New function for *Escherichia coli* xanthosine phosphorolase (xapA): genetic and biochemical evidences on its participation in NAD⁺ salvage from nicotinamide

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**Abstract**

**Background:** In an effort to reconstitute the NAD⁺ synthetic pathway in *Escherichia coli* (*E. coli*), we produced a set of gene knockout mutants with deficiencies in previously well-defined NAD⁺ *de novo* and salvage pathways. Unexpectedly, the mutant deficient in NAD⁺ *de novo* and salvage pathway I could grow in M9/nicotinamide medium, which was contradictory to the proposed classic NAD⁺ metabolism of *E. coli*. Such *E. coli* mutagenesis assay suggested the presence of an undefined machinery to feed nicotinamide into the NAD⁺ biosynthesis. We wanted to verify whether xanthosine phosphorolase (xapA) contributed to a new NAD⁺ salvage pathway from nicotinamide.

**Results:** Additional knockout of xapA further slowed down the bacterial growth in M9/nicotinamide medium, whereas the complementation of xapA restored the growth phenotype. To further validate the new function of xapA, we cloned and expressed *E. coli* xapA as a recombinant soluble protein. Biochemical assay confirmed that xapA was capable of using nicotinamide as a substrate for nicotinamide riboside formation.

**Conclusions:** Both the genetic and biochemical evidences indicated that xapA could convert nicotinamide to nicotinamide riboside in *E. coli*, albeit with relatively weak activity, indicating that xapA may contribute to a second NAD⁺ salvage pathway from nicotinamide. We speculate that this xapA-mediated NAD⁺ salvage pathway might be significant in some bacteria lacking NAD⁺ *de novo* and NAD⁺ salvage pathway I or II, to not only use nicotinamide riboside, but also nicotinamide as precursors to synthesize NAD⁺. However, this speculation needs to be experimentally tested.

**Keywords:** Purine nucleoside phosphorylase, Nicotinamide riboside, Salvage pathway, Pyridine nucleotide cycles

**Background**

Nicotinamide adenine dinucleotide (NAD⁺) and NAD⁺ phosphate (NADP⁺) are two of the most important coenzymes in cells. They act as either electron donors or electron acceptors in more than 300 enzymatically catalyzed oxidoreductions [1,2]. NAD⁺ also plays an essential role in producing ATP, and is involved in various cellular processes as a substrate for a number of degradation enzymes [3-9]. Abnormal regulation of NAD⁺ metabolism may result in or is associated with serious metabolic disorders and diseases, such as diabetes, cancers, neurological disorders and cardiovascular disease [2,10-17]. Furthermore, the disruption of NAD⁺ synthesis can cause growth suppression and cell death [18-21].

NAD⁺ can be synthesized *de novo* from simple amino acid precursors such as tryptophan or aspartate, or converted from intermediates such as nicotinamide (NAM), nicotinic acid (NA) or nicotinamide riboside (NR) via salvage pathways, which are designated as salvage pathways I (i.e., (NAM→) NA→NaMN [nicotinic acid mononucleotide]→deNAD [deamino-NAD]→NAD⁺), II (i.e., NAM→NMN [nicotinamide mononucleotide]→NAD⁺), and III (i.e., NR→NMN→NAD⁺), respectively.
All three pathways are in fact interconnected. However, some organisms (e.g., humans and other vertebrates) may lack a nicotinamidase (pncA; EC 3.5.1.19) to prevent NAM from entering pathway I, whereas others (e.g., *Escherichia coli*) lack a nicotinamide phosphoribosyltransferase (NMPRT; EC 2.4.2.12) to prevent NAM from entering pathway II [13,27]. In yeast, pathway I may be extended by first converting NR to NAM [23].

Some NAD⁺-consuming enzymes may break down NAD⁺ to form various types of ADP-ribosyl groups, in which the NAM moiety is the most common end-product [28,29]. In a variety of physiological events, some of these enzymes (e.g., poly ADP ribose polymerases [PARPs]) can be significantly activated, such as during the regulation of apoptosis, DNA replication, and DNA repair [30], thus potentially leading to the rapid depletion of intracellular NAD⁺, and associated accumulation of NAM [21]. Since NAM is also known as a strong inhibitor of several NAD (P)⁺-consuming enzymes, uncontrolled NAM accumulation may negatively affect not only NAD⁺ metabolism, but also cellular functions such as gene silencing, Hst1-mediated transcriptional repression, and life span of cells [31-34]. Therefore, NAD⁺ salvage pathways I and II are...
important not only in regenerating NAD⁺, but also in preventing the accumulation of NAM. While NAM may be converted to NMN by NMPRT (pathway II) or NAB by pncA (pathway I), there were no reports on other enzymes that might act on NAM.

In the present study, we have discovered by genetic and biochemical approaches that xanthosine phosphorylase (xapA; also known as purine nucleoside phosphorylase II [PNP-II], EC 2.4.2.1) is also capable of converting NAM to NR in E. coli. XapA was originally identified from E. coli, and known to catalyze the reversible ribosyltransfer on purine nucleosides including xanthosine, inosine and guanosine [35-37]. Our data has not only assigned a novel function to xapA, but also uncovered a potential new route in the NAD⁺ salvage, in which the pathway III is extended by using NAM as an alternative precursor in xapA-possessing organisms.

Results

Genetic disruption of NAD⁺ de novo biosynthesis and NAD⁺ salvage pathway I in Escherichia coli

In an effort to uncover the new function of E. coli xapA in NAD⁺ salvage pathway from nicotinamide, we produced a set of gene knockout mutants deficient in previously defined NAD⁺ synthetic pathways, including NAD⁺ de novo and NAD⁺ salvage pathways I and III for genetic investigation purpose (see Table 1, Additional file 1: Figure S1 and Additional file 2: Table S1). We first generated a mutant strain deficient in NAD⁺ de novo pathway (BW25113ΔnadC) that was unable to survive in the M9 minimal medium, but could restore the growth to a level comparable to the wild-type BW25113 when NA or NAM was supplied to allow NAD⁺ synthesized via NAD⁺ salvage pathway I (Figure 2 and Table 2).

We then generated double-deletion mutant BW25113ΔnadCΔpncA to also interrupt the conversion from NAM to NA in NAD⁺ salvage pathway I. This mutant was expected to only survive in the absence of NA, but not NAM due to the lack of NAD⁺ salvage pathway II in E. coli (Figure 1). The growth of BW25113ΔnadCΔpncA mutant in the absence of NA was confirmed as expected, but we also unexpectedly observed its survival in M9/NAM medium, albeit with a much slower growth rate (i.e., 380.8 min generation time vs. 53.4 min for BW25113ΔnadC mutan) (Table 2 and Figure 2). This result suggested the presence of another unknown salvage pathway can participate in the conversion of NAM from medium into NAD⁺.

Genetic evidence on the involvement of xapA in NAD⁺ salvage pathway

The ability for BW25113ΔnadCΔpncA to grow in M9/NAM medium implied a previously undefined enzyme (s) might be involved in feeding NAM into the NAD⁺ synthesis. The poor efficiency in utilizing NAM was indicative of the presence of an enzyme that might use NAM as an atypical substrate, but the activity was sufficient for bacterial growth when other NAD⁺ intermediates were unavailable. Based on the substrate preference of

| Table 1 Escherichia coli strains and plasmids used in this study |
|-----------------|-----------------|-----------------|
| Strains or plasmids | Genotypes and comments | Source or reference |
| Strain            | Routine cloning host | In-house collection |
| BW25113           | ΔlacZ4787 hsdR514 ΔaraBAD)567 ΔrhaBAD)568 rph-1 | CGSC* |
| BW25113ΔnadC      | BW25113 with chromosomal nadC deletion | This study |
| BW25113ΔnadCΔpncA | BW25113 with chromosomal nadC and pncA deletion | This study |
| BW25113ΔnadCΔpncAΔxapA | BW25113 with chromosomal nadC, pncA, and xapA deletion | This study |
| BW25113ΔnadCΔpncAΔnadR | BW25113 with chromosomal nadC, pncA, and nadR deletion | This study |
| BW25113ΔnadCΔpncAΔxapAΔnadR | BW25113 with chromosomal nadC, pncA, xapA and nadR deletion | This study |
| Plasmid           | Gene knockout procedure | CGSC* |
| pKD13             | Gene knockout procedure | CGSC* |
| pKDa6             | Gene knockout procedure | CGSC* |
| pCP20             | Gene knockout procedure | CGSC* |
| pBAD-hisA         | bla⁺ | In-house collection |
| pBAD-EGFP         | pBAD-hisA with EGFP gene | This study |
| pBAD-xapA         | pBAD-hisA with xapA gene | This study |
| pET28a            | Kana⁺ | In-house collection |
| pET28-xapA        | pET28a with xapA gene | This study |
| pEGFP-N2          | Template for PCR amplification of EGFP gene | In-house collection |

*CGSC is the E. coli Genetic Stock Center of Yale University.*
xapA towards purine nucleosides and the fact that its sister enzyme deoD (PNP-I) is able to use NR as non-
typical substrate to form NAM in vitro [38], we hypothe-
sized that xapA might be a candidate enzyme responsible
for converting NAM to NR. To test this hypothesis, we
developed three multiple gene deletion mutants, namely,
BW25113ΔnadCΔpncAΔxapA, BW25113ΔnadCΔpncAΔnadR, and BW25113ΔnadCΔpncAΔxapAΔnadR (Table 1). Among them, the growth of BW25113ΔnadCΔpncAΔxapA was worse than that of BW25113ΔnadCΔpncA in the
M9/NAM medium (i.e., 620.4 min generation time in
BW25113ΔnadCΔpncAΔxapA vs. 380.8 min in BW25113ΔnadCΔpncA) (Figure 2 and Table 2). When a
complementary plasmid pBAD-xapA (but not the control
vector pBAD-EGFP) was reintroduced into this triple-
deletion mutant, its growth rate was restored to a similar
time corresponding to NR (Figure 4A and 4C). Further posi-
tive MS/MS analysis at m/z 255 detected two major peaks
in these assays was prepared by a hydrolysis of 5′-phosphate groups from NMN by CIAP. The ability for xapA to
use NAM as a less efficient substrate to produce NR that
could be routed into the pathway III (i.e., NAM → NR →
NAD⁺) in vivo.

Biochemical evidence on the conversion of NR from NAM
by E. coli xapA

The genetic data on the involvement of xapA in converting
NAM to NR was further validated by biochemical assays
using recombinant xapA protein that was expressed using
an E. coli expression system and purified into homogeneity
(see Additional file 1: Figure S2). Standard NR sample used
in these assays was prepared by a hydrolysis of 5′-phosphate groups from NMN by CIAP. The ability for xapA to
convert NAM to NR was first confirmed by HPLC-ESI-
MS/MS assay. In reactions catalyzed by recombinant xapA and
CIAP (positive control), selected-ion monitoring chro-
matogram (SIM) detected a single peak at the retention
time corresponding to NR (Figure 4A and 4C). Further posi-
tive MS/MS analysis at m/z 255 detected two major peaks
with m/z at 255 and 123, representing NR (255 Da) and the
NAM (123 Da) moiety, respectively (Figure 4B and 4D),

Table 2 Generation time (minutes) of Escherichia coli strains in different culture media*

| No. | Strain | Pathway Deficiency | Medium M9 | Medium M9 + NAD⁺ | M9 + NA | M9 + NAD⁺ |
|-----|--------|--------------------|-----------|-----------------|--------|-----------|
| 1   | BW25113| None               | + 65.8    | + 49.8          | + 50.5 | + 49.4    |
| 2   | ΔnadC  | dn                 | – –       | – –             | – –    | – –       |
| 3   | ΔnadCΔpncA| dn, l               | – –       | + 50.3          | + 49.2 | – 380.8   |
| 4   | ΔnadCΔpncAΔxapA| dn, l               | – –       | + 49.2          | + 50.0 | – 620.4   |
| 5   | ΔnadCΔpncAΔxapAΔpBAD-xapA| dn, l               | – NT      | + NT            | – –    | – 376.4   |
| 6   | ΔnadCΔpncAΔxapAΔpBAD-EGFP| dn, l               | – NT      | + NT            | – –    | – 626.8   |
| 7   | ΔnadCΔpncAΔnadR| dn, l, III          | – –       | + 51.1          | + NT   | – –       |
| 8   | ΔnadCΔpncAΔxapAΔnadR| dn, l, III          | – –       | + 49.7          | + NT   | – –       |

*Notes: NA, nicotinic acid; NAM, nicotinamide; NAD⁺, nicotinamide adenine dinucleotide; NT, not tested; –, No proliferation; +, proliferation; dn, de novo NAD⁺
synthesis; I, NAD⁺ salvage pathway I; III, NAD⁺ salvage pathway III.
Figure 3 Dose-dependent effects of NAD⁺ on the growth of *Escherichia coli* mutant with triple-deletion (BW25113ΔnadCΔpncAΔxapA).

**A)** Growth curve of the mutant in M9 minimal medium supplied with various concentration of NAD⁺.  
**B)** The relationship of the inverse of the NAD⁺ concentration (from 0.1 to 1 μg/ml) to the bacterial generation time in M9/NAD⁺ medium for 7 h.  
**C)** The relationship of the NAD⁺ concentration (from 0.1 to 1 μg/ml) to the OD₆₀₀ of the mutant grown in M9/NAD⁺ medium for 7 h.

Figure 4 Biochemical evidence on the synthesis of NR from NAM catalyzed by *E. coli* xapA as determined by HPLC-ESI-MS/MS.

**A)** Selected-ion monitoring (SIM) chromatogram at m/z 254.3-255.3 Da of NR converted from NAM by recombinant xapA.  
**B)** Positive ESI-MS/MS spectrum of the NR peak produced by xapA and eluted from HPLC showing an ion fragmentation pattern characteristic to NR, including two major peaks representing NR and the NAM moiety with m/z at 255 and 123, respectively.  
**C)** SIM chromatogram of NR converted from NAM by CIAP as positive control.  
**D)** Positive ESI-MS/MS spectrum of the NR peak produced by CIAP and eluted from HPLC. The retention time and MS/MS spectra were identical to those produced by standard NR control, confirming the synthesis of NR from NAM by xapA. See Figure 1 for abbreviations.
which confirmed the xapA-catalyzed production of NR from NAM.

Further kinetic analysis showed that the $K_m$ value towards NAM was 5.81 mM, and the $V_{max}$ was at 400 nmol/min/mg protein. The kinetic data indicated that xapA in *E. coli* was much less efficient in using NAM to synthesize NR than using typical substrate ($K_m$ at 5.81 mM on NAM vs. 72 μM on xanthosine) [37], or when compared with other NAD$^+$ salvaging enzymes (e.g., $K_m$ values at 70 μM and 2 μM for pncA and pncB on NAM and NA, respectively) [39,40], but similar to those of deoD (PNP-I) from calf and *E. coli* (i.e., 1.48 mM and 0.62 mM, respectively) in converting the non-typical substrate NR to NAM [38].

The contribution of xapA in NAD$^+$ salvaging was also confirmed in bacterial mutants cultured in M9/NAM medium, in which the consumption of extracellular NAM by the triple-deletion (BW25113ΔnadCΔpncAΔxapA) was reduced by 95% in comparison to that by the double-deletion BW25113ΔnadCΔpncA (Figure 5A). The consumption of extracellular NAM was restored when vector expressing xapA (but not the EGFP control) was reintroduced to the triple-deletion (Figure 5A). The level of intracellular NAD$^+$ was detectable in BW25113ΔnadCΔpncA (150 ng), but virtually undetectable in BW25113ΔnadCΔpncAΔxapA (Figure 5B). Again, the intracellular NAD$^+$ level could be restored by reintroducing xapA into the triple-deletion, but not by EGFP (Figure 5B).

**Discussion**

**Contribution of xapA to an alternative NAD$^+$ salvage pathway from NAM**

Xanthosine phosphorylase (xapA, EC 2.4.2.1) is a second purine nucleoside phosphorylase (PNP-II) in *E. coli*. Similar to PNP-I (deoD), it mainly functions in the purine metabolism by carrying out both phosphorylation and synthesis of purine and purine deoxy-/ribonucleosides [41]. Here we first obtained genetic evidence that xapA was probably involved in NAD$^+$ salvage in *E. coli*. We also provided more direct biochemical evidences that xapA was able to synthesize NR from NAM. Both bacterial growth experiments and enzyme kinetic data indicated that xapA used NAM in a much less efficient way than using its typical substrates (i.e., purine analogs), suggesting that NAM served only as a non-typical substrate, which was comparable to the PNP-I. Therefore, the capability to convert NAM to NR appeared to be a “side effect” for xapA. However, such a side-effect was sufficient to maintain the survival of *E. coli* by feeding NAM into the salvage pathway III when all other NAD$^+$ synthetic pathways were unavailable and only NAM was present in the minimal medium. For clarity, we designated the xapA-mediated extension of NAD$^+$ salvage pathway III as the salvage pathway IIIb (i.e., NAM → NR → NMN → NAD$^+$) (Figure 1).

**Potential uses of xapA-mediated salvage pathway in drug development**

The true biological function of pathway IIIb may be less significant in *E. coli*, as this bacterium is able to synthesize NAD$^+$ via multiple routes (i.e., *de novo*, NAD$^+$ salvage pathways I and III). However, we speculate that it may be highly significant for some other pathogenic bacteria that lack NAD$^+$ *de novo*, NAD$^+$ salvage pathway I and/or II for NAD$^+$ synthesis. One of the examples might be the gram-negative coccobacillus *Pasteurella multocida* that causes a range of diseases in humans and animals. It appears to be V-factor-independent, indicating its capability to utilize NAM as the pyridine nucleotide, as well as NAD$^+$, NMN and NR to synthesize NAD$^+$ [42]. Analysis of NAD$^+$ biosynthesis pathways reveals that *P. multocida* lacks NAD$^+$ *de novo* and NAD$^+$ salvage pathway I but possesses NAD$^+$ salvage pathway II and NAD$^+$ salvage pathway III for the presence of nadV, NMPRT homolog in bacteria, and nadR [26] (Figure 1B). Furthermore, a PNP homologue (see Additional file 3: Text S1) is also present in the *P. multocida* genome. Accordingly, it seems reasonable to speculate that *P. multocida* may synthesize NAD$^+$ from NAM through NAD$^+$ salvage pathway II and/or NAD$^+$ salvage pathway.

![Figure 5 Consumption of extracellular NAM (A) to form intracellular NAD$^+$ (B) by four strains of *Escherichia coli* derived from BW25113 cultured in M9/NAM medium until the strain BW25113ΔnadCΔpncA reached the mid-log phase. Strain 1, BW25113ΔnadCΔpncA; strain 2, BW25113ΔnadCΔpncAΔxapA; strain 3, BW25113ΔnadCΔpncAΔxapA/pBAD-xapA; and strain 4, BW25113ΔnadCΔpncAΔxapA/pBAD-EGFP.](http://www.biomedcentral.com/1471-2180/14/29)
IIIb. However, the hypothesis on the potential contribution of NAD⁺ salvage pathway IIIb to NAD⁺ biosynthesis in such bacteria remains to be tested. If the hypothesis is confirmed, the xapA or its isoform(s) may be explored as a novel target for developing therapeutics.

In fact, the NAD⁺ salvage pathways of human is similar to that of *P. multocida* in that humans lack NAD⁺ salvage pathway I, but possess NMPRT-mediated NAD⁺ salvage pathway II and NRK (isozyme of nadR)-mediated NAD⁺ salvage pathway III (Figure 1A) [23,24,43]. NMPRT is highly expressed in many types of tumor cells, including human hematologic malignancies, to maintain adequate levels of NAD⁺ [44–46]. Inhibitor(s) of NMPRT, such as FK866, has been in Phase II clinical trials [47,48]. However, NAM was found to have an antidote potential for the cellular effects of FK866 [49], which indicates that the NAD⁺ synthesis pathways from NAM may be not completely disrupted. As the PNP-mediated new salvage pathway is also present in mammals (see Additional file 2: Table S2 and Additional file 3: Text S2), it remains to be tested whether human PNP (counterpart of xapA) is also able to utilize NAM to synthesize NR as an alternative to pathway II (i.e., via pathway IIIb), thus responsible for the slow anti-cancer action of FK866. In fact, the enzymes involved in the pathway IIIb, such as human PNP and NRK, are all effective anticancer drug targets [50,51]. When the inhibitors of PNP and/or NRK are used in combination with FK866, rapid NAD⁺ depletion and NAM accumulation may occur, hopefully increase the anticancer efficacy or widen the antitumor spectra, or even conquer the drug resistance.

Conclusions

We have provided genetic and biochemical evidences showing that xanthosine phosphorylase (xapA) in *E. coli* is able to utilize nicotinamide (NAM) as an atypical substrate to synthesize nicotinamide riboside (NR), which extends the NAD⁺ salvage pathway III to use NR as an alternative precursor (i.e., pathway IIIb). This unexpected discovery not only assigns a new function to xapA, but also increases our current knowledge on the NAD⁺ biosynthesis and pyridine nucleotide cycles.

Methods

**Bacterial strains, plasmids, media and reagents**

The BW25113 strain of *E. coli* served as a parent strain for generating mutants with single to multiple gene deletions within the NAD⁺ synthetic pathways (see Table 1 for a list of strains and plasmids used in this study). Bacteria were cultured in lysogeny broth (LB), LB agar, M9 broth or M9 agar as described [53]. When required, supplements were typically used at the following final concentrations: 100 μg/ml of ampicillin, 50 μg/ml of kanamycin, 1 mmol/liter of L-arabinose, 10 μg/ml of NAM, 10 μg/ml of NA, and 10 μg/ml of NAD⁺. All chemicals were purchased from Sigma-Aldrich (St. Louis, MO) with purity at ≥99%. NAM was further purified with high-performance liquid chromatography (HPLC) to remove minor contaminating NA.

**Genetic construction of various NAD⁺ synthesis pathway-deficient mutants**

A series of *E. coli* mutants with single to multiple gene deletions in the NAD⁺ *de novo* and salvage pathways were constructed from the wild-type BW25113 strain using a λ Red-mediated recombination system as described (Table 1) [53,54]. Briefly, PCR products were generated from template plasmids carrying a kanamycin resistant (KmR) gene flanked by FLP-recognition target sites using primers with 36-nucleotide extensions that were homologous to regions adjacent to the genes to be inactivated and (see Additional file 2: Table S3 for primer sequences). The chromosomal genes were replaced by the corresponding PCR products via the λ Red-mediated recombination system. The resulting KmR colonies were selected and verified by PCR and sequencing of the PCR products, and the kanamycin resistant cassette was removed by introducing pCP20 helper plasmid that carried the yeast Flp recombinase and ampicillin resistant gene (AmpR). The Red and FLP helper plasmids were subsequently cured by growth at 37°C because they are temperature-sensitive replicons.

**Phenotypic determination of NAD⁺ synthesis deficiency by selective media**

The phenotypic deficiencies of mutants were validated by their capabilities to utilize different precursors to
synthesize NAD⁺ in various selective media. All strains were washed twice in M9 minimum medium to remove trace amounts of nutrients and resuspended in specified selective media. For plate growth assay, 0.2 μl suspensions of the E. coli strains (OD600 = 0.1) were dotted onto agar plates containing M9 alone or M9 plus either NA or NAM. Plates were incubated at 37°C for 12 h or longer. For determining growth rates, strains were diluted in specified liquid media (OD600 = 0.005), cultured at 37°C and OD600 values were measured every hour as described [53]. The generation times (T_d) were calculated during the exponential phase of growth according to the formula: 

\[ T_d = (t_2 - t_1) \times \frac{\log(2)}{\log(q_2/q_1)} \]

where \( t_1 \) and \( t_2 \) represented times, \( q_1 \) and \( q_2 \) represented the number of cells at \( t_1 \) and \( t_2 \), respectively. Additionally, the dose-dependent effect of NAD⁺ on the triple-deletion strain (BW25113ΔnadCΔpncAΔxapA) was measured in M9 medium containing NAD⁺ at various concentrations (i.e., 0, 0.1, 0.33, 1, 3.3, and 10 μg/ml). The growth rate and generation time of this mutant were determined as described above.

**Genetic validation on the involvement of xapA in NAD⁺ salvage pathway**

To further validate the involvement of xapA in NAD⁺ salvage pathway, a genetic complementation experiment was performed by reintroducing xapA into the triple-deletion mutant (BW25113ΔnadCΔpncAΔxapA). The xapA ORF was amplified and reconstructed into pBAD-hisA at the EcoRI and Xhol sites. The same pBAD-hisA vector carrying the enhanced green fluorescence protein (EGFP) gene (pBAD-EGFP) was constructed as control. The plasmids were then transformed into the BW25113 ΔnadCΔpncAΔxapA strain. Transformed cells were cultured on LB plates containing ampicillin, and the positive clones were selected for growth phenotypic examination. The growth rates of the transformed cells in M9/NAM medium were determined as described above.

**Cloning, expression and purification of recombinant E. coli xapA**

The open reading frame (ORF) of xapA was amplified by PCR (see Additional file 2: Table S3 for primer sequences) from E. coli genomic DNA using the high-fidelity Pfu DNA polymerase, and cloned into pET28a expression vector (Novagen) flanking the EcoRI and HindIII sites as described [53]. The resulting pET28-xapA was sequenced from 110 – 2,000 Da; 2) the selected ion monitoring (SIM) scans were set at m/z 254.8 for NR, m/z 123.0 for NAM, and m/z 334.8 for NMN; and 3) the MS/MS scans were set at 254.8@cid 18 for NR, 123.0@cid 30.0 for NAM, and 334.8@cid 19 for NMN. The isolation width was set to 2,000 Da; 3) the MS/MS scans were set at m/z 254.8 for NR, m/z 123.0 for NAM, and m/z 334.8 for NMN; and 3) the MS/MS scans were set at 254.8@cid 18 for NR, 123.0@cid 30.0 for NAM, and 334.8@cid 19 for NMN. The isolation width was set to 1.0 Da, and the ejected ions were detected by the electron multiplier with a gain at 5 × 10⁶. Data were analyzed by Xcalibur Software version 1.4 (Thermo Scientific).
Kinetic parameters for xapA enzyme were determined by measuring the decreased absorbance of NAM at 262 nm with a Synergy H1 microplate reader (BioTek, USA) as described [55]. The reaction was performed in 50 mM MES buffer (pH 6.0) containing 20 mM R1P, 0.1 mg/ml xapA protein and varied concentrations of NAM at 37°C for 30 min. Michaelis-Menten plots and the linear transformations (Lineweaver-Burk, Hanes-Woolf) were used for determining the kinetic parameters.

Quantitative analysis of NAD⁺ synthesis on the xapA-mediated NAD⁺ salvage pathway from NAM

We also directly tested the utilization of NAM by xapA in the bacterial mutants by measuring their consumption of extracellular NAM and the production of NAD⁺ in cells. In this experiment, four mutants (i.e., BW25113ΔnadCΔpncA, BW25113ΔnadCΔpncAΔxapA/pBAD-xapA and BW25113ΔnadCΔpncAΔxapA/pBAD-EGFP) were cultured in the M9/NAM medium. The cultures were maintained until the BW25113ΔnadCΔpncA strain reached the mid-log phase. A volume of the bacterial suspensions containing approximately 1 × 10⁹ BW25113ΔnadCΔpncA cells was collected by centrifugation at 15,000 × g for 10 min. Equal volumes of the other three strains were also collected. After centrifugations, bacterial pellets and supernatants were separately collected. The supernatants were freeze-dried for measuring extracellular NAM. The pellets were resuspended in 2 ml of deionized water and ultrasonicated for 10 min. After centrifugation at 15,000 × g for 15 min at 4°C, supernatants were collected and freeze-dried for measuring intracellular NAD⁺. The concentrations of NAD⁺ and NAM were determined by HPLC-ESI-MS as described above.

Statistical analysis

All experiments were performed independently for at least three times. Statistically significant differences were calculated by two-tailed Student's t-test using SPSS software (version 19.0) (http://www-01.ibm.com/software/analytics/spss/).

Additional file 1: PCR verification of gene deletions in the E. coli mutants. ST1-ST6 represents BW25113, BW25113ΔnadC, BW25113ΔxapA, BW25113ΔnedCΔpncAΔxapA, BW25113ΔnedCΔpncAΔxapAΔpncR and BW25113ΔnedCΔpncAΔxapAΔpncR. Figure S2. SDS-PAGE (12%) analysis of recombinant xapA protein expressed in E. coli. Lanes 1: protein marker; lane 2: cell-free extract before induction with IPTG; lane 3: cell-free extract after IPTG induction; lane 4: recombinant xapA protein. Figure S3. Potential contribution of xapA-mediated conversion from NAM to NR (marked by an asterisk) in the pyridine nucleoside cycles (PNCs). Pathways unique to E. coli or vertebrates are marked.

Additional file 2: Table S1. The expected product sizes (bp) for PCR of the four specified genes in different strains used in the study. Table S2.
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