathway of NAD$^+$ biosynthesis; Asp, de novo biosynthesis of NAD$^+$ from aspartic acid; Trp, de novo biosynthesis of NAD$^+$ from tryptophan.

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Through our sequence similarity search, only two of the six homologs in the de novo synthesis pathway starting from tryptophan were identified. Previously, nic1-1 and nic4 mutants were reported to grow on medium supplemented with 3-HA, a metabolite produced in the tryptophan pathway [18]. We find that the growth defect of nic1-1 cannot be rescued by the addition of 3-HA (Figure 1) and this agrees with our finding that NCI1 encodes NMNAT, which acts downstream of 3-HA. In addition, 3-HAO, the enzyme that uses 3-HA as a substrate, is not present in the Chlamydomonas genome sequence. The nic4 mutant is no longer existent in the Chlamydomonas strain collection and was never mapped ([19], www.chlamydb.html). Therefore, we are unable to test its grow ability on medium provided with 3-HA. Similar to our finding, 3-HA and other intermediates found in the tryptophan pathway fail to rescue nicotinamide requiring mutants in Chlamydomonas eugametos [70]. Recent studies indicate that nicotinamide riboside (NR) and nicotinic acid riboside (NaR) are NAD$^+$ precursors in yeast and mammalian cells [71–73]. Enzymes involved in the NR and NaR salvage pathways include nicotinamide riboside kinase (NRK1), purine nucleoside phosphorylase (PNP1), uridine hydrolase (URH1), and methylthioadenosine phosphorylase (MEU1). Similarity searches using yeast protein sequences identified only one PNP1-like protein in Chlamydomonas. In addition, 3-HAO, which acts downstream of 3-HA, was identified. Previously, NMNAT, which acts downstream of 3-HA. In addition, 3-HAO, which acts downstream of 3-HA, was identified. Therefore, we are unable to test its grow ability on medium provided with 3-HA. Similar to our finding, 3-HA and other intermediates found in the tryptophan pathway fail to rescue nicotinamide requiring mutants in Chlamydomonas eugametos [70]. Recent studies indicate that nicotinamide riboside (NR) and nicotinic acid riboside (NaR) are NAD$^+$ precursors in yeast and mammalian cells [71–73]. Enzymes involved in the NR and NaR salvage pathways include nicotinamide riboside kinase (NRK1), purine nucleoside phosphorylase (PNP1), uridine hydrolase (URH1), and methylthioadenosine phosphorylase (MEU1). Similarity searches using yeast protein sequences identified only one PNP1-like protein in Chlamydomonas, but none of the other proteins. Thus, it is unlikely that Chlamydomonas contains the NR/NaR salvage pathway.

In the study of longevity, several model organisms (S. cerevisiae, D. melanogaster, and mouse) have been widely used. Caloric restriction leads to extended life span in these organisms, but the mechanisms behind these findings are not well understood. Studies indicate that caloric restriction-mediated longevity links to upregulation of Sir2 in yeast [41,74], flies [75], and mammals [76] but is independent of Sir2 expression in worms [77]. However, increasing the dosage of Sir2 in C. elegans leads to longer life span [40]. Our observation that mutant cells with a longer life span have increased Sir2 expression suggests a link between Chlamydomonas Sir2-like genes and longevity. It is intriguing that only the nic13-1 mutant strain has increased levels of Sir2. Since nic13-1 mutants should have increased levels of the intermediate, NaAD, we attempted to ask if exogenous NaAD altered Sir2 levels. Exogenous NaAD failed to rescue upstream mutants, which suggests that it was not effectively imported into cells (Figure 2).

We assayed replicative aging in Chlamydomonas using centriole or basal body age as our marker. In the wild-type populations, the biflagellate cells contain a grandmother centriole (at least three cell cycles old) and a daughter centriole. We can recover biflagellate cells by virtue of their ability to swim. The cells that are biflagellate represent the oldest cells in the population. We find that wild-type cells fail to divide after 38–40 generations while the nic13-1 mutant continues for at least 10 more cell divisions. We suggest that this aging may include aging of the centrioles. Recent studies on fruit fly germline stem cells [78] and mouse neural progenitor cells [79] indicate that the mother centriole stays with the self-renewing daughter stem cell while the daughter centriole goes with the differentiating daughter cell. As cells age, misorientation of centrioles accumulates and eventually causes cell cycle delay or arrest in mouse neural progenitor cells. Using Chlamydomonas as a model system to study aging, we can further pursue the link between NAD$^+$ metabolism, Sir2-like genes, and centriole aging. Whether overexpression of Sir2 in Chlamydomonas causes extended life span as shown in other organisms needs additional experimentation.

A recent study on mammalian SIRT1 indicates that it is involved in regulation of circadian rhythm via transcriptional regulation of several key genes [80]. It is currently unclear whether other SIRT proteins have similar effect on circadian rhythm. Given that synchronous Chlamydomonas cell culture can be easily achieved by alternating light/dark cycles, we foresee Chlamydomonas as a model to explore the effect of SIRT2 (SIRT6-like) and SIRT1 (SIRT4-like) on circadian rhythms [81].

In conclusion, the results presented in this work underscore several key advantages of using Chlamydomonas as a model system for further studies of NAD$^+$ metabolism. The Chlamydomonas genome contains a single copy of each of the proteins that make up the plant-specific de novo NAD$^+$ biosynthesis pathway. However, unlike Arabidopsis, which is homozygous lethal for the first three enzymes, all five Chlamydomonas mutants show conditional lethality. Consequently, Chlamydomonas will facilitate future studies on
metabolites involved in NAD⁺ biosynthesis. *Chlamydomonas* also contains a single copy of the genes in the mammal-specific 2-step NAD⁺ salvage pathway. The fact that mammals contain multiple isoforms of NAMPT and that this enzyme is essential to viability impede NAMPT-blocking drug studies in mammal-based model systems. As such, NAMPT targeted drug screens using *Chlamydo-
monas* avoid the many confounding factors that are inherent in current screening methods. Our centriole aging results demonstrate how *Chlamydomonas* may be a valuable model organism for future studies in cellular and organelle aging.

**Materials and Methods**

*Chlamydomonas* strains and spotting assay

*Chlamydomonas reinhardtii* strains, CC-14 (*nic15-1; mtε*), CC-124 (*mt−*), CC-125 (*mtδ*), CC-407 (*C8, mtε*), CC-408 (*C9, mt−*), CC-503 (*ac92; mtε*), CC-599 (*nic1-1; mtε*), CC-620 (*R3, mtε*), CC-621 (*NO, mt−*), CC-864 (*nic13-1; mtε*), CC-1079 (*ac12; th9; nic2-1; mtε*), CC-1690 (*21gr, mt−*), CC-1691 (*614εc, mt−*), and CC-3657 (*nic2-1; mtε*), were obtained from *Chlamydomonas* Center (Duke University) and maintained on solid rich growth (R) medium [82] containing 15 mM nicotinic acid (NA, dissolved in water), nicotinamide mononucleotide (NMN, dissolved in water), 10 mM nicotinate adenine dinucleotide (NaAD, dissolved in water), hydroxyanthranilate (3-HA, dissolved in DMSO). The plates were ed with one of the following compounds: 10 mM DTT, 0.5 mM dNTP, 0.2 μM primer, 40 U of RNase-OUT (Invitrogen), and 200 U of SuperScript II reverse transcriptase (Invitrogen). The reaction was performed according to manufacturer’s recommendation (Invitrogen). To remove RNA from the reaction, 2 units of RNase H (Invitrogen) were added at the end of reaction and incubated at 37 °C for 20 min.

Amplification of the NAMPT coding region requires nested PCR due to highly repetitive sequences found in the gene. Five μl cDNA (1/10 of the reaction volume) from above was used in a 50 μl PCR reaction using a 3′ RACE primer and a gene-specific primer (nic-1-3) that binds 4 nucleotides downstream of the predicted start codon. The reaction, which contained 1× KlentaqLA buffer (pH 9.2), 0.8 mM dNTP, 10% DMSO, 1 mM MgCl₂, 0.5 μl KlentaqLA polymerase [83], was transferred directly from ice to a thermocycler (Bio-Rad, Hercules, CA) that was preheated to 93°C. The reaction conditions were: 93°C 5 min, 30 cycles of (93°C 15 sec, 53°C 15 sec, and 68°C 5 min), and 70°C 10 min. The resultant 2.2 kb fragment was used as template for a second round of amplification. A forward primer (nic1-20) that starts 98 nucleotides downstream of the predicted start codon and a reverse primer (nic-1-24) that ends at the predicted stop codon were used. The resultant fragment was gel purified and subjected to DNA sequencing.

For amplification of other genes, 1 μl cDNA was used in a 20 μl PCR reaction containing 0.4 U Phusion DNA polymerase (Finnzymes, Woburn, MA), 1× GC buffer (Finnzymes), 0.2 mM dNTP, 3% DMSO, and 0.2 μM each of forward and reverse primers. The general reaction condition was 98°C 30 sec, 30 cycles of (98°C 10 sec, 72°C 20 sec, and 72°C 30–45 sec), and 72°C 10 min. T is the lower Tm of the primers calculated by the Finnzymes’ Tm calculator. Different sets of primers were used to cover the whole coding region of individual genes. The PCR products were subjected to gel purification and DNA sequencing to identify exon-intron boundaries.

**Identification of Chlamydomonas homologs via sequence similarity search**

Protein sequences of *Arabidopsis thaliana* ASO, QS, QPT, NMNAT, NS (listed in Table 1), human NAMPT (NP_005737), yeast SIR2 (NP_010242), and human SIRT4 (NP_036372) were used in TBLASTN against JGI [Joint Genome Institute] *Chlamydo-
monas reinhardtii* genome version 4.0 [JGI v4.0, http://genome.jgi-psf.org/Chlre4/Chlre4.home.html] with expected E-values less than or equal to 1E-5 (1E-3 for SIR2 and SIRT4). The resultant genes were checked for EST coverage. Genes without full-length EST coverage, *QS, NMNAT, NS, NAMPT, SRT1*, and *SRT2*, were subjected to exon-intron predictions using GreenGenie 2 [http://bifrost.wustl.edu/cgi-bin/greenlegen2/greenlegen2] [33]. The predicted coding regions were used as guidelines in primer design for RT-PCR to amplify the actual coding regions of these genes.

**Chlamydomonas NAD⁺ Biosynthesis**

Amplification of coding regions by RT-PCR

*Chlamydomonas* total RNA was prepared as previously described [84]. Five μg of total RNA from wild-type cells were used for cDNA synthesis using a 3′ RACE poly (dT)-adapter primer (Integrated DNA Technologies, Iowa City, IA) in a 30 μl reaction, which contains 1× RT buffer (Invitrogen, San Diego, CA), 10 mM DTT, 0.5 mM dNTP, 0.2 μM primer, 40 U of RNase-OUT (Invitrogen), and 200 U of SuperScript II reverse transcriptase (Invitrogen). The reaction was performed according to manufacturer’s recommendation (Invitrogen). To remove RNA from the reaction, 2 units of RNase H (Invitrogen) were added at the end of reaction and incubated at 37°C for 20 min.

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For amplification of other genes, 1 μl cDNA was used in a 20 μl PCR reaction containing 0.4 U Phusion DNA polymerase (Finnzymes, Woburn, MA), 1× GC buffer (Finnzymes), 0.2 mM dNTP, 3% DMSO, and 0.2 μM each of forward and reverse primers. The general reaction condition was 98°C 30 sec, 30 cycles of (98°C 10 sec, 72°C 20 sec, and 72°C 30–45 sec), and 72°C 10 min. T is the lower Tm of the primers calculated by Finnzymes’ Tm calculator. Different sets of primers were used to cover the whole coding region of individual genes. The PCR products were subjected to gel purification and DNA sequencing to identify exon-intron boundaries.

**Colorfy for protein sequence alignment**

Multiple sequence alignments (MSA) were color-coded using the online MSA column percentage composition coloring tool, Colorfy [http://bifrost.wustl.edu/colorfy]. Colorfy takes as input any standard ALN format MSA (e.g. default CLUSTAL output) [93] and outputs the corresponding color-coded MSA.
DNA was dried using Savant SpeedVac (Thermo Scientific, Waltham, MA) and resuspended in 50 μl water. The concentration of DNA was determined by spectrophotometry at 260 nm (Eppendorf Biophotometer 6131, Westbury, NY). Approximately 20 ng of genomic DNA was used in PCR and the resultant PCR products were gel-purified and subjected to DNA sequencing. In the nic1-1 cells, the region that carries mutations was amplified by the primer set nic1-10 and nic1-11. In the nic15-1 cells, the region that contains a point mutation was amplified by nic15-3F and nic15-3R.

BAC and plasmid DNA manipulation

*Chlamydomonas* BAC DNA was prepared using Qiagen Plasmid MidiPrep kit. To prepare the pNIC15a plasmid, the BAC (32L22) DNA was digested with *Xmn*I and a 6.1 kb fragment was isolated and cloned into a pBlueScript II SK vector (Stratagene, La Jolla, CA). This fragment contains a 1 kb upstream sequence, the full-length *NIC15* gene, and a 2.5 kb downstream sequence, which is predicted to be part of an unknown zinc finger protein (protein id 150664). To prepare the pNIC1-56 plasmid, a 7.1 kb Km fragment from the BAC (10M24) DNA was cloned into a pBlueScript II SK vector. The plasmid contains a 0.7 kb upstream sequence, the full-length *NIC1* gene, and a 4.7 kb downstream sequence, which is predicted to contain an unknown protein that has a HAD-superfamily hydrolase domain.

*Chlamydomonas* transformation

This protocol is modified from Iomini et al [87]. *Chlamydomonas* cells were inoculated in 100 ml liquid R medium for three days under continuous illumination with gentle shaking until cells reached a concentration of ~5×10^8 cells/ml. Cells were collected by centrifugation at 4°C. Cells were gently resuspended on ice in R+100 mM mannitol to the final concentration of ~4×10^8 cells/ml. Two hundred fifty μl of cells (~1×10^8 cells) were used for transformation with 1 μg of BAC DNA or plasmid DNA with the (nic-1 strain) or without (the nic15-1, nic2-1, and nic13-1 strains) the addition of 1 μg of pSI103, which confers resistance to paromomycin [53], for cotransformation. Cells and DNA were added to an electroporation cuvette (4mm gap, Bio-Rad) and incubated in a 16°C water bath for 5 min before electroporation, which was performed in a Bio-Rad Gene Pulser II with the following setting: 0.75 kv, 25 μF, and 50 Ω. Cells were electroporated with one pulse and incubated at room temperature for 10 min before transferring to 50 ml R+100 mM mannitol liquid medium and incubated overnight at room temperature with continuous illumination. Cells were resuspended gently in 1 ml 25% cornstarch in R medium and spread onto 5 R plates with 15 μl/1 3-AP (nic15-1, nic2-1, and nic13-1 strains) or 5 R plates with 10 μg/ml paromomycin (nic1-1 cells). Colonies appear within 5–7 days at 25°C. The nic1-1 transformants were tested subsequently on medium with 3-AP.

UV-mutagenesis of the nic13-1 cells

nic13-1 cells were inoculated in 200 ml liquid R medium provided with 16 μM NAM for 4 days until cells reached a density of ~10^9 cells/ml. These cells were collected and spread evenly on an R+NAM medium plate. The cells were subjected to UV irradiation at 70 mJoules (Stratagene UV stratalinker 1800, Cedar Creek, TX) and recovered in the dark overnight. The plate was divided into 13 sections and cells were scraped off the plate and spread on 13 R+3-AP plates. 3-AP resistant colonies were observed one week later. Genomic DNA from individual cell lines, wild-type, and nic13-1 cells were prepared as above and a short region was amplified by primers nic13-20F and nic13-3R by Phusion DNA polymerase. The PCR products were subjected to overnight digestion with *Sfi*I at 25°C and separated on a 2% agarose gel.

Real-time RT-PCR

*Chlamydomonas* total RNA was extracted from ~10^6 cells using Qiagen RNAeasy Mini Kit (Qiagen, Valencia, CA). Cells were homogenized by passing through a 20-gauge needle fitted to a 1 ml RNase-free syringe 20 times. The lysate was centrifuged and RNA extraction was performed according to manufacturer’s recommendation. One microgram of total RNA from each strain was treated with 1 U of RNase-free DNase I (Fermentas, Glen Burnie, MD) at 37°C for 30 min and the reaction was terminated by adding 1 μl of 25 mM EDTA and incubating at 65°C for 10 min. The DNase I-treated RNA was added into a 20 μl reverse transcription reaction that contains 200 ng random primers (Invitrogen), 1× RT buffer (Invitrogen), 5 mM DTT, 0.5 mM dNTP, 20 U of RNaseOUT (Invitrogen), and 100 U of SuperScript III reverse transcriptase (Invitrogen). The reaction was performed according to manufacturer’s recommendation (Invitrogen).

For real-time PCR, cDNA obtained from above was diluted 1:10 and 2 μl was used in a 20 μl SYBR Green-PCR reaction [88] which contains 1× homemade PCR buffer (10 mM Tris-HCl, pH8.8, 50 mM KCl, 2 mM MgCl2; 0.1% Triton X-100; 1× SYBR Green I mix (1× SYBR Green, Molecular Probes); 10 nM Fluorescein, Bio-Rad; 0.1% Tween-20; 0.1 mg/ml BSA; 5% DMSO); 200 μM dNTP; 0.5 μM primers; and 1.6 μl TAQ DNA polymerase [89]. The reactions were carried out using a Bio-Rad iCycler iQ under the following conditions: 95°C 3 min, 40 cycles of (95°C 10 sec and 57°C 45 sec), followed by the melting curve program. The transcript levels of individual genes were standardized by an internal control, *CRT1*, which encodes the ribosomal protein S14 [90]. Gene expression was set to 100% in wild-type cells and the relative expression levels in various mutants were plotted as % increasing or decreasing related to transcript levels in wild-type cells. Results represent data from 2 biological replicates.

**Chlamydomonas** aging

nic13-1 cells were crossed to uni3-1 (CC4179) cells and the nic13-1; uni3-1 double mutants were identified by 3-AP sensitivity and the presence of cells with 0, 1, or 2 flagella. Both *NIC13; uni3-1* and *nic13-1; uni3-1* cells were inoculated in 20 ml liquid R medium supplied with 16 μM NAM. The top 5 ml of liquid was transferred to a new test tube containing R+NAM every 12 hours. ~100 cells were plated on R+NAM plates and the fraction of cells that formed colonies was counted under dissecting microscope after 8–10 days.

**Supporting Information**

**Figure S1** The nic13-1 mutant strain has a missense mutation in aspartate oxidase (ASO). Protein sequence alignment of ASO from various organisms was performed by ClustalW [83] and the result is shown using Colorfy. Colorfy groups the twenty amino acids into eight separate conservation groups [{G, A}, {V, L, I, }, {F, Y, W}, {C, M}, {K, R, H}, {D, E, N, Q}, {S, T}, {P}]. Percentage composition is defined on a per column basis and categorized as Majority Identity, Conserved Minority or Insufficient Conservation. A column is Majority Identity when at least 61% of the amino acids in that column are identical. A column is Conserved Minority when at least 61% of the amino acids in that column
belong to the same conservation group and no amino acid makes up more than 60% of that column. A column is Insufficient Conservation when its composition fails to satisfy any of the prior two conditions. Columns are colored based on percentage composition: Blue: 61 to 70; Green: 71 to 90; Gold: 91 to 100. Colors codes are divided into two shades, dark and light. A Majority Identity column can have up to two colors in the column: dark to indicate the positions of the identity amino acid and light to indicate positions of amino acids belonging to the same group as the identity amino acid. A Conserved Minority is colored the light color of the corresponding percentage composed of the majority amino acid group. Columns categorized as Insufficient Conservation are left uncolored. If a column satisfies Majority Identity at a lower percentage and Conserved Minority at a higher percentage, the Majority Identity categorization takes precedence and the column is colored per the Majority Identity percentage. The nucleotide sequences and the corresponding protein sequences around the mutation point for wild-type and nic15-1 are shown in the box. The mutated nucleotide is underlined and the changed amino acid is shown in bold. The color of individual amino acids corresponds to their identity percentages among different organisms. At, Arabidopsis thaliana; Bs, Bacillus subtilis; Cr, Chlamydomonas reinhardii; Ec, Escherichia coli; Ol, Ochrobactrum luminescens; Os, Oryza sativa; Ot, Ostreococcus tauri; Pp, Pyrococcus abyssi; Pt, Pseudomonas thiooxidans; Vc, Volvox carteri ; Zm, Zea mays.

Figure S2 The nic7-1 mutant strain has a missense mutation in quinolinyl synthetase (QS). Protein sequence alignment of QS from various organisms was performed by ClustalW and the result is shown by Colorfy. The nucleotide sequences and the corresponding protein sequences around the mutation point for wild-type and nic7-1 are shown in the box. The mutated nucleotide is underlined and the changed amino acid is shown in bold. The color of individual amino acids corresponds to their identity percentages among different organisms. Found at: doi:10.1371/journal.pgen.1001105.s001 (2.46 MB TIF)

Figure S3 The nic2-1 mutant strain has a deletion of a single nucleotide in quinolinyl phosphoribosyltransferase (QPT). Protein sequence alignment of QPT from various organisms was performed by ClustalW and the result is shown by Colorfy. The conserved quinolinyl-binding sites are indicated by blue reverse triangles. Partial nucleotide and the corresponding protein sequences for wild-type and nic2-1 are indicated in the box. The deleted nucleotide is underlined in the wild-type. The deletion causes a frame shift that results in a stop codon (*) at amino acid 240. An, Aspergillus nidulans; Hs, Homo sapiens; Mm, Mus musculus; Nc, Neurospora crassa; Sc, Saccharomyces cerevisiae; Xi, Xenopus laevis.

Found at: doi:10.1371/journal.pgen.1001105.s003 (2.13 MB TIF)

Figure S4 The nic1-1 mutant strain contains a premature stop codon in nicotinamide/nicotinate mononucleotide adenyllyltransferase (NMNAT). Protein sequence alignment of NMNAT from various organisms was performed by ClustalW and the result is shown by Colorfy. Partial nucleotide and the corresponding protein sequences for wild-type and nic1-1 are indicated in the box. The mutated nucleotides are underlined, and gray boxes indicate the codons. The amino acid changes are indicated by bold letters. The asterisk indicates a stop codon. Ce, Caenorhabditis elegans; Dm, Drosophila melanogaster; Sp, Schizosaccharomyces pombe.

Found at: doi:10.1371/journal.pgen.1001105.s004 (2.50 MB TIF)

Figure S5 The nic13-1 mutant has a missense mutation in NAD+ synthase (NS). Protein sequence alignment of NS from various organisms was performed by ClustalW and the result is shown by Colorfy. Partial nucleotide and the corresponding protein sequences for wild-type and nic13-1 are indicated in the box. The mutated nucleotides are underlined and the mutated amino acid is indicated by bold letters.

Found at: doi:10.1371/journal.pgen.1001105.s005 (4.63 MB TIF)

Figure S6 Sequence alignment of nicotinamide phosphoribosyltransferase (NAMPT) from various organisms. Protein sequence alignment of NAMPT was performed by ClustalW and the result is shown by Colorfy.

Found at: doi:10.1371/journal.pgen.1001105.s006 (1.93 MB TIF)

Figure S7 Sequence alignment of SIRT7/Sirt2 from various organisms. Protein sequence alignment was performed by ClustalW and the result is shown by Colorfy.

Found at: doi:10.1371/journal.pgen.1001105.s007 (1.77 MB TIF)

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Author Contributions

Conceived and designed the experiments: HL, SKD. Performed the experiments: HL, SKD. Analyzed the data: HL, ALK, SKD. Contributed reagents/materials/analysis tools: ALK. Wrote the paper: HL, SKD.

References


