

## Bioinformatic Analysis of Strawberry NDH-H Gene

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**Keywords:** NDH-H; research object; physical and chemical properties.

**Abstract.** NDH-H has always been known as a key factor of Hydrogen ion metabolism pathway in plant testa. Recent studies show that chlororespiration and cyclic electron flow mediated by NDH may coordinate to alleviate the over-reduction of stroma, thus to keep operation of CO<sub>2</sub> assimilation at certain extent under heat stress condition. In this research we chosen NDH-H gene of 13 kinds species, downloaded their nucleotide and protein sequence from NCBI as the research object, found strawberry NDH-H gene via bioinformation analyses, constructed phylogenetic tree. At the same time, we analyzed the strawberry NDH-H gene of physical and chemical properties and its protein structure and so on. The phylogenetic tree showed that strawberry and *Malus x domestica* were closest relative. By the protein prediction, we found that the protein owed one proper signal peptide without obvious transmembrane regions.

### 1. Introduction

NDH-H has always been known as a key factor of Hydrogen ion metabolism pathway in plant testa. Recent studies show that chlororespiration and cyclic electron flow mediated by NDH may coordinate to alleviate the over-reduction of stroma, thus to keep operation of CO<sub>2</sub> assimilation at certain extent under heat stress condition[1]. As the endosymbiont evolved into an organelle, the plastid retained a greatly reduced genome with many of the cyanobacterial genes being transferred to the host nuclear genome. Although most functional cp-tonuclear gene transfers occurred early in plastid evolution[2], such transfers have been a continual evolutionary process[3], and the cp genome (plastome) of photosynthetic land plants typically encodes 68–82 conserved protein-coding genes[4-7]. The study chosen NDH-H-like gene of 13 kinds species, downloaded their nucleotide and protein sequence from NCBI as the research object, found strawberry NDH-H gene via bioinformation analyze so as to provide reference for further study and utilization.

### 2. Result and Analysis

#### 2.1 Strawberry NDH-H Find and Phylogenetic Tree Construction of NDH-H

Run BLAST in the *Fragaria × ananassa* database of GDR and Strawberry GARDEN respectively using *Arabidopsis thaliana* NDH-H as a sample. Select the sequence with ideal S and C value, we find that FAN\_iscf00079132.1 is strawberry NDH-H.

We have chosen NDH-H-like gene of 13 kinds species (Table 1), downloaded their nucleotide and protein sequence from NCBI as the research object, analyzed

phylogenetic tree on the genetic distance base (Figure 1). The relationship between strawberry and petunia is closer than others, due to they all contain a lot of anthocyanins probably.

Table 1. Basic information of *ndh-h* gene in different species

Species	mRNA Accession Number	Protein Accession Number	Amino Acid Number
<i>Fragaria vesca</i>	XM_004300664.2	NP_764579841	2378
<i>Prunus persica</i>	XM_007209819.2	NP_1162557396	2,039
<i>Prunus avium</i>	XM_021954618.1	1220048676	1,950
<i>Prunus mume</i>	XM_008240407.2	1027110558	1,906
<i>Ziziphus jujuba</i>	XM_016035329.1	1009146309	1,726
<i>Manihot esculenta</i>	XM_021769310.	1216280848	1,716
<i>Vitis vinifera</i>	XM_010654642.2	1105496133	2,168
<i>Jatropha curcas</i>	XM_012223503.2	1173833864	1,882
<i>Glycine max</i>	XM_003525090.3	955321540	1,962
<i>Momordica charantia</i>	XM_022293720.1	1229791775	1,870
<i>Cicer arietinum</i>	XM_004503838.2	828317514	2,000
<i>Lupinus angustifolius</i>	XM_019603041.1	1117349479	1,975
<i>Malus x domestica</i>	XM_008371310.2	1039874863	1,876

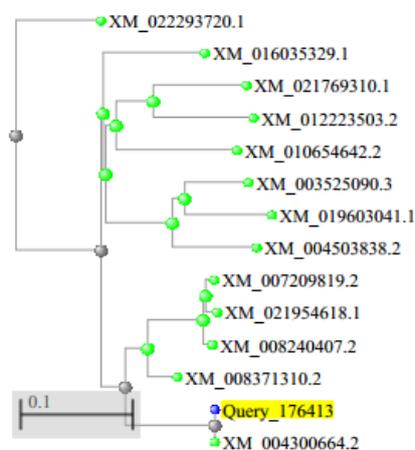


Figure 1. Phylogenetic Tree of Strawberry NDH-H.

## 2.2 Strawberry Ndh-H Protein Physical Analysis

Analyze strawberry NDH-H protein physical feature using ProtPran. Result shows as following: the protein is composed by 1611bp, molecular weight is 132904.25, theoretical pI is 5.00, electric neutrality, molecular formula is C4866H8163N1611O2075S319. Because the N-terminal of the sequence considered is A (Ala), the estimated half-life is 4.4 hours in mammalian reticulocytes (in vitro), 20 hours in yeast (in vitro) and 10 hours in *Escherichia coli* (in vitro). The instability index (II) is computed to be 45.68, so the protein is unstable. The aliphatic index of the protein is 26.01. Grand average of hydropathicity (GRAVY): 0.660.

Amino acid composition result is settings as following (Table 2): the peptide chain consists many Ala as 29.0%.

Table 2. Strawberry *ndh-h* gene amino acid composition

Amino Acid	Count	Percentage
Ala (A)	419	29.0%
Cys (C)	319	19.8%
Gly (G)	410	25.5%
Thr (T)	463	28.7%

## 2.3 Strawberry Ndh-H Protein Signal Peptide Forecast

Forecast strawberry NDH-H protein signal peptide using SignalP 4.1. Result shows as following (Figure 2). There is one signal peptide in the NDH-H between 22th base and 23th base.

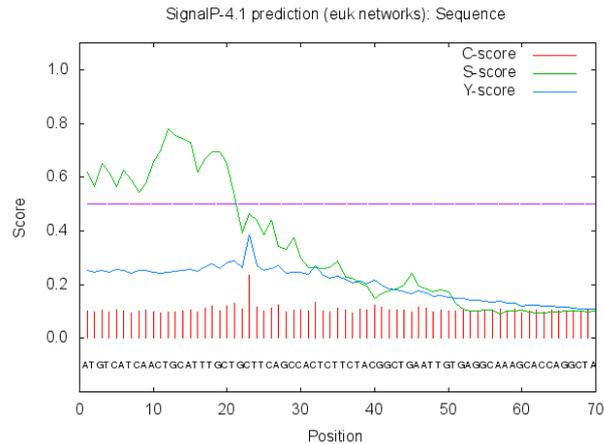


Figure 2. Signal peptide forecast of strawberry NDH-H.

### 2.4 Strawberry Ndh-H Protein Transmembrane Domain Forecast

Forecast strawberry NDH-H protein transmembrane domain using TMHMM Server. Result shows as following (Figure 3). There isn't transmembrane domain in the strawberry NDH-H, thus the protein is not cytomembrane receptor or located on cytomembrane.

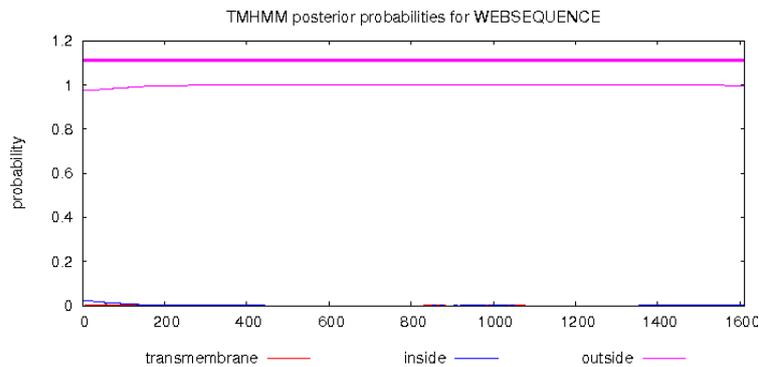


Figure 3. Transmembrane domain forecast of strawberry NDH-H.

## 3. Materials and Methods

Sequences access from NCBI (<https://www.ncbi.nlm.nih.gov/>). BLAST run in GDR (<https://www.rosaceae.org/>), and Strawberry GARDEN(<http://strawberry-garden.kazusa.or.jp/>). Phylogenetic tree is constructed via MEGA6.0, forecast strawberry NDH-H protein signal peptide using SignalP 4.1 (<http://www.cbs.dtu.dk/services/SignalP/>), forecast strawberry NDH-H protein transmembrane domain using TMHMM Server (<http://www.cbs.dtu.dk/services/TMHMM/>).

## 4. Conclusion

As suggested by Krause (2012) [8], parasitism may prompt adaptive gene loss. Some orchids still contain the whole set of NDH-related genes. The emergence of the heterotrophic stage of these orchids may have occurred very recently, and thus the NDH-related genes are still retained due to insufficient time for selection to eliminate them. Our analyses suggest that in contrast to nonorchid monocots, NDH complex genes in Orchidaceae may be evolving under relaxed selective constraints and may ultimately be lost. Further investigations into the correlation between CO<sub>2</sub> fixation, growth habit, type of trophic strategy and NDH activity would be helpful to elucidate the mechanism and function of the NDH complex in plants. In addition to some photoautotrophic orchids, many non-orchid photoautotrophic plants also exhibit The exploration on strawberry TT12, which is forward gene to strawberry NDH-H, have been attempt in our lab, we would focus on the interaction between strawberry TT12 and NDH-H so as to provide reference for further study and utilization.

## Acknowledgments

I thank my teachers: Haoru Tang, for the directions, Jiangan He for the discussion. This work was financially supported by National Innovation Experiment Program for University Students (201510626005) fund.

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