

Article

Genome-Wide Identification and Light-Induced Expression Analysis of the *BPC* Gene Family in *Peucedanum praeruptorum* Dunn

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Abstract

The BASIC PENTACYSTEINE (*BPC*) family represents a group of plant-specific transcription factors with established functions in developmental regulation and environmental adaptation. Although *BPC* genes have been catalogued in diverse plant species, their genome-wide characterization and light-dependent expression dynamics remain unexplored in the medicinal herb *Peucedanum praeruptorum* Dunn. Here, we report the systematic identification of eight *PpBPC* loci from the *P. praeruptorum* genome assembly through comprehensive bioinformatic screening. Evolutionary reconstruction grouped these eight members into three distinct clades (designated A, B, and C). Comparative genomic analyses revealed pronounced syntenic conservation between *PpBPCs* and their counterparts in *Arabidopsis thaliana*, *Angelica sinensis*, and *Daucus carota*. Members clustered within the same phylogenetic group displayed analogous exon-intron architectures and conserved motif repertoires, and all possessed the characteristic GAGA-binding domain. Examination of transcript abundance across organs demonstrated that clade A and C members shared broadly overlapping expression signatures in root, stem, and leaf tissues, whereas clade B genes exhibited organ-prevalent patterns. When seedlings were treated with three monochromatic light regimes, the *PpBPC* family displayed heterogeneous transcriptional responses, with individual clades showing distinct wavelength sensitivities. In particular, *PpBPC6* and *PpBPC8* were strongly activated by blue light. Collectively, these data delineate the foundational landscape of the *PpBPC* family and highlight candidate members likely involved in light signal transduction, thereby establishing a framework for future mechanistic dissection of light-responsive gene regulation in *P. praeruptorum*.

Keywords: *Peucedanum praeruptorum* Dunn; *BPC*; gene family; expression pattern; light response



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1. Introduction

Peucedanum praeruptorum Dunn belongs to the genus *Peucedanum* of the Apiaceae family, whose dried roots are used as the traditional Chinese medicine *Peucedani Radix* [1]. With a long-standing history of clinical application, *Peucedani Radix* exerts therapeutic effects of descending “Qi”, resolving phlegm, dispelling wind and clearing heat. Clinically, it is indicated for cough, excessive sputum, chest oppression and asthma, making it a commonly prescribed herb for respiratory disorders [2]. *P. praeruptorum* is widely distributed throughout China, with its major producing regions concentrated in Zhejiang, Anhui, Guizhou, Hubei, Sichuan, Jiangxi and Hunan Provinces [3]. Marked divergences in climate, soil and topography exist across these regions, among which variations in altitude and light regimes are particularly pronounced. Such environmental heterogeneity directly leads to regional differences in plant growth, bioactive constituent accumulation and medicinal quality [4,5]. Notably, Guizhou Province is one of the primary production regions of *P. praeruptorum* in China. Its distinctive karst topography, featuring fragmented and rugged terrain, restricts arable land to scattered intermountain basins and slopes, thereby resulting in high microenvironmental heterogeneity [6]. In the cultivation regions of *P. praeruptorum* in Guizhou Province, altitude varies drastically from 600 to 1800 m. Altitudinal gradients induce pronounced variations in light regimes, temperature, humidity, and soil properties, which profoundly modulate the growth, development, and physiological metabolism of *P. praeruptorum*.

The BASIC PENTACYSTEINE (BPC) gene family is a plant-specific transcription factor family, whose members harbor a highly conserved C-terminal domain composed of five cysteine residues [7]. Through specific recognition of GAGA-repeat elements within target gene promoters, BPC proteins exert transcriptional control over downstream loci [8]. Beyond the conserved core domain, substantial divergences exist in conserved motifs among members of different BPC protein subfamilies, and the composition of these motifs further ensures the conservation and functional divergence of subfamily genes. Regulating plant growth and development constitutes the core function of the BPC gene family, which is mainly involved in floral organ development, embryogenesis, seed formation, and maintenance of the shoot apical meristem [9–13]. In *Arabidopsis thaliana*, AtBPC proteins regulate the normal differentiation of floral organs; the *bpc1-2 bpc2 bpc3* triple mutant exhibits pleiotropic defects, including enlargement of the inflorescence meristem and flowers with supernumerary floral organs [14]. Overexpression of *CjBPC1*, derived from the ornamental flower-*Camellia japonica*, in *A. thaliana* leads to severe defects in siliques and seeds [15]. In apple (*Malus domestica*), *MdBPC2* negatively regulates auxin synthesis, which specifically reduces plant height and inhibits root development [16].

Beyond developmental control, mounting evidence points to the involvement of BPC factors in stress signaling and hormonal pathways. The promoters of BPC gene family members harbor cis-acting elements responsive to light, phytohormones, developmental cues, and various abiotic/biotic stresses, implying their versatile biological functions. Research on members of the *BjuBPC* gene family in mustard showed that *BjuBPC9* exhibits specific responsiveness to blue light, suggesting its role in enhancing mustard adaptability to high-altitude environments with strong blue-violet light [17]. Furthermore, BPC gene family members in tobacco [18], alfalfa [19], pear [20], cotton [21], and cucumber [22] play important roles in responses to salt, drought, low temperature, and hormone stresses.

Therefore, given the complexity and heterogeneity of growing environments across major producing regions—particularly in Guizhou Province—investigations into the BPC gene family of *P. praeruptorum* and its responsiveness to different light qualities are of great significance. Identification of key light-responsive candidate genes will help unravel the molecular regulatory mechanisms underlying microhabitat adaptation in *P. praeruptorum*.

2. Materials and Methods

2.1. Plant Materials and Light Quality Treatments

The *Peucedanum praeruptorum* Dunn used as experimental material was kindly provided by Professor Xiaobo Zhang. Bolting-stage plants grown under natural conditions in the Chinese Medicine Resource Nursery of Guizhou University of Traditional Chinese Medicine were collected for tissue-specific expression analysis. Two-month-old seedlings were subjected to light-quality treatments. Seedlings were cultivated in an artificial climate chamber at a constant temperature of 22 °C with a 16 h light/8 h dark photoperiod for 7 days. Four light-quality regimes were applied: white light (full spectrum, 400–700 nm), blue light (450 nm), red light (660 nm), and far-red light (730 nm).

2.2. Data Sources

The genome data of *P. praeruptorum* [1], *Angelica sinensis* [23], and *Daucus carota* [24] are listed in Supplementary Table S1. BPC protein sequences of *A. thaliana* were obtained from the TAIR database (<https://www.arabidopsis.org>).

2.3. Identification and Physicochemical Characterization of the PpBPC Gene Family

A dual strategy combining sequence homology and domain-based screening was adopted to identify BPC family members in *P. praeruptorum*. First, the seven AtBPC protein sequences served as queries in BLASTP searches (implemented within TBtools-II v2.390) against the predicted *P. praeruptorum* proteome, applying a stringent E-value threshold of 1×10^{-20} . After removing redundant hits, the preliminary candidate pool was further filtered using the HMMER web service (<https://www.ebi.ac.uk/Tools/hmmer/search/hmmscan>, accessed on 7 April 2026) with the Hidden Markov Model profile of the GAGA conserved domain (PF06217) obtained from the Pfam database (<http://pfam.xfam.org/>, accessed on 7 April 2026) [25]; only proteins harboring this signature domain were retained. To ensure domain completeness, all surviving candidates were examined with NCBI Batch CD-Search (<https://www.ncbi.nlm.nih.gov/Structure/bwrpsb/bwrpsb.cgi>, accessed on 7 April 2026), and sequences displaying truncated or partial GAGA domains were discarded manually. This pipeline yielded eight non-redundant BPC homologs in *P. praeruptorum*, which were sequentially named PpBPC1 through PpBPC8. Genomic and coding sequences (CDS) corresponding to each locus were extracted for further investigation.

The physicochemical attributes of the deduced PpBPC proteins—including residue count, molecular mass, theoretical pI, instability index, and grand average of hydropathicity (GRAVY)—were computed with the ProtParam utility on the ExPASy platform (<http://web.expasy.org/protparam/>, accessed on 7 April 2026). Predicted subcellular targeting was assessed using Plant-mPLoc 2.0 (<http://www.csbio.sjtu.edu.cn/bioinf/plant-multi/>, accessed on 7 April 2026).

2.4. Chromosomal Localization and Collinearity Analysis of PpBPC Genes

Chromosomal coordinates of PpBPC loci were determined and graphically rendered with TBtools-II (v2.390) [26]. Intraspecific collinearity scanning was performed via the integrated MCScanX toolkit within TBtools-II to detect duplication-derived gene pairs in the *P. praeruptorum* genome. MCScanX was run using default settings except for E-value = 1×10^{-10} and Number of Hits = 5. The software output file geneLinkedRegion.tab displays collinear gene pairs. To examine cross-species conservation, interspecific synteny analyses were conducted between *P. praeruptorum* and *A. thaliana*, *A. sinensis*, and *D. carota*. Subsequently, the KaKs_Calculator plugin embedded in TBtools-II was employed to compute nonsynonymous (Ka) and synonymous (Ks) substitution rates along with

their ratios (Ka/Ks) for each duplicated pair, enabling inference of the selective regimes operating during BPC family evolution.

2.5. Phylogenetic Analysis of the PpBPC Gene Family

Amino acid sequences of BPC proteins from *A. thaliana*, *P. praeruptorum*, *A. sinensis*, and *D. carota* were subjected to multiple sequence alignment via the MUSCLE algorithm within MEGA12 [27]. The resulting alignment was used to infer an interspecific phylogenetic tree by the Neighbor-Joining (NJ) approach under the Poisson substitution model with pairwise gap deletion; clade support was estimated from 1000 bootstrap pseudoreplicates. Orthology and paralogy assignments among BPC sequences were deduced from this tree, and the topology was refined and displayed using iTOL (<https://itol.embl.de>).

In parallel, an intraspecific NJ phylogeny was reconstructed exclusively from PpBPC protein sequences under identical parameters (Poisson model, pairwise deletion, 1000 bootstrap replicates) to delineate subgroup affiliations within the *P. praeruptorum* BPC repertoire.

2.6. Gene Structure and Motif Analysis of PpBPC Genes

Conserved sequence motifs across PpBPC proteins were discovered with the MEME Suite plugin bundled in TBtools-II (v2.390), allowing up to 10 motifs ranging from 6 to 50 residues in width. Motifs consistently recovered from the majority of PpBPC members were selected for detailed comparative analysis. Upstream regulatory regions (2 kb relative to the transcription start site) of each *PpBPC* gene were isolated using TBtools-II (v2.390) and interrogated for cis-regulatory elements via the PlantCARE database (<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>, accessed on 7 April 2026). Annotations classified as “unknown” or corresponding to generic transcriptional machinery (e.g., TATA-box and CAAT-box) were filtered out, whereas elements linked to light signaling, phytohormone responses, developmental processes, abiotic stress, and metabolic pathways were retained for subsequent analyses. Finally, the phylogenetic topology, motif architecture, and exon–intron configuration of the *PpBPC* family were integrated into a unified graphical summary using the visualization engine of TBtools-II (v2.390) to facilitate structure–function inference.

2.7. Tissue-Specific Expression Analysis of PpBPC Genes

Total RNA was isolated from root, stem, and leaf samples of bolting-stage *P. praeruptorum* (described in Section 2.1) with the Maxwell[®] RSC simplyRNA Tissue Kit (Cat. No. AS1340, Promega (Shanghai) Biotech Co., Ltd., Shanghai, China). Three biological replicates were prepared for roots, stems and leaves separately. One biological replicate corresponds to one independent individual *P. praeruptorum* plant. The root, stem and leaf tissues of a single biological replicate were all collected from the same individual plant, and unified sampling standards were adopted for all three tissue types to control tissue variation. First-strand cDNA was synthesized using the PrimeScript[™] RT reagent Kit (Perfect Real Time, Cat. No. RR037A, Takara Bio Inc., Kusatsu, Shiga, Japan) in accordance with the supplier’s protocol. Quantitative real-time PCR (qRT-PCR) was carried out with 1:50-diluted cDNA template, TB Green[™] Premix Ex Taq[™] II (Takara), and a Bio-Rad real-time PCR detection system. *PpUBC9* was employed as the endogenous normalizer [28]. Primer information is compiled in Supplementary Table S2. Transcript abundance was quantified by the $2^{-\Delta\Delta C_t}$ method. Statistical computations and graph generation were performed with Microsoft Excel 2019, SPSS 27.0.1, and GraphPad Prism 10, respectively. One-way analysis of variance (one-way ANOVA) followed by Duncan post-hoc test was conducted to detect significant differences among groups, and multiple comparison analyses with significance letter labeling were visualized in GraphPad Prism 10.

2.8. qRT-PCR Expression Analysis of PpBPC Genes Under Different Light Quality Treatments

Leaf tissue was harvested from *P. praeruptorum* seedlings subjected to white, blue, red, and far-red light regimes (Section 2.1). Total RNA extraction, qRT-PCR amplification, and quantification were executed as detailed in Section 2.7 to profile the transcriptional behavior of *PpBPC* genes under differential light-quality conditions.

3. Results

3.1. Genome-Wide Identification and Physicochemical Characterization of the PpBPC Gene Family

BLASTP interrogation of the *P. praeruptorum* genome using the seven *A. thaliana* BPC queries, followed by validation of the PF06217 conserved domain, uncovered eight BPC-type loci, which were assigned the identifiers PpBPC1 through PpBPC8. Physicochemical characterization (Table 1) showed that the encoded polypeptides span 278 to 352 amino acids with predicted molecular masses between 31.63 and 39.22 kDa. Computed pI values fell within 8.83–9.81, indicating that all eight proteins carry a net positive charge at neutral pH. Instability indices ranged from 43.98 to 65.96; since every member exceeded the threshold of 40, the entire set is predicted to be unstable according to ProtParam. Aliphatic indices varied between 54.86 and 69.58, while the uniformly negative GRAVY scores point to a hydrophilic character for all PpBPC proteins. Plant-mPloc 2.0 predicted nuclear localization for every PpBPC protein. The coexistence of the PF06217 domain and nuclear localization signal predicts that these proteins act as transcription factors.

Table 1. Physicochemical characterization of the *PpBPC* gene family proteins.

Gene ID	Gene Name	Number of Amino Acid	Molecular Weight	pI	Instability Index	Aliphatic Index	GRAVY	Subcellular Localization
Ppra_2G0010400	<i>PpBPC1</i>	343	38.73	8.83	52.29	56.06	−0.8	Nucleus
Ppra_3G0005040	<i>PpBPC2</i>	352	39.22	9.51	61.67	55.43	−0.747	Nucleus
Ppra_4G0007820	<i>PpBPC3</i>	290	32.60	9.81	57.73	54.86	−0.716	Nucleus
Ppra_4G0019390	<i>PpBPC4</i>	310	35.41	9.68	44.91	69.58	−0.739	Nucleus
Ppra_4G0027120	<i>PpBPC5</i>	287	31.63	9.69	43.98	59.13	−0.687	Nucleus
Ppra_6G0000030	<i>PpBPC6</i>	323	36.11	9.53	65.96	59.85	−0.825	Nucleus
Ppra_6G0030300	<i>PpBPC7</i>	288	32.04	9.49	51.4	60.63	−0.66	Nucleus
Ppra_8G0026350	<i>PpBPC8</i>	311	35.64	9.79	53.22	59.65	−0.833	Nucleus

3.2. Chromosomal Localization and Collinearity Analysis of the PpBPC Gene Family

Mapping of *PpBPC* loci to chromosomes using TBtools-II (v2.390) revealed a scattered distribution across five chromosomes (Figure 1). Chromosome 4 accommodated the largest cluster (three genes), Chr6 carried two members, and Chr2, Chr3, and Chr8 each harbored a single locus.

Analysis of intragenomic duplication patterns (Figure 2A) demonstrated that *PpBPC* genes predominantly originated through whole-genome duplication (WGD), large segmental duplications, and proximal duplication events, yielding four collinear gene pairs. These results highlight WGD/large segmental duplication and proximal duplication as the primary drivers of *PpBPC* family expansion. Calculation of K_a/K_s ratios for *BPC* collinear pairs among *P. praeruptorum*, *A. thaliana*, *A. sinensis*, and *D. carota* produced values between 0.068 and 0.521. All ratios were substantially below 1, signifying that the *PpBPC* family has been subjected to robust purifying selection throughout its evolutionary trajectory (Figure 2B).

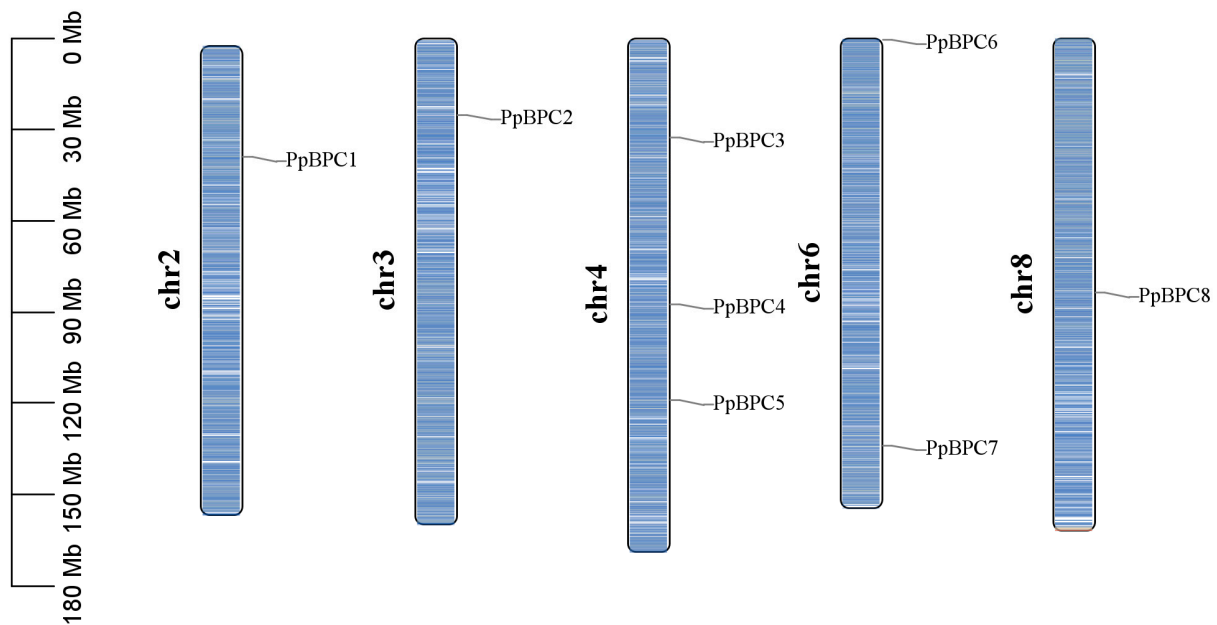


Figure 1. Genomic distribution of *PpBPC* loci across *P. praeruptorum* chromosomes. Eight *PpBPC* genes are positioned on 5 of the 11 chromosomes. Chromosome identifiers are shown on the left; the scale bar (far left) denotes chromosome length.

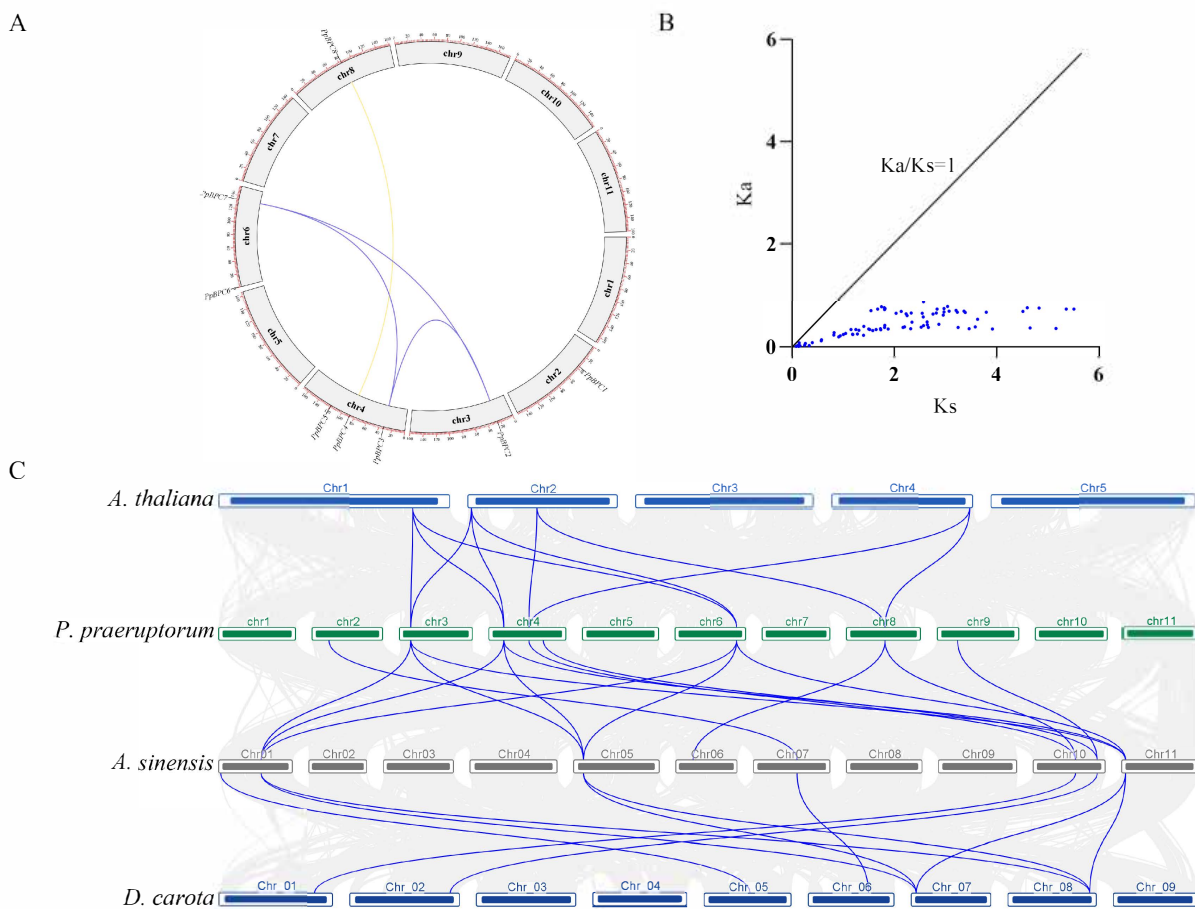


Figure 2. Synteny and selective pressure assessment of the *PpBPC* family. (A) Intragenomic collinearity among *PpBPC* members. (B) K_a/K_s ratios for duplicated *PpBPC* pairs. (C) Cross-species synteny of *BPC* loci involving *A. thaliana*, *P. praeruptorum*, *A. sinensis*, and *D. carota*.

Cross-species synteny assessment further underscored the evolutionary conservation of *BPC* loci. Thirteen collinear *BPC* pairs were detected between *P. praeruptorum* and *A. thaliana* (Figure 2C), 14 pairs with *A. sinensis*, and 10 pairs linking *A. sinensis* and *D. carota*, collectively implying deep functional preservation of this gene family across plant lineages.

3.3. Phylogenetic Relationship Analysis of the *PpBPC* Gene Family

To clarify the evolutionary positioning of *PpBPC* genes, a multi-species phylogenetic reconstruction was performed using aligned *BPC* protein sequences from *A. thaliana*, *P. praeruptorum*, *A. sinensis*, and *D. carota* (Figure 3). The topology revealed that *PpBPC* genes conform to the canonical tripartite organization previously documented in other plants: Group A (14 members), Group B (11 members), and Group C (4 members). Interestingly, *BPC* sequences from the three Apiaceae representatives (*P. praeruptorum*, *A. sinensis*, *D. carota*) tended to coalesce into a shared branch before diverging with their *A. thaliana* orthologs.

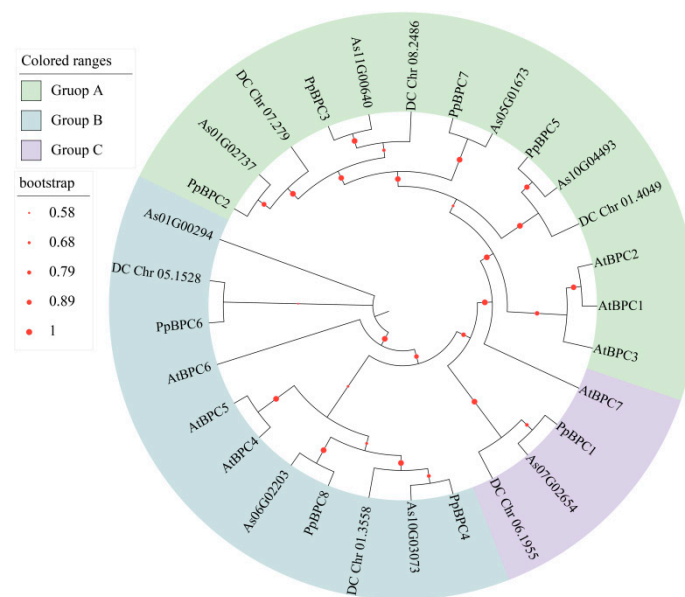


Figure 3. Evolutionary relationships of *BPC* proteins from four plant species. The neighbor-joining tree incorporates sequences from *A. thaliana* (7), *P. praeruptorum* (8), *A. sinensis* (8), and *D. carota* (6), with 1000 bootstrap iterations. Three major clades (A, B, C) are resolved. Red dots on branches indicate bootstrap support (range: 0.58–1).

3.4. Gene Structure and Conserved Motif Analysis of *PpBPC* Gene Family Members

Domain architecture inspection verified that every *PpBPC* protein possesses the hallmark GAGA domain (Figure 4A,C). Exon–intron organization was largely uniform within each phylogenetic subgroup, with limited structural deviations observed in a minority of genes. MEME-based motif discovery identified ten highly conserved elements across the *PpBPC* family (Figure 4B). Motifs 1, 2, and 5 were universally present. By contrast, Motifs 4, 6, 7, and 10 were confined to Group A proteins, and Motif 9 was exclusive to Group B. Within each subgroup, the linear order and composition of motifs were highly consistent, suggesting a tight coupling between motif architecture and protein-level function.

Gene structure comparison (Figure 4D) revealed a striking dichotomy: Group A *PpBPC* genes are entirely devoid of introns, whereas each member of Groups B and C contains a single intron. This structural demarcation aligns closely with the phylogenetic grouping, offering important clues about the mode and tempo of *BPC* gene evolution.

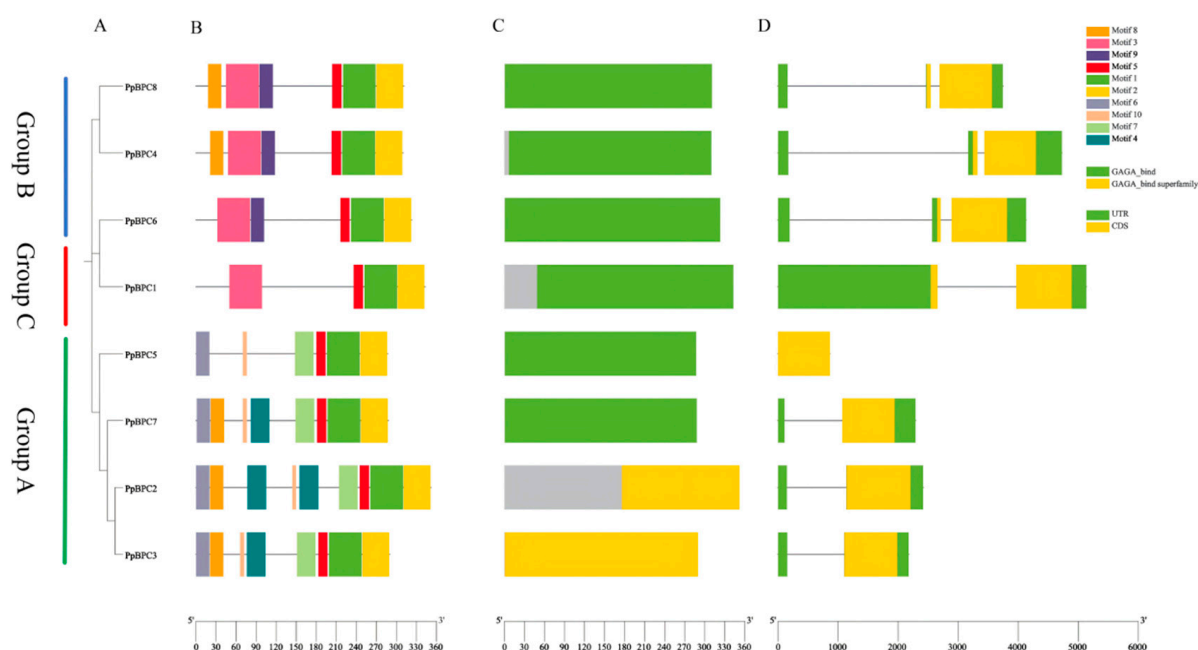


Figure 4. Structural characterization of PpBPC proteins. (A) NJ tree grouping PpBPC members into clades A–C (color-coded). (B) Ten conserved motifs detected by MEME, with distinct colors per motif. (C) GAGA domain architecture (green and yellow boxes). (D) Exon–intron configuration; yellow and green denote CDS and UTR regions, respectively. Gene order matches the phylogeny throughout.

3.5. Cis-Acting Element Analysis of PpBPC Gene Family Members

To gain insight into potential transcriptional control mechanisms, the 2 kb promoter segments upstream of each *PpBPC* start codon were scanned for cis-regulatory elements (Figure 5A). All eight upstream regions contained an array of regulatory motifs (Figure 5B) that fall into four broad functional categories: light-responsive elements, hormone-responsive elements, growth/development and environmental stress-related elements, and metabolism-associated elements (Figure 5C).

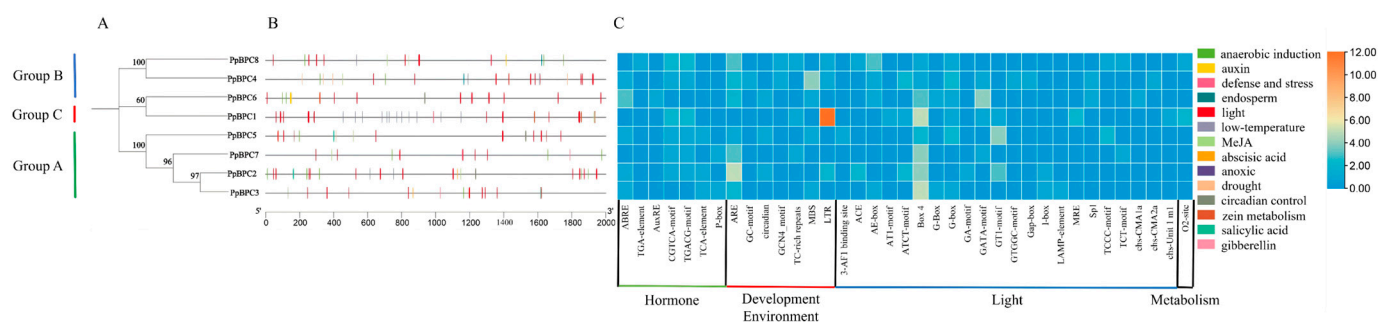


Figure 5. Cis-regulatory landscape of PpBPC promoters. (A) Phylogenetic grouping of PpBPC proteins. (B) Spatial distribution of regulatory motifs within the promoter regions, indicated by colored boxes. (C) Quantitative heatmap of cis-element abundance across four functional categories; bar graph summarizes total element counts, and shaded cells report copy numbers per element type.

Among the phytohormone-associated elements, binding sites linked to abscisic acid (ABA), auxin, gibberellin (GA), methyl jasmonate (MeJA), and salicylic acid (SA) signaling were identified, with distribution across *PpBPC2*, *PpBPC3*, *PpBPC4*, *PpBPC5*, *PpBPC6*, and other family members. Specifically, ABA-responsive motifs were present in *PpBPC2*–*PpBPC6*; auxin-responsive sites were restricted to *PpBPC6* and *PpBPC8*; GA-responsive elements were found in *PpBPC3* and *PpBPC7*; MeJA-responsive elements were widespread

(*PpBPC1*, *PpBPC2*, *PpBPC4*, *PpBPC5*, *PpBPC7*, *PpBPC8*); and SA-responsive elements were detected in *PpBPC2*, *PpBPC3*, and *PpBPC5*.

Elements pertinent to growth/development and environmental challenges were also identified. Circadian-controlled and endosperm-development motifs targeted *PpBPC2*, *PpBPC5*, *PpBPC6* and *PpBPC4*, *PpBPC8*, respectively. Stress-associated motifs included anaerobic induction signals (present in *PpBPC2–PpBPC8*), anoxia-specific motifs (*PpBPC4* only), drought-responsive elements (*PpBPC3–PpBPC6*), low-temperature-responsive elements (principally *PpBPC1*, plus *PpBPC2*, *PpBPC4*, and *PpBPC8*), and defense/stress elements (*PpBPC1*, *PpBPC7*, *PpBPC8*).

Light-responsive motifs constituted the most abundant category and were detected in the promoters of every *PpBPC* gene, pointing to pervasive regulation by light signaling pathways. Metabolism-linked elements, predominantly zein-metabolism motifs, were identified in *PpBPC1* and *PpBPC8* and may be connected to prolamin biosynthesis and turnover.

3.6. Tissue-Specific Expression Analysis of the *PpBPC* Gene Family

Quantitative real-time PCR was employed to delineate the organ-level expression landscape of *PpBPC* genes in bolting-stage plants (Figure 6A,B). Three distinct expression patterns emerged. *PpBPC1*, *PpBPC2*, and *PpBPC3* displayed a coordinated profile with peak transcript levels in stems, intermediate abundance in leaves, and minimal expression in roots. *PpBPC4*, *PpBPC5*, and *PpBPC7* exhibited another shared pattern, characterized by strongest expression in stems, moderate levels in roots, and the lowest signal in leaves. *PpBPC6*, in contrast, was most highly expressed in leaves, followed by stems and then roots. By comparison, *PpBPC8* showed a unique distribution, achieving maximal transcript accumulation in roots, with lower levels in leaves and stems.

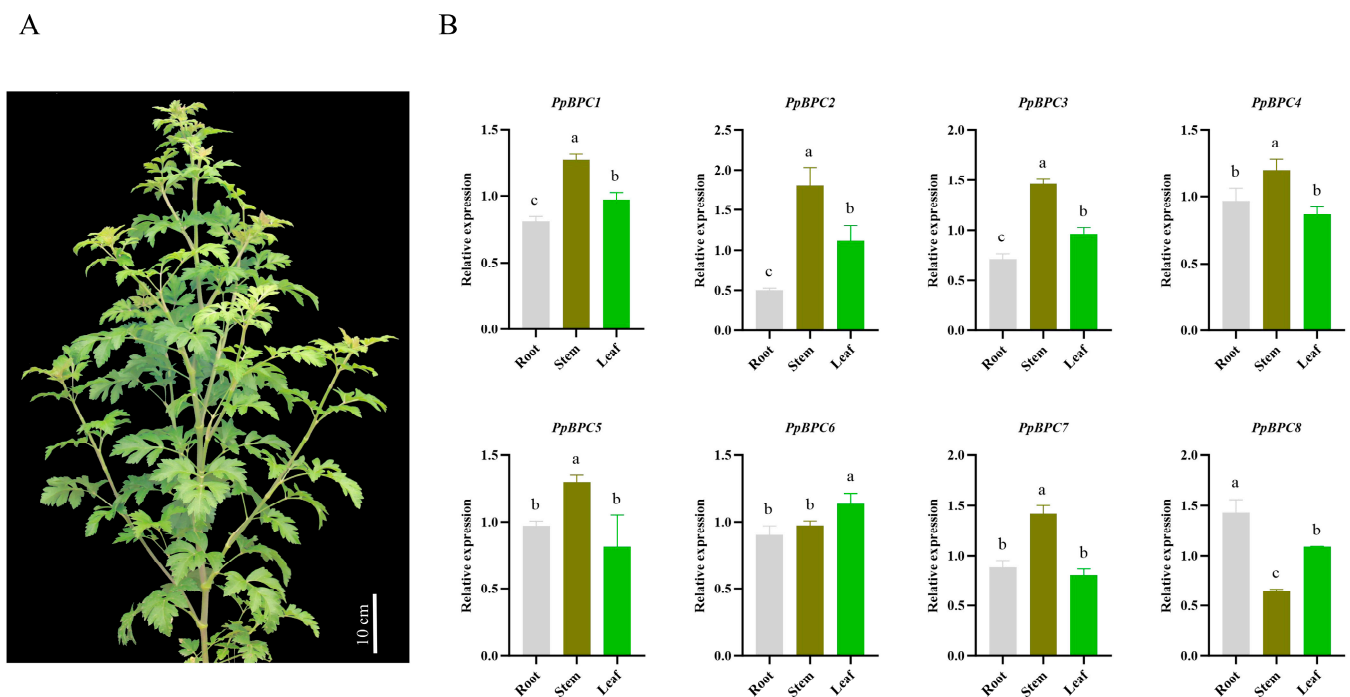


Figure 6. Organ-specific transcript profiles of *PpBPC* genes at the bolting stage. (A) Whole-plant morphology of a bolting-stage *P. praeurptorum* individual. (B) qRT-PCR-based quantification of *PpBPC* transcript levels in root, stem, and leaf tissues. One-way ANOVA followed by Duncan post-hoc test was performed using Microsoft Excel 2019 and SPSS 27.0.1. All bar charts were drawn in GraphPad Prism 10, with error bars representing the standard deviation (SD) of three biological replicates. Letters (a–c) above bars denote statistically significant differences among organs ($p < 0.05$).

3.7. Expression Analysis of *PpBPC* Genes Under Different Light Quality Treatments

Given the widespread occurrence of light-responsive cis-regulatory elements across all *PpBPC* promoters, we next tested whether these elements correspond to functional light-dependent transcriptional modulation. Seedlings were exposed to blue, red, and far-red light, with white-light-grown plants serving as the normalization baseline for comparative analysis (Figure 7).

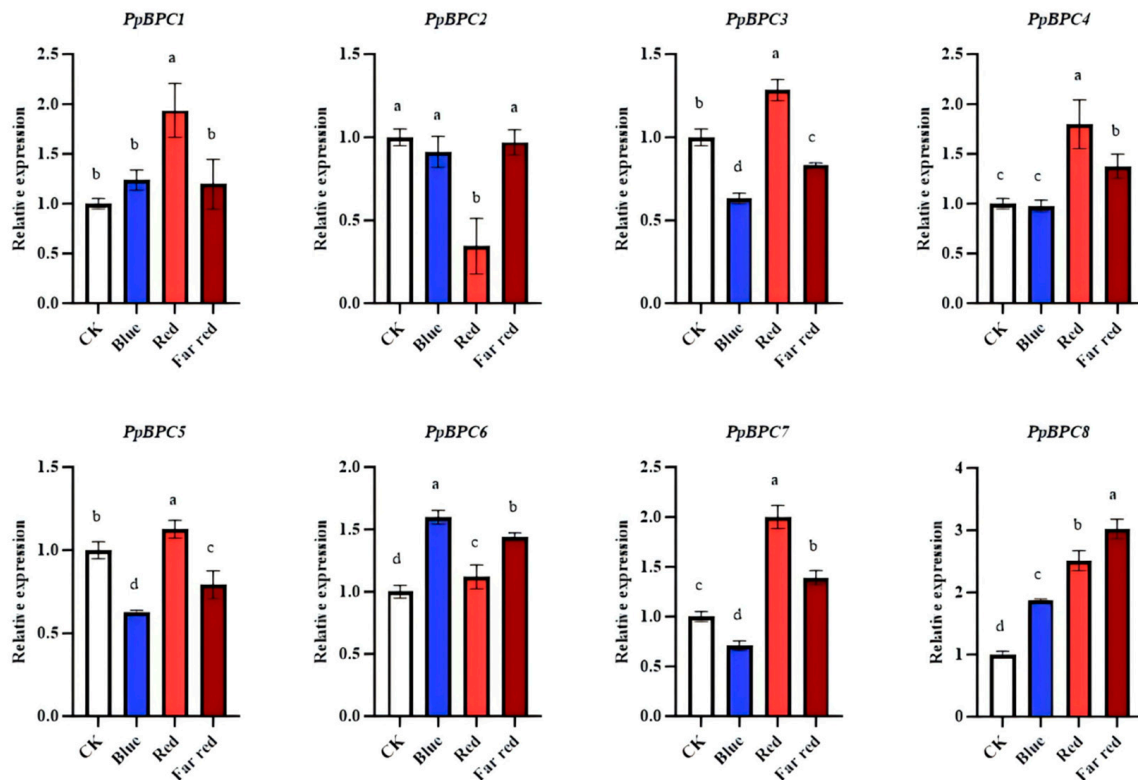


Figure 7. Light-quality-dependent expression of *PpBPC* genes measured by qRT-PCR. White light (full spectrum) was employed as the reference condition (CK; expression set to 1). One-way ANOVA followed by Duncan post-hoc test was performed using Microsoft Excel 2019 and SPSS 27.0.1. All bar charts were drawn in GraphPad Prism 10, with error bars representing the standard deviation (SD) of three biological replicates. Letters (a–d) above bars denote statistically significant differences among organs ($p < 0.05$).

The eight *PpBPC* genes exhibited heterogeneous responses depending on the wavelength applied. Under blue light, *PpBPC6* and *PpBPC8* were significantly upregulated relative to the white-light control; *PpBPC1*, *PpBPC2*, and *PpBPC4* remained statistically unchanged; and *PpBPC3*, *PpBPC5*, and *PpBPC7* showed significant downregulation. Red light treatment resulted in a broad activation: *PpBPC1* and *PpBPC3–PpBPC8* were all significantly upregulated, with *PpBPC2* as the sole member exhibiting significant suppression. Far-red light exposure significantly elevated the expression of *PpBPC4*, *PpBPC6*, *PpBPC7*, and *PpBPC8* relative to the control, whereas *PpBPC1* and *PpBPC2* showed no significant alteration and *PpBPC3* and *PpBPC5* were significantly repressed.

4. Discussion

Light serves as one of the most influential environmental inputs governing plant growth, developmental transitions, and metabolic output [29,30]. Upon light perception, signaling cascades converge on transcription factors that act as molecular switches to reprogram downstream gene networks, thereby enabling plants to tailor their physiology to the prevailing light environment [31–34]. Among these regulatory hubs, BASIC

PENTACYSTEINE (*BPC*) transcription factors have emerged as important participants in light-modulated processes [17]. Genome-wide surveys of the *BPC* family have now been completed for a range of species, including *A. thaliana* [10], soybean [35], barley [36], rice [37], cucumber [22], coconut [38], *B. napus* [39,40], and *B. juncea* [17]. *P. praeruptorum* is a medicinally valuable species in China, and its growth characteristics, secondary metabolite synthesis, and environmental response mechanisms have drawn increasing research attention [16,41–44]. Nevertheless, a comprehensive catalogue and functional appraisal of its *BPC* complement has been lacking. The present study addresses this gap by identifying eight *PpBPC* members and analyzing their sequence features, evolutionary relationships, organ-specific transcript profiles, and dynamic expression in response to blue, red, and far-red light treatments. These results lay the groundwork for understanding how *BPC*-mediated transcriptional regulation contributes to development and light signal processing in *P. praeruptorum*.

Evolutionary and structural data indicated that the *BPC* family is broadly conserved across plant taxa, with the GA-binding domain representing the most highly constrained region, while auxiliary domains and N-terminal activation regions display substantial sequence variability. This pattern mirrors a general principle of plant *BPC* evolution: strong selective pressure on the DNA-binding core preserves the fundamental regulatory capacity needed for viability, whereas diversification of accessory domains and transactivation regions provides the raw material for functional innovation. Moreover, the combination of conserved DNA-binding modules and multiple gene duplication mechanisms likely maintains a degree of functional buffering within the *PpBPC* family. Interspecific synteny analyses confirmed that *BPC* orthologous regions and their flanking chromosomal segments are well preserved across species boundaries, and that *BPC* gene pairs have consistently evolved under purifying selection. These observations agree with earlier work in *A. thaliana* demonstrating widespread functional overlap among *AtBPC* paralogs. The presence of an intact GAGA domain in every family member, together with evidence that *PpBPC* duplicated copies were generated by diverse duplication modes, provides a molecular rationale for the functional redundancy and regulatory robustness observed in this family. Within a given phylogenetic group, motif content and organization are highly uniform; across groups, however, pronounced sequence divergence is evident—a pattern consistent with subfunctionalization, neofunctionalization, or pseudogenization following rounds of polyploidization, although definitive mechanistic evidence awaits future functional validation experiments. Domain-centric analysis alongside phylogenetic inference indicates that the core functional region of *PpBPC* genes operates under tight evolutionary constraint, and the overall tempo of functional evolution appears comparatively restrained. Investigation of the origins of gene family expansion revealed that WGD/large segmental duplication and proximal duplication represent the principal forces driving the proliferation of the *PpBPC* repertoire, a scenario congruent with the known genomic history of Apiaceae—two ancestral polyploidization events coupled with lineage-specific chromosomal structural variations in *P. praeruptorum* [1]. Redundant gene copies produced by WGD and proximal duplication presumably undergo the aforementioned processes of functional divergence over evolutionary time to accommodate the regulatory requirements of plant development, with the interplay between structural variation in genes and the rewiring of spatiotemporal expression patterns serving as a central driving factor. This evolutionary logic appears to be a recurrent theme across *BPC* families from phylogenetically diverse plant species [10,17,22,35–40].

In contrast to the *A. thaliana* *BPC* family, where extensive functional divergence and mutual antagonism among subgroups have been reported [45], transcript profiling in *P. praeruptorum* revealed that Group A and Group C members possess largely overlapping

tissue-level expression signatures, suggestive of functional redundancy particularly in the context of stem development at the bolting stage. By comparison, Group B members displayed markedly distinct expression patterns, indicative of adaptive specialization. Notably, *PpBPC6* transcript levels peaked in leaf tissue, whereas *PpBPC8* was predominantly expressed in roots, implying that these two genes may serve as organ-specific regulators of leaf and root development, respectively. These findings resonate with observations in other species: in apple, *MdBPC2* affects leaf morphology and suppresses root growth [16], and disruption of *CsBPC2* in cucumber compromises root elongation [46]. Collectively, these observations point to an evolutionarily conserved involvement of *BPC* factors in root developmental programs across diverse plant species.

Promoters function as the primary interface through which genes sense and integrate developmental and environmental information [47–50]. Our promoter dissection showed that all eight *PpBPC* upstream regions are populated by a diverse repertoire of functional cis-elements spanning four major categories: light responsiveness, growth/development and stress responses, hormone signaling, and metabolism. This regulatory complexity implies that the *PpBPC* family may coordinate internal developmental programs with external stress adaptation through the convergence of multiple signaling inputs. The ubiquity of light-responsive elements across all *PpBPC* promoters suggests that light may act as a major upstream signal regulating the transcriptional output of this gene family.

The current study further substantiated the influence of distinct light wavelengths on *PpBPC* expression. Red light exerted a predominantly positive effect, significantly upregulating seven of the eight *PpBPC* members (all except *PpBPC2*, which showed no significant expression change). This broad transcriptional activation aligns with the well-characterized role of red light in promoting plant growth and development and is consistent with the established involvement of *BPC* genes in developmental regulation. Blue and far-red light, by contrast, elicited bidirectional responses: certain *PpBPC* genes were induced, others were repressed, and a subset remained relatively stable. Given the close association of blue and far-red wavelengths with photomorphogenic programs, the observation that *PpBPC6* and *PpBPC8* were strongly upregulated under both blue and far-red conditions implies that these two loci may be involved in light-mediated morphogenic regulation in *P. praeruptorum*, and they could serve as potential candidate genes for further research on plant light responses.

Nevertheless, we refrain from establishing a direct intrinsic regulatory linkage between the organ-specific expression of *PpBPC6*/*PpBPC8* and their light-inducible expression profile in this work. The leaf/root-biased expression of *PpBPC6* and *PpBPC8* was characterized in mature bolting-stage field plants, whereas their light responsiveness was identified in chamber-grown seedlings. Follow-up experiments with uniform plant materials at identical developmental stages under standardized culture conditions are required to validate whether light signals shape their tissue-specific expression patterns. Another limitation of the present study is that sampling was performed at day 7 of light treatment. Since light-induced gene expression exhibits obvious time dependence, we will include multiple time points in our subsequent experiments.

5. Conclusions

In summary, this work presents the first genome-wide characterization of the *BPC* transcription factor family in *P. praeruptorum*, encompassing eight members whose physico-chemical properties, evolutionary history, and transcriptional behavior were systematically examined. Meanwhile, these findings identify candidate light-responsive *PpBPC* genes and provide a basis for future functional studies on light-regulated transcriptional responses in *P. praeruptorum*. However, these findings are preliminary data derived from *P. praeruptorum*

samples collected at different growth stages with diverse light-quality treatments; further gene functional verification is therefore necessary to validate the above conclusions.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/horticulturae12080905/s1>, Table S1: Reference genome sources; Table S2: Primers for qRT-PCR analysis.

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