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Phylogenetic analysis and expression profiling of *Nuclear Factor-Y* gene family in *Dendrobium catenatum* Lindl. (Orchidaceae)

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A R T I C L E I N F O

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A B S T R A C T

Nuclear factor-Y (NF-Y) are transcription factors that play vital role in various developmental processes such as flowering, embryogenesis, root formation, nodulation and stress tolerance. In the present study, 27 *NF-Y* genes were identified in *Dendrobium catenatum* which were grouped into three sub-families: DcNF-YA (5), DcNF-YB (10) and DcNF-YC (12), on the basis of presence of specific conserved domains. The phylogenetic relationship between DcNF-Y protein sequences with their orthologs in *Vanilla planifolia* and *Arabidopsis thaliana* confirmed the classification of these proteins into the specified three groups. Physico-chemical characterization reported a wide range in the protein length (111 to 433 amino acids), with DcNF-YAs being longer than the others. Strong interaction between most of the DcNF-Y proteins suggests towards the formation of complexes which might be playing a role in different developmental processes. Gene architectural studies predicted the presence of multiple (3–6) introns in *DcNF-YA* in contrast with the intron-less status of majority of *DcNF-YB* and *DcNF-YC* genes. The abundance of stress related cis-regulatory elements in the promoter regions of *DcNF-Y* genes indicate the potential of these genes in stress tolerance. Additionally, variable expression of these genes in diverse tissues point towards their widespread role in growth and development. This work can act as a harbinger for functional characterization of *NF-Y* genes with a view for genetic improvement in *Dendrobium catenatum* Lindl.

1. Introduction

Nuclear factor-Y (NF-Y) is a class of transcription factor that play decisive role in diverse developmental pathways in plants. These are also present in other eukaryotes as CCAAT-binding factor (CBF) or heme activator protein (HAP). NF-Ys are composed of three sub-families i.e. NF-YA, NF-YB and NF-YC, so named due to presence of specific subunits. The NF-YB is further sub-grouped into LEC (Leafy cotyledon) and non-LEC categories. Each NF-Y protein contains a centrally conserved domain for DNA binding and sub-unit interactions. NF-Y are represented by single gene in yeast and mammals while it is encoded by multiple genes in plants (Petroni et al., 2012). This gene family has been characterised in various plants such as *Arabidopsis thaliana* (30; Petroni et al., 2012), *Brachypodium distachyon* (36; Cao et al., 2011), *Camellia sinensis* (35; Wang et al., 2019), *Citrus grandis* (24; Mai et al., 2019), *Cucumis sativus* (27; Chen et al., 2020), *Glycine* max (59; Quach et al., 2015), *Hordeum vulgare* (23; Panahi et al., 2019), *Manihot esculenta* (51; He et al., 2019), *Musa acuminate* (44; Yan et al., 2019), *Pinus tabuliformis* (28; Guo et al., 2021), *Prunus persica* (24; Li et al., 2019), *Ricinus communis* (25; Wang et al., 2018), *Sorghum bicolor* (42; Malviya et al., 2016) and *Vanilla planifolia* (25; Arora et al., 2020). There are various reports which suggest about the role of NF-Y in various developmental processes such as embryogenesis (Lotan et al., 1998), nodule development (Combier et al., 2006), flowering (Chen et al., 2007), root elongation (Ballif et al., 2011), chlorophyll synthesis (Stephenson et al., 2011), etc. NF-YA1 in *Arabidopsis* has role in male gametogenesis (Mu et al., 2013). *MtNF-YA1* showed higher gene expression during early stages of nodule development (Baudin et al., 2015). *AtNF-YB9* (*AtLEC1*) gene was reported in regulating embryogenesis (West et al., 1994; Lotan et al., 1998). Overexpression of *LEC1* increased seed oil formation in maize (Shen et al., 2010) while loss-of-function of *LEC1* resulted in the formation of cotyledon (West et al., 1994). Overexpression of *CgNF-YB9* affected the sucrose metabolism by decreasing sucrose and increasing fructose and glucose in *Citrus grandis* (Mai et al., 2019). Various studies regarding the role of *NF-Y* genes in mitigating stress has also been reported. *ZmNF-YA3* was found to have dual role in flowering and drought and temperature tolerance in maize (Su et al., 2018). In wheat, *TaNF-YB3* help in tolerance to drought stress (Yang et al., 2017). Differential

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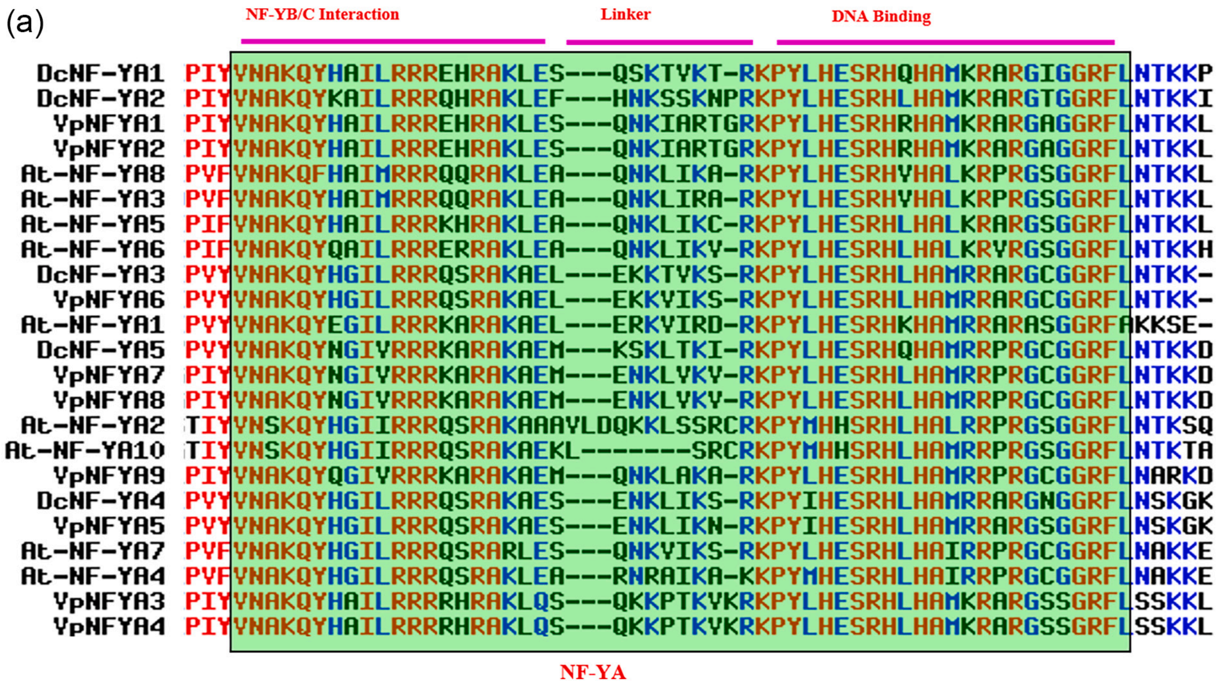

Fig. 1. Multiple sequence alignment of NF-Y proteins of *Dendrobium catenatum*, *Vanilla planifolia* and *Arabidopsis thaliana.* a) NF-YA b) NF-YB c) NF-YC.

expression of *CsaNF-Y* genes was observed in drought and salt stress in *Cucumis sativus* (Chen et al., 2020). In *Picea wilsonii*, overexpression of *PwNF-YB3* increased drought and salt tolerance in *Arabidopsis* (Zhang et al., 2015). Ectopic expression of *GmNF-YA3* from soybean resulted in increased drought tolerance in *Arabidopsis* (Ni et al., 2013). Similarly, *CdtNF-YC1* from hybrid bermudagrass (*Cynodon dactylon* × *Cynodon transvaalensis*) increased drought and salt tolerance in *Paspalum vaginatum* (Wu et al., 2018).

Dendrobium catenatum is an economically important orchid species known for its medicinal and floricultural potential. But due to various man-made and environmental disturbances such as habitat destruction, unprecedented exploitation and climate change has pushed the orchid plants towards endangerment. Efforts are required to strengthen these growth and stress tolerance to facilitate development of robust plants. The sequenced genome of *Dendrobium catenatum* Lindl. (PRJNA262478; Zhang et al., 2016) offers valuable opportunity to identify and characterize gene specific to these molecular processes. *NF-Y* gene family is one such important candidate to study. Resultantly, a study was performed to identify and characterize *NF-Y* gene family in *D. catenatum*. This study aims to illuminate the role of *NF-Y* genes in growth and development and stress responses which in turn can pave way for future functional studies.

2. Materials and methods

2.1. Identification of putative NF-Y proteins in Dendrobium catenatum

Dendrobium catenatum NF-Y (DcNF-Y) sequences were identified by performing BLASTp searches using NF-Y sequences of *Arabidopsis thaliana* (Siefers et al., 2009) and *Vanilla planifolia* (Arora et al., 2020) in NCBI. The threshold cut-off was set at e-value of 1×10^{-10}. The sequences were confirmed by the presence of conserved domain i.e. smart00521 (CBF), pfam02045 (CBFB_NFYA), pfam00808 (CBFD_NFYB_HMF) of cl23735 (H4) superfamily and cl30738 (HAP5) in Conserved Domain Database (CDD; https://www.ncbi.nlm.nih.gov/Structure/cdd/cdd.shtml) and pfam database (https://pfam.xfam.org). NCBI BLAST search was also conducted to identify orthologous proteins of NF-Y family in *V. planifolia*, *A. thaliana* and *D. catenatum*. The conserved domains of respective sub-units were identified and marked with MultAlin (http://multalin.toulouse.inra.fr/multalin/). Motif analysis was conducted using MEME (http://meme-suite.org/tools/meme) with motif width of 6–60; total of ten motifs with zero or one occurrence per sequence were predicted.

2.2. Phylogenetic analysis

The phylogenetic tree between NF-Y proteins of *V. planifolia*, *A. thaliana* and *D. catenatum* was constructed by neighbour-joining tree method using MEGA X with thousand bootstrap replications after aligning the sequences using MUSCLE (https://www.megasoftware.net).

2.3. Physico-chemical and interaction studies in DcNF-Y proteins

Physical and chemical features of proteins such as protein length, molecular weight (MW), aliphatic index (AI), isoelectric point (pI) and grand average of hydropathicity (GRAVY) values were calculated using PROTPARAM (https://web.expasy.org/protparam/). An interaction network of DcNF-Y protein was made with high confidence interaction score (0.7) using String (https://string-db.org/).

2.4. Gene construction and promoter analysis

The gene architecture was constructed using CDS and gene sequences in GSDS (http://gsds.gao-lab.org/). Promoter region was predicted 1.5 kb upstream from the starting position of the gene and was subjected to PlantCARE database (http://bioinformatics.psb.ugent.be/webtools/plantcare/html/). The position of 12 cis-regulatory elements was visualized by MEME using any number of repition and 6–10 width size. The various cis-elements identified in three sub-families were subjected to Venn diagram and were categorised into four groups based on the developmental function associated with these elements (http://bioinformatics.psb.ugent.be/webtools/Venn/).

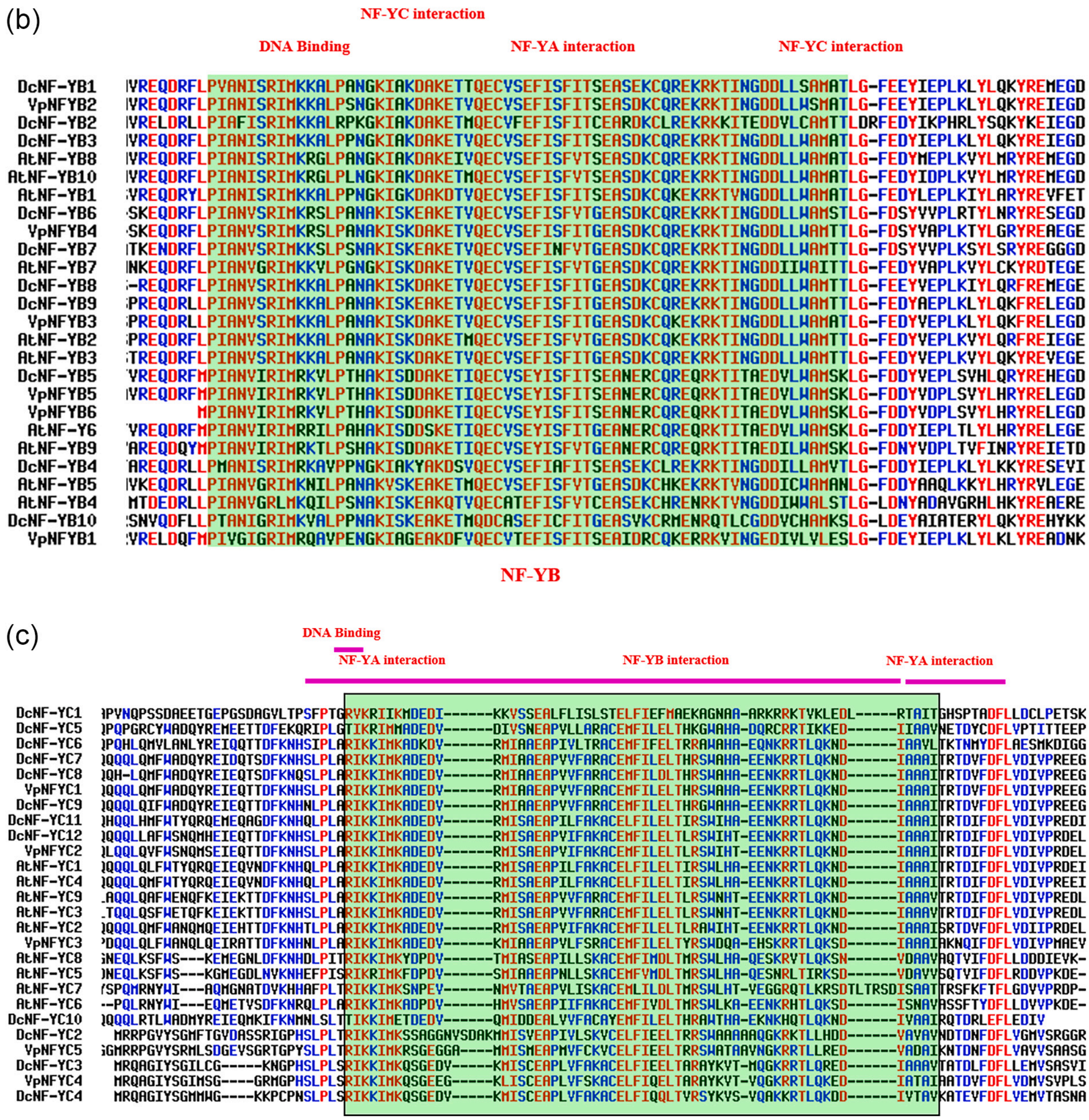

Fig. 1. (*continued*).

2.5. Expression profiling

The expression level of *NF-Y* genes in different tissues such as flower buds (SRX2251519), pollinia (SRX2938662), leaf (SRX2251517), stem (SRX2251516) and root (SRX2938667) was calculated by using the number of hits obtained in SRA BLAST of CDS sequences of the putatively identified genes (https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&BLAST_SPEC=SRA&LINK_LOC=blasttab#i). These hits were used to estimate the RPKM values in different tissues for each gene (Mortazavi et al., 2008) and a heat map was developed using ClustVis visualizing tool with correlation clustering of the genes (https://biit.cs.ut.ee/clustvis/).

3. Results

In *Dendrobium catenatum*, 27 sequences were identified and classified into three sub-families as five in NF-YA, 10 in NF-YB and 12 NF-YC. The classification of the protein sequences was performed with the help of conserved domain searches in NCBI CDD. The DcNF-YA protein sequences showed identity with smart00521 and pfam02045 which had similarity with NF-YA domain. Similarly, DcNF-YB and DcNF-YC sequences showed similarity with PF00808 in Pfam database but showed variability in CDD search, where DcNF-YB sequences had similarity with pfam00808 while DcNF-YC sequences matched with cl30738 in NCBI CDD. Except in case of DcNF-YC1, it showed pfam00808 as domain identification feature but the sequence was shifted to NF-YC because of its sequence similarity with AtNF-YC3 and VpNF-YC1. The DcNF-Y sequences were further confirmed with the help of related orthologous sequences of *Vanilla planifolia* and *Arabidopsis thaliana* (Supplementary Table 1).

The protein sequences of three NF-Y sub-families were aligned separately to determine the degree of conservation in the domain region and this revealed the presence of DNA binding domain and a sub-unit binding domain. DcNF-YA proteins had two interaction domains and one DNA binding domain, which were separated by a linker. DcNF-YB

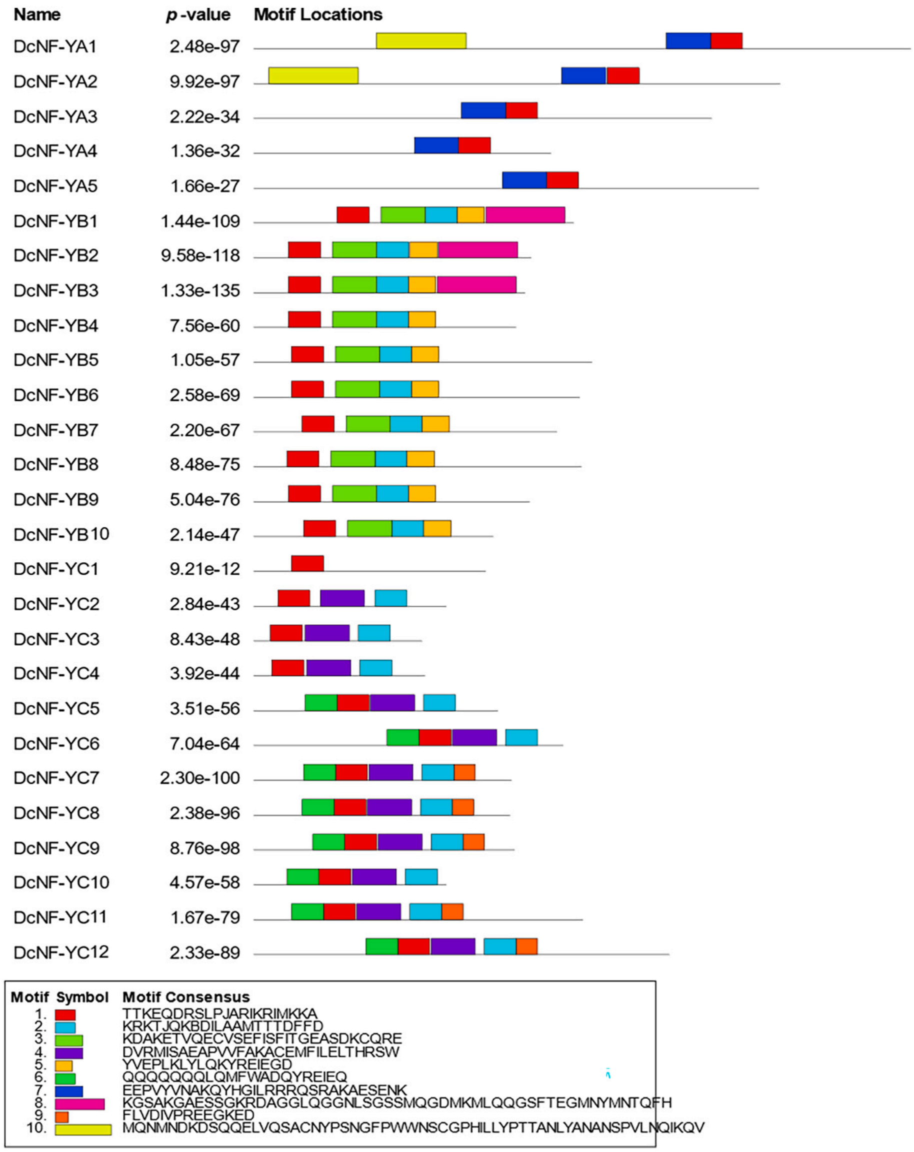

Fig. 2. The structural placement of conserved motifs in DcNF-Y proteins.

proteins had a DNA-binding domain, a NF-YA interaction domain, and a NF-YC interaction domain. DcNF-YC proteins had four domains: two NF-YA interaction domains separated by NF-YB interaction domain and the DNA-binding domain was present in the first NF-YA interacting domain (Fig. 1).

The distribution and arrangement of motifs in DcNF-Y proteins was assessed by MEME server (Fig. 2). DcNF-YA protein sequences were marked by the predominant presence of motif 1 and motif 7 and additionally, motif 10 was observed in DcNF-YA1 and DcNF-YA2. DcNF-YB is characterised by presence of motif 1, motif 2, motif 3, motif 5 and motif 8 while motif 1, motif 2 and motif 4 were conserved in most of DcNF-YC sequences except DcNF-YC1 where only motif 1 was present. A phylogenetic relationship was established between *Arabidopsis thaliana, Dendrobium catenatum* and *Vanilla planifolia*. The tree was categorised into three sub-families: NF-YA, NF-YB and NF-YC. Also, protein sequences of *D. catenatum* showed closer relation with *V. planifolia* than with *A. thaliana* (Fig. 3).

The CDS length of the *DcNF-Y* genes ranged from 336 bp (*DcNF-YC3*) to 1302 bp (*DcNF-YA1*) as given in Table 1. The protein length varied from 111 (DcNF-YC3) to 433 (DcNF-YA1) amino acids. DcNF-YAs were generally longer than others with an average length of 322aa. The average molecular weight was 22,757.40 Da with range varying from 12,214.21 Da to 48,768.39 Da. The average value of aliphatic index (AI), isoelectric point (pI) and GRAVY across three sub-families was 67.51, 7.2 and − 0.57, respectively (Table 1).

The interaction network between the NF-Y proteins showed that DcNF-YB9 interacts with DcNF-YA2, DcNF-YA4, DcNF-YC6, DcNF-YC10 and DcNF-YC12 while DcNF-YB5 interacts with DcNF-YC6, DcNF-YC10 and DcNF-YC12 suggesting that the formation of complex protein interactions could play an important role in different developmental processes (Fig. 4).

DcNF-YA had four introns except in case of *DcNF-YA1* and *DcNF-YA3* which had 5 introns each (Fig. 5). *DcNF-YB* genes were intron-less except *DcNF-YB1*, *DcNF-YB2* and *DcNF-YB3* which had 4 introns and *DcNF-YB4* had 2 introns. All of *DcNF-YC* were intron-less with exception of *DcNF-YC6* where a single intron was found. Moreover, most of the introns were present in zero phase pointing towards the conserved nature of the genes.

A total of 95 unique cis-regulatory elements were identified across three NF-Y sub-families in *D. catenatum* where 5, 14 and 11 unique elements were found in *DcNF-YA*, *DcNF-YB* and *DcNF-YC*, respectively (Fig. 6a). A total of 39 elements such as ERE, CAAT-box, W box, TCA-

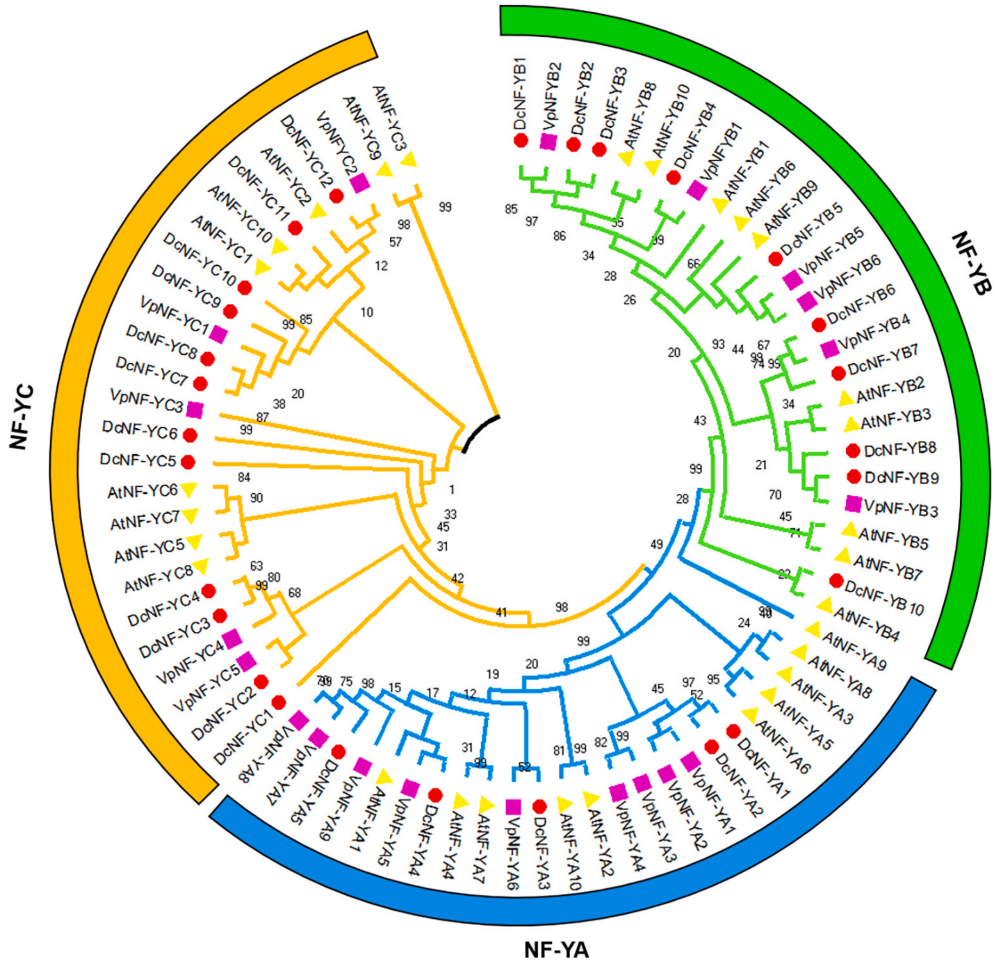

Fig. 3. Phylogenetic relationship between NF-Y proteins of *Arabidopsis thaliana*, *Dendrobium catenatum* and *Vanilla planifolia*.

Table 1
Physical and chemical properties of DcNF-Y proteins.

IDs	CDS length *(bp)*	Protein Length *(aa)*	MW *(Da)*	pI	Instability Index	Aliphatic Index	GRAVY
DcNF-YA1	1302	433	48,768.39	9.69	59.1	57	−0.851
DcNF-YA2	1044	347	38,242.54	9.13	52.1	59.39	−0.807
DcNF-YA3	909	302	33,420.49	9.3	59.97	57.28	−0.817
DcNF-YA4	591	196	21,332.7	6.79	61.99	58.83	−0.703
DcNF-YA5	1002	333	36,438.03	9.31	41.85	62.1	−0.631
DcNF-YB1	636	211	23,219.1	6.92	49.65	64.79	−0.565
DcNF-YB2	552	183	20,146.98	8.69	48.32	58.2	−0.676
DcNF-YB3	540	179	19,492.81	5.5	59.88	59.5	−0.721
DcNF-YB4	522	173	20,117.26	6.44	53.96	85.14	−0.308
DcNF-YB5	672	223	24,618.27	5.98	41.42	64.3	−0.635
DcNF-YB6	648	215	23,330.74	8.77	66.98	49.19	−0.795
DcNF-YB7	603	200	20,746.88	7.69	40.77	49.75	−0.698
DcNF-YB8	651	216	22,598.89	5.97	48.5	46.16	−0.707
DcNF-YB9	549	182	19,728.98	6.22	48.06	58.23	−0.729
DcNF-YB10	477	158	18,105.76	9.24	55.28	70.38	−0.679
DcNF-YC1	462	153	16,650.02	5.59	59.73	80.46	−0.423
DcNF-YC2	384	127	13,731.79	9.3	47.62	85.98	−0.136
DcNF-YC3	336	111	12,214.21	8.5	49.28	88.83	−0.073
DcNF-YC4	342	113	12,740.04	9.42	41.04	78.5	−0.220
DcNF-YC5	486	161	18,175.36	4.5	43.82	71.55	−0.588
DcNF-YC6	615	204	23,559.23	9.88	55.26	73.19	−0.546
DcNF-YC7	513	170	19,528.95	5.45	55.06	70.71	−0.655
DcNF-YC8	510	169	19,373.79	5.45	58.94	71.12	−0.622
DcNF-YC9	519	172	19,693.21	5.65	50.85	76.16	−0.540
DcNF-YC10	384	127	15,013.04	5.48	33.69	83.78	−0.586
DcNF-YC11	654	217	23,465.35	4.98	53.05	68.89	−0.394
DcNF-YC12	825	274	29,997.05	5.28	65.07	73.47	−0.322

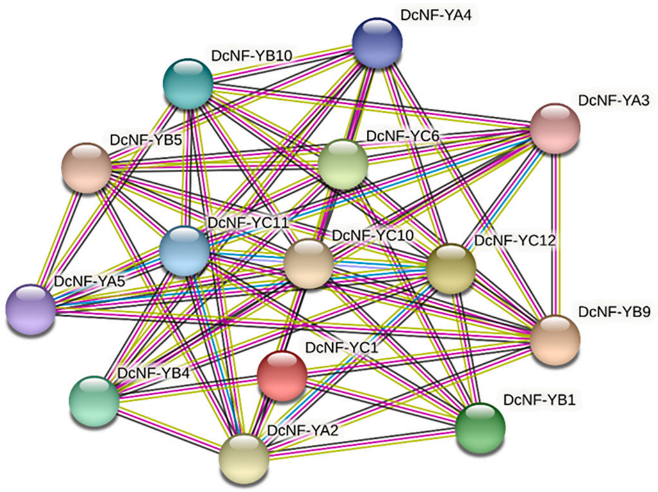

Fig. 4. String based interaction network between DcNF-YA, DcNF-YB and DcNF-YC proteins.

element, WUN-motif etc., were common to all three *NF-Y* sub-families in *D. catenatum.* The location of some of these elements on the promoter region of the genes was visualized in Fig. 6b. These cis-regulatory elements were divided into four groups: light, stress, hormone and growth & development. Light associated cis-regulatory elements such as G-box, Box 4, GA motif, TCT-motif, GATA motif, MRE, GA motif and many others were present across *NF-Y* gene family with G-box being the most abundant. Beside these, hormone responsive elements such as ABRE, CGTCA-motif, GARE-motif, TGACG-motif, TGA-element, P-box, etc. were also present. ABRE related to abscisic acid was the most predominant cis-regulatory motif in *DcNF-Ys*. However, cis-regulatory elements (GCN4_motif, HD-Zip 1, RY-element) related to growth and development were least in number (Fig. 6c).

Expression levels between different tissues such as root, stem, leaves, pollinia and flower bud was assessed across *DcNF-Y* genes (Fig. 7). It was observed that *DcNF-YA2* and *DcNF-YC3* showed high expression in stem while 11 out of 27 *DcNF-Y* genes showed high transcript levels in the root tissue. *DcNF-YB7, DcNF-YB9* and *DcNF-YB10* were more prominent in roots. *DcNF-YC11* had the highest expression in leaves. Most genes expressed in pollinia belong to *NF-YB* and *NF-YC* where about 70% of *DcNF-YBs* had high expression levels in pollinia. Their expression levels were moderate in flower buds signifying the role of these gene in reproduction. This variable expression of the *DcNF-Ys* in different tissues of *Dendrobium catenatum* suggests that this gene family play profuse role in different developmental pathways during plant growth.

4. Discussion

Nuclear factor-Y gene family is a vital transcription factor family having prominent role in embryogenesis, root formation, stress tolerance and many other developmental processes in plants. Due to the enormous importance of this family, a study was conducted to identified and characterised these genes in an economically important orchid plant, *Dendrobium catenatum*. The 27 *NF-Y* genes were identified in *Dendrobium catenatum*. The multigene nature of the family has also been reported in many other plants such as *Citrus grandis* (Mai et al., 2019), *Manihot esculenta* (He et al., 2019), *Vanilla planifolia* (Arora et al., 2020) and many others. The proteins were sub-grouped into three sub-families; NF-YA (5), NF-YB (10) and NF-YC (12) on the basis of specific conserved domains. Similar observations have been made in *Hordeum vulgare* (Panahi et al., 2019) and in *Glycine* max (Quach et al., 2015). The result of multiple sequence alignment in *D. catenatum* is in line with the previous published reports on *Camellia sinensis* (Wang et al., 2019), *Juglans regia* (Quan et al., 2018) and *Prunus persica* (Li et al., 2019) which shows the presence of DNA binding and NF-Y interacting domains. Several reports have indicated that all the three sub-families i.e. NF-YA, NF-YB and NF-YC as identified by their conserved domains that interact, form complex and bind with DNA at CCAAT site of the promoter region (Myers and Holt III, 2018). The conserved organizations of the specific domains in each subfamily suggest that these transcription factors remained highly conserved during plant evolution thus contributing to their vital developmental roles (Chen et al., 2020).

Evolutionary analysis between NF-Y proteins of *Arabidopsis thaliana*, *Vanilla planifolia* and *Dendrobium catenatum* revealed that these proteins cluster into three subfamilies i.e. NF-YA, NF-YB and NF-YC. Moreover,

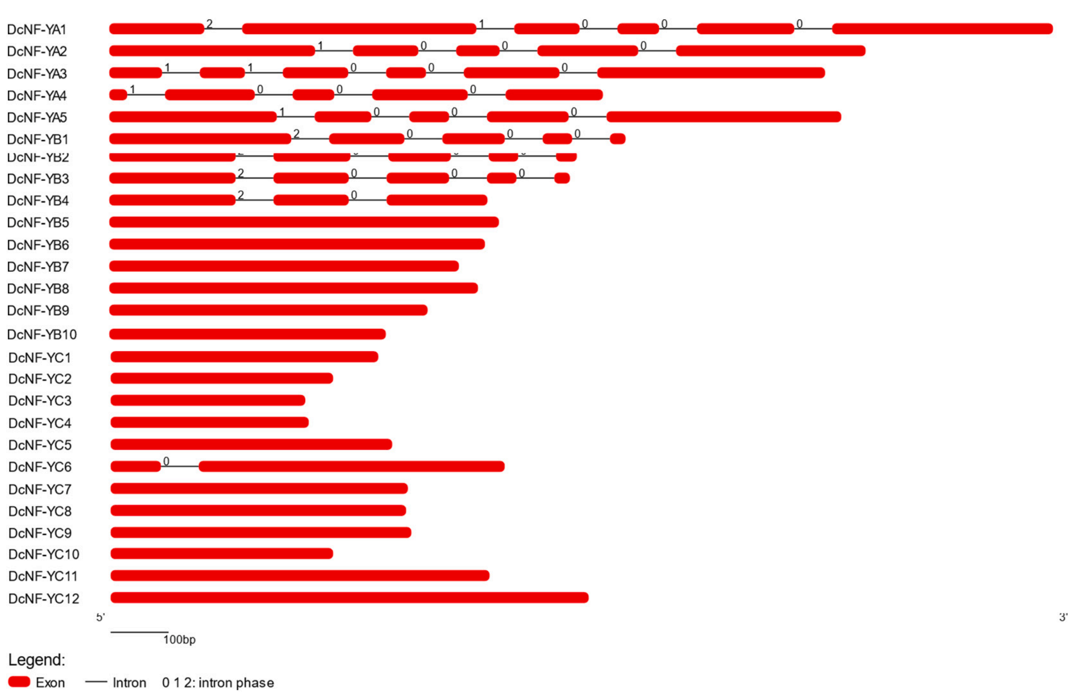

Fig. 5. Gene structure organization of *DcNF-Y* genes constructed by GSDS.

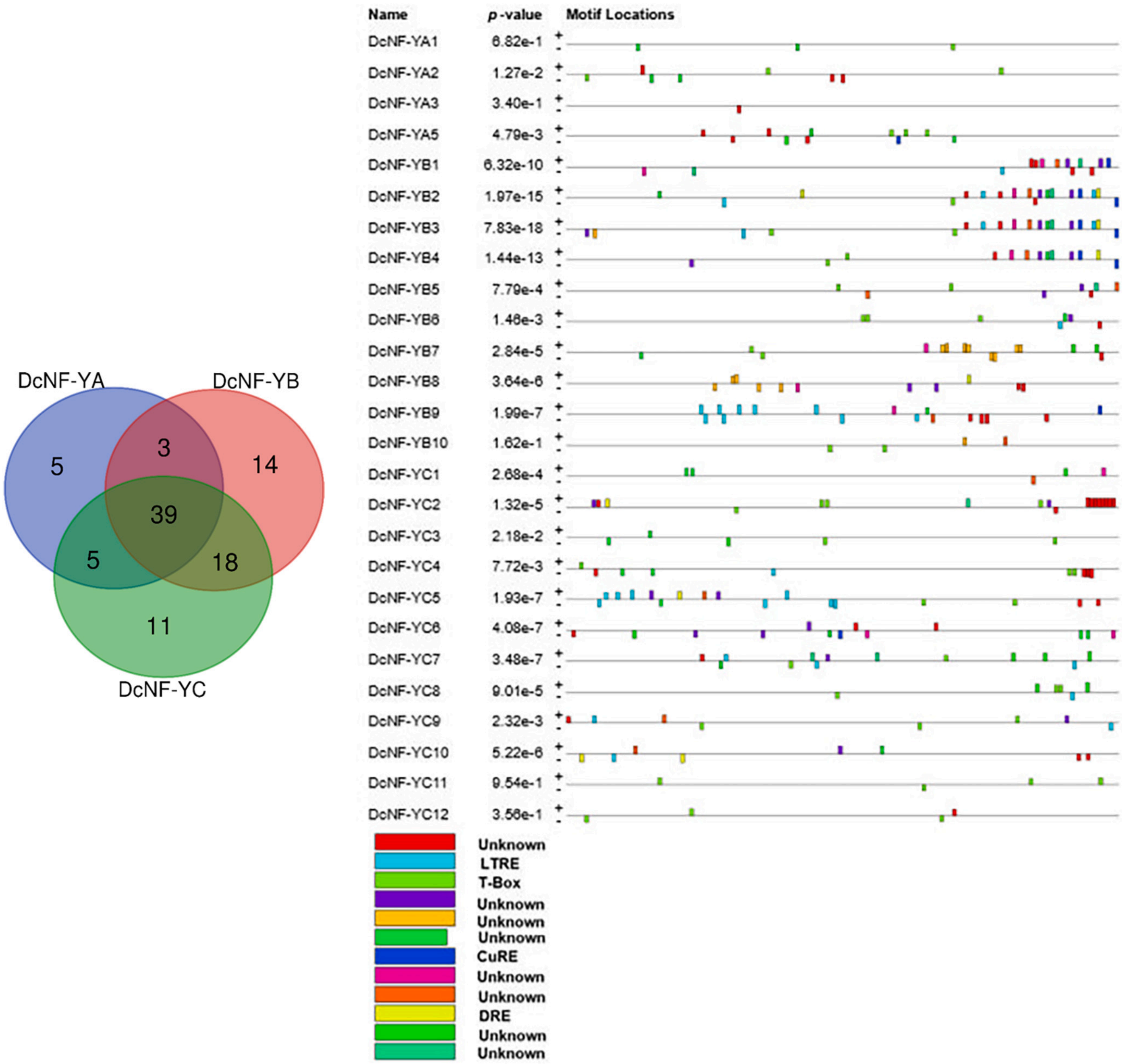

Fig. 6. a. Venn diagram depicting the presence of common and unique cis-regulatory elements (CREs) in the 1.5 kb promoter region. b. Positional visualization of twelve CREs in the promoter region of the respective genes. c. Graphical representation of the numerical variation between light, hormone, growth and stress responsive cis-regulatory elements in DcNF-Ys.

DcNF-Y proteins are more similar with VpNF-Y counterparts than with AtNF-Y sequences. Such relationships have been observed in cucumber where proteins from dicot cucumber and *Arabidopsis* were relatively more similar than with monocot rice (Chen et al., 2020). NF-YB was further classified into LEC-1 and non-LEC1 groups as found in *Brachypodium* (Cao et al., 2011) and tea (Wang et al., 2019). LEC group contains AtNF-YB6, AtNF-YB9, VpNF-YB5, VpNF-YB6 and DcNF-YB5. The members of LEC group have seed specific role as observed in both *Arabidopsis* and *Vanilla* (Petroni et al., 2012; Arora et al., 2020).

According to earlier studies, *NF-YA* genes had 3–6 introns whereas variations were reported in *NY-YB* and *NF-YC* (Feng et al., 2015; Wang et al., 2018; Chen et al., 2020). The similar observations have been made in this study where 4–5 introns were present in *DcNF-YA*. Most of the *DcNF-YB* and *DcNF-YC* were intron-less which is also in accordance with reports on chickpea where 11 *NF-YB*s and 7 *NF-YC*s were intron less (Chu et al., 2018). The comparable observation has also been made in banana (Yan et al., 2019), cucumber (Chen et al., 2020) and apple (Qu et al., 2021) where majority of the *NF-YB* and *NF-YC* genes had no introns. The similar organization of gene structure in indications towards plausible conservation of NF-Y gene family during the evolution of plant history.

A total of 95 cis-regulatory elements were found in the promoter region of *DcNF-Y* genes. The light responsive elements were the most abundant ones followed by hormone responsive elements. Stress responsive elements such as ARE, LTR, MBS, TC-rich repeats and WUN-motifs were present in *DcNF-Y* and similar observations have been made in case of cucumber suggesting their role in mitigating stress conditions (Chen et al., 2020). The presence of hormonal responsive elements such

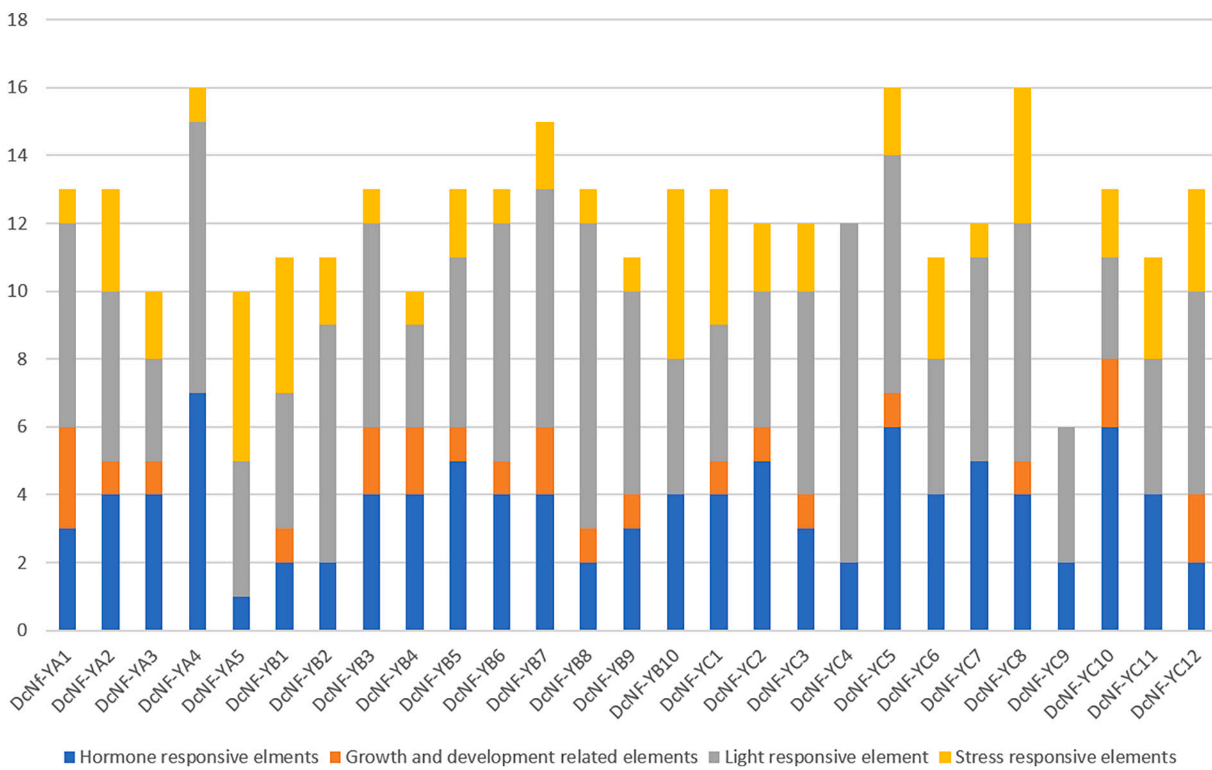

Fig. 6. (*continued*).

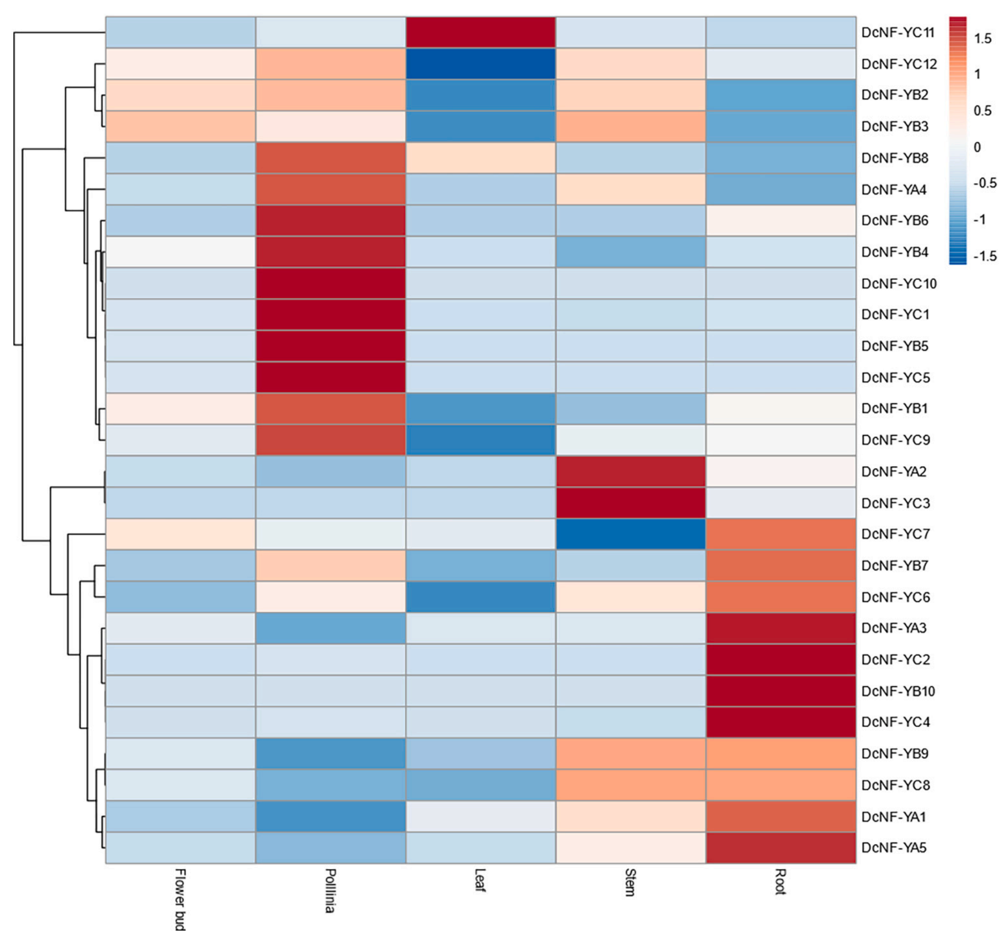

Fig. 7. Expression analysis of *DcNF-Y* genes across different tissues such as flower bud, pollinia, leaf, stem and root.

as ABRE, ERE, CGTCA-motif, TCA-element, TGA-element, GARE-motif etc. in *D. catenatum* is in accordance with the results obtained in the study done on cucumber (Chen et al., 2020). G-box element was the most common light responsive elements and similar results have been reported in apple (Qu et al., 2021).

Expression of *NF-Y* genes was studied in various tissues *DcNF-YA3, DcNF-YB10, DcNF-YC2* and *DcNF-YC4* had root specific expression. Similarly, in cucumber, *CsaNF-YA3* and *CsaNF-YB13* transcripts were abundant in roots (Chen et al., 2020). *MdNF-YA9, MdNF-YB8, MdNF-YB18* and *MdNF-YB19* had high expression in roots of *Malus domestica* (Qu et al., 2021). In *Brassica napus*, *BnNF-YA1, BnNF-YA2, BnNF-YA3, BnNF-YB14, BnNF-YC4* and *BnNF-YC5* had high transcript levels in root (Liang et al., 2014). Also, *Vanilla planifolia* and *Triticum aestivum* showed similar observations where *NF-YA* transcript levels were high in roots (Arora et al., 2020; Stephenson et al., 2007). *DcNF-YB6* and *DcNF-YB7* homologous to *VpNF-YB4* showed moderated expression in roots and similar observation has been made in the previous study. *DcNF-YC3, DcNF-YC8* and *DcNF-YC12* were expressed in stem and this could be corroborated with the fact that *MaNF-YC3* showed strong expression in the stem of banana (Yan et al., 2019). DcNF-YA2 had high level of expression in stem tissue. This was in line with the study on *Brassica napus* where *BnNF-YA3* was highly expressed in stem (Liang et al., 2014). *DcNF-YB2* and *DcNF-YB3* showed expression in the floral buds of *D. catenatum*. Similar observations were made in case of cucumber where *CsaNF-YB9* expression was in male flowers (Chen et al., 2020). The high expression levels of *BnNF-YB10* and *BnNF-YB11* in flowers of *B. napus* were reported (Liang et al., 2014). Also, *BdNF-YB6* of *Brachypodium distachyon* and *HvNF-YB1* of *Hordeum vulgare* were reported to increase flowering in *Arabidopsis* (Cao et al., 2011; Liang et al., 2012). Also, *RcNF-YB9* expression was more prominent in male flowers in *Ricinus communis* (Wang et al., 2018). This could help in functional analysis of NF-Y members in plants where flowering trait is of commercial importance. The expression of *DcNF-YC6, DcNF-YC7* and *DcNF-YC12* were observed both in vegetative and reproductive tissues and it was in line with the study on peach where *PpNF-YC1* was present both in vegetative tissues and reproductive tissues (Li et al., 2019). This suggest showing that the NF-Y genes might play different roles during development of plant.

5. Conclusions

The present study categorically identifies and characterises members of the *NF-Y* gene family in *Dendrobium catenatum*. Twenty-seven DcNF-Y proteins were identified and categorised into three sub-families, NF-YA, NF-YB and NF-YC, based on presence of specific conserved domains and phylogenetic analysis. Variable expression levels of *DcNF-Y* genes in different tissues indicated the diverse potential of these transcription factors in plant growth and development which can be further functionally tapped for the genetic improvement in this economically important orchid species.

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Authors' contributions

DG performed the experimental procedure, compiled the results and drafted the manuscript. JKS envisioned the project, designed the experiment and revised the manuscript.

Declaration of Competing Interest

There is not conflict of interest between authors.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.plgene.2022.100365.

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