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iTRAQ-based proteomic and physiological analyses of broccoli sprouts in response to exogenous melatonin with $ZnSO_4$ stress†

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Exogenous melatonin (10 μM) enhances $ZnSO_4$ (4 mM) stress tolerance and regulates the isothiocyanate content of broccoli sprouts. Nevertheless, the molecular mechanism underlying the role of melatonin in isothiocyanate metabolism under $ZnSO_4$ stress is unclear. The effects of exogenous melatonin on growth and isothiocyanate metabolism in broccoli sprouts under $ZnSO_4$ stress during germination were investigated by physio-biochemical methods, quantification of relative gene expression levels, and the isobaric tags for the relative and absolute quantitation (iTRAQ) labelling technique. Compared with sprouts under $ZnSO_4$ stress alone, sprout length, fresh weight and free calcium content increased significantly in sprouts under $ZnSO_4$ stress plus melatonin treatment while electrolyte leakage and malonaldehyde content decreased. The glucosinolate content and myrosinase activity also significantly increased in sprouts under $ZnSO_4$ stress plus melatonin treatment compared with the control, and thus the isothiocyanate and sulforaphane content increased markedly. Meanwhile, the expression of glucoraphanin biosynthesis genes, such as *MYB28*, *CYP83A1*, *AOP2*, *BoSAT1*, and *BoHMT1* was significantly induced by melatonin in sprouts under $ZnSO_4$ stress. Furthermore, compared with sprouts under $ZnSO_4$ stress alone, a total of 145 proteins in broccoli sprouts under $ZnSO_4$ stress plus melatonin treatment showed differential relative abundances. These proteins were divided into 13 functional classes and revealed that pathways for sulfur metabolism, glucosinolate biosynthesis, selenocompound metabolism, biosynthesis of secondary metabolites and peroxisome were significantly enriched. The present study indicates that exogenous melatonin alleviates the adverse effects of $ZnSO_4$ stress on sprout growth and promotes glucoraphanin biosynthesis and the hydrolysis of glucoraphanin to form isothiocyanates in broccoli sprouts.

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1. Introduction

Broccoli sprouts have been widely consumed as functional foods and have become increasingly popular due to their high content of bioactive compounds, including flavonoids, ascorbic acid, anthocyanins and isothiocyanates (ITCs).[1–3] Among these, ITCs have raised scientific interest for their potential to reduce the risk of diseases including cancer,[4,5] inflammatory diseases[6,7] and cardiovascular diseases.[8,9] In a plant cell, ITCs can be metabolised from glucosinolates (GLSs) *via* myrosinase (MYR, EC 3.2.1.147). The ITC sulforaphane (4-methylsulfinylbutyl isothiocyanate) is the most promising anticancer agent with its unique properties in cancer prevention and treatment.[10] For these reasons, there is immense interest in accumulating ITCs in broccoli sprouts. Germination under abiotic stress, especially $ZnSO_4$ stress, is the most common and effective way of enhancing ITC content in broccoli sprouts.[11–13] However, the growth and development of sprouts are found to be markedly inhibited under $ZnSO_4$ stress, although the ITC content increases significantly.[13]

Melatonin (*N*-acetyl-5-methoxytryptamine) is a bioactive indole derivative that widely exists in plants. Previous research has shown that melatonin, as a master regulator, plays significant roles in modulating plant metabolism and regulating the growth and development of plants.[14,15] In multiple plant species, melatonin treatment can reduce the negative effects associated with stressors, and enhance tolerance to biotic and abiotic stress through the scavenging of reactive oxygen species and modulation of stress-related genes.[16,17] Moreover, in the secondary metabolism of the plant, melatonin induces the biosynthesis of flavonoids,[18,19] anthocyanins[20,21] and carotenoids,[22] among other molecules.[23] Similarly, according to our previous study, exogenous melatonin (10 μM) counters the harmful effects of $ZnSO_4$ stress (4 mM) and enhances sulforaphane content in broccoli sprouts during germination. Studies indicate that exogenous melatonin may be an ideal

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biotechnological target for improving ITC-enriched broccoli sprouts grown under stressful conditions.[24] Nevertheless, the molecular mechanism underlying the role of melatonin in the resistance to $ZnSO_4$ stress is still unclear.

Based on the issues above, in the present study, an isobaric tag for the relative and absolute quantitation (iTRAQ) labelling technique was employed to characterise the proteomic changes in broccoli sprouts under $ZnSO_4$ and $ZnSO_4$ plus melatonin treatment. The results of physiological and biochemical assays, gene expression levels and comparative proteomic analyses help to clarify the mechanisms by which ITC metabolism in broccoli sprouts is affected in response to $ZnSO_4$ plus melatonin treatment.

2. Experimental

2.1. Plant growth and experimental design

Broccoli seeds (*Brassica oleracea* L. var. Italica) were surface sterilised by soaking in 1% (v/v) sodium hypochlorite for 15 min and then steeped in distilled water at 30 °C for 4 h. The soaked seeds were spread evenly on a transparent square case (8.5 cm × 9 cm × 8 cm) filled with vermiculite and irrigated with distilled water. The cases were transferred to a controlled environment chamber with a 16 h light/8 h dark cycle at an air temperature of 30 °C. After 1 day of germination, treatments were applied as follows: (1) control check (CK, distilled water); (2) $ZnSO_4$ treatment (Zn, 4 mM $ZnSO_4$); (3) melatonin treatment (MT, 10 μM melatonin); (4) $ZnSO_4$ plus melatonin treatment (ZM, 4 mM $ZnSO_4$ + 10 μM melatonin). Broccoli sprouts were randomly sampled on days 4 and 6, and freeze-dried or stored frozen at −20 °C for further biochemical measurements. The concentrations of the solutions used and the germination times were selected based on our earlier experiments.

2.2. Determination of sprout length, fresh weight, malondialdehyde content, and electrolyte leakage

For the determination of the sprout length and fresh weight (FW), 30 sprouts from each treatment group were randomly selected, and their lengths and weights were measured. The content of malondialdehyde (MDA) was measured based on the method of Madhava and Sresty.[25] The electrolyte leakage was measured with a conductivity meter (DDS-307, China) according to the method of Dionisio-Sese and Tobita.[26]

2.3. Measurements of myrosinase activity, glucosinolate content, isothiocyanate content and sulforaphane content

The MYR activity was measured according to Burow *et al.*[27] with minor modifications. Sprouts were grinded in ice bath conditions with 3 mL 0.1 M phosphate buffer (pH 6.5), and centrifuged at 4 °C at 10 000*g* for 15 min. Supernatant (0.5 mL) was mixed with 0.5 mL sinigrin (0.25 mM). The content of glucose was determined using a Glucose Kit (F006-1-1, Nanjing Jiancheng Biological Engineering Research Institute, China). The MYR activity was expressed as nmol glucose formed per minute and mg total protein. The total GLS content was determined according to Guo *et al.*[28] The content of ITCs was determined according to the method of Jiao *et al.*[29] The content of sulforaphane was determined according to Guo *et al.*[30]

2.4. Determination of total antioxidant capacity and peroxidase activity

The total antioxidant capacity (T-AOC) and peroxidase (POD) activity were determined using a Plant T-AOC Assay Kit (A015-1-2, Nanjing Jiancheng Bioengineering Research Institute, China) and a Plant POD Assay Kit (A084-3, Nanjing Jiancheng Bioengineering Institute, China), respectively.

2.5. Determination of intracellular free calcium

The intracellular free calcium was measured according to the method of Cheng *et al.*[31]

2.6. RNA extraction and quantitative real-time PCR analysis

Total RNA was isolated from broccoli sprouts using an E.Z.N.A.™ Plant RNA Kit (R6827-01, OMEGA, USA) as described in the manufacturer's instructions. The RNA samples were reverse transcribed into cDNA by a PrimeScript™ RT Master Mix Kit (RR036A, Takara, Japan). Triplicate quantitative assays were performed on each cDNA using SYBRR Premix Ex-Taq™ (RR420A, Takara, Japan) and the ABI 7500 sequence detection system (Applied Biosystems, Calif., USA) according to the manufacturer's protocol. The sequence-specific primers used in the present study are listed in ESI Table S1.†

2.7. Protein extraction, digestion, and iTRAQ labelling

The total protein in 4 day-old broccoli sprouts was extracted using a Plant Total Protein Extraction Kit (PE0230, Sigma, USA). The protein concentration was determined using a Pierce™ Coomassie Protein Assay Kit (23200, Thermo Scientific, USA) using bovine serum albumin as the standard. The sample was reduced, alkylated, and then submitted to digestion with trypsin according to the method developed by Cheng *et al.*[31] Afterwards, each sample was labelled separately using the iTRAQ 8-Plex Kit (4381662, Sigma-Aldrich, USA) according to the manufacturer's instructions. Finally, all samples were combined and lyophilised.

2.8. LC-MS/MS and data analysis

The labelled samples were fractionated using a Thermo UHPLC U3000 Pump system (Thermo Fisher Scientific, San Jose, CA) with an ACQUITY UPLC BEH C18 RP column (1.7 μm particle size, 2.1 × 100 mm; Waters, USA). Detailed specific parameters for the LC-MS/MS analysis are given in our previous research.[31,32] The raw MS/MS files were processed using the Proteome Discoverer Software 1.4 (ESI Table S2 and ESI Fig. S2†). Protein identification was performed using the Sequest HT engine against the uniprot *Arabidopsis thaliana* database. The search parameters were as follows: trypsin was selected as the enzyme, with the tolerance set at one missed cleavage, a peptide allowance of 10 ppm, and an MS and MS/MS allowance of 0.02 Da. To be identified as important differentially abundant proteins (DAPs), a protein needed to contain at least one unique peptide with a *p*-value less than 0.05 and a fold change greater than 1.5 or less than 0.67.[32] Identified

proteins were annotated with their biological functions according to KEGG (http://www.genome.jp/kegg/) and the literature. Information on the DAPs was obtained from the Universal Protein Resource (http://www.uniprot.org/). Pathway enrichment analysis was performed using KOBAS 3.0 (http://kobas.cbi.pku.edu.cn/).

2.9. Statistical analysis

All data are expressed as mean values ± standard deviations of tests on three replicate independent broccoli sprouts. The data obtained were statistically analysed by one-way ANOVA and Tukey's test, and a p-value of less than 0.05 was considered significant. Relative gene expression was analysed by the $2^{-\Delta\Delta C_t}$ method.[33]

3. Results and discussion

3.1. Effect of melatonin on growth performance, sprout length, fresh weight, malondialdehyde content, and electrolyte leakage of broccoli sprouts

Compared with the control, $ZnSO_4$ treatment significantly inhibited the growth and development of broccoli sprouts (Fig. 1I), decreasing the sprout length and fresh weight (Fig. 1II and III). As indicators of membrane damage, electrolyte leakage and MDA content dramatically enhanced in broccoli sprouts under $ZnSO_4$ treatment ($p < 0.05$) (Fig. 1IV and V). Fig. 1I shows that the growth of broccoli sprouts was better after exogenous melatonin was applied than under $ZnSO_4$ stress alone. After germinating for 4 and 6 days under $ZnSO_4$ plus melatonin treatment, the sprout length and fresh weight showed increases while electrolyte leakage and MDA content decreased significantly ($p < 0.05$) compared with $ZnSO_4$ treatment alone (Fig. 1II–V). The above facts provide evidence that melatonin counters the adverse effects of $ZnSO_4$ stress in broccoli sprouts.

3.2. Effect of melatonin on glucosinolate content, isothiocyanate content, sulforaphane content, and myrosinase activity of broccoli sprouts

In plants, GLSs can be hydrolysed by MYR into ITCs. As shown in Fig. 2, compared with the control, the content of ITCs, sulforaphane and GLSs, and the MYR activity in broccoli sprouts all increased significantly during germination under $ZnSO_4$ and

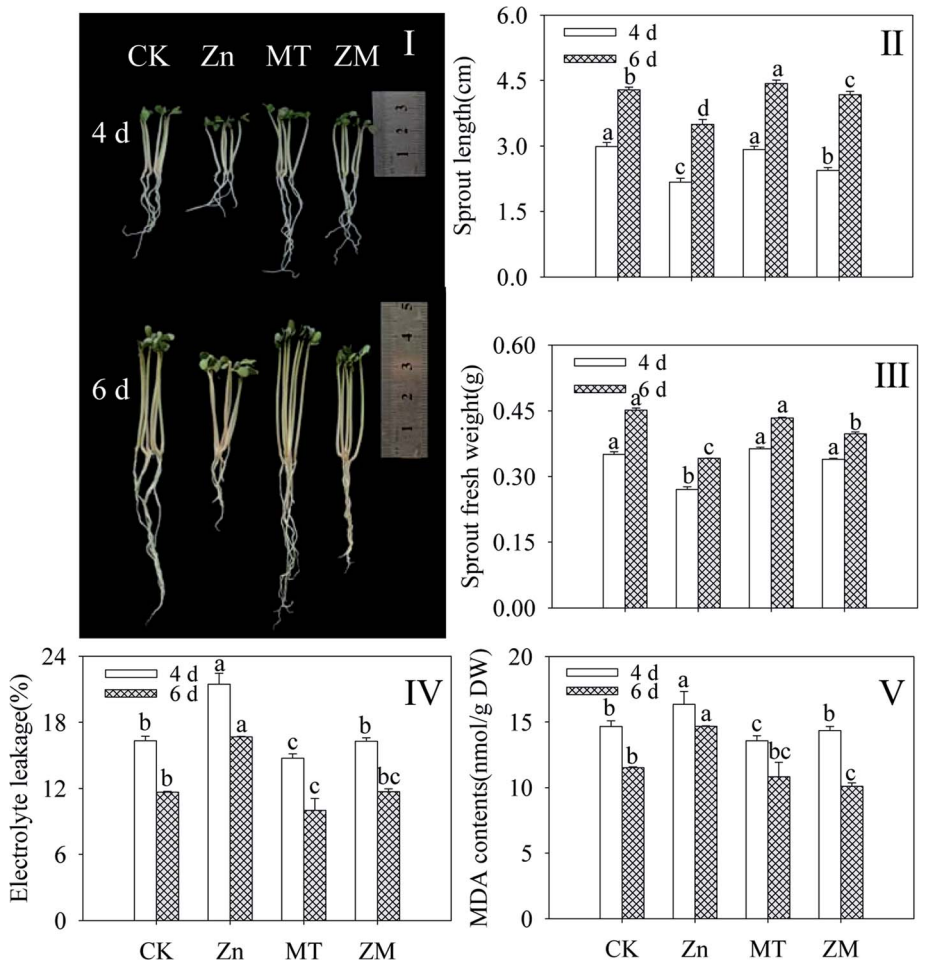

Fig. 1 Effect of exogenous melatonin on growth performance (I), sprout length (II), fresh weight (III), electrolyte leakage (IV), and MDA content (V) of broccoli sprouts under $ZnSO_4$ treatment during germination. Each data point represents the average of three independent biological replications (average ± SD). Lower case letters reflect the significance of the differences in indexes between treatments at the given germination times ($p < 0.05$). CK: control; Zn: $ZnSO_4$; MT: melatonin; ZM: $ZnSO_4$ + melatonin.

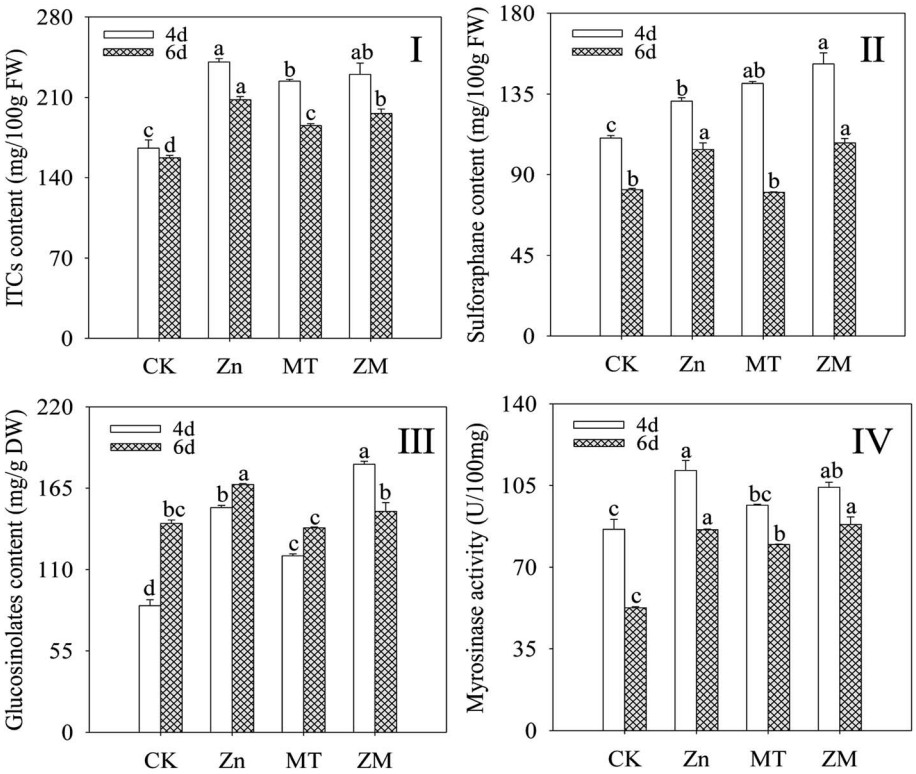

Fig. 2 Effect of exogenous melatonin on ITC content (I), sulforaphane content (II), GLS content (III), and MYR activity (IV) of broccoli sprouts under $ZnSO_4$ treatment during germination. Each data point represents the average of three independent biological replications (average ± SD). Lower case letters reflect the significance of the differences in indexes between treatments at the given germination times ($p < 0.05$). CK: control; Zn: $ZnSO_4$; MT: melatonin; ZM: $ZnSO_4$ + melatonin.

$ZnSO_4$ plus melatonin treatments ($p < 0.05$). Melatonin significantly enhanced the GLS and sulforaphane content after germination for 4 days ($p < 0.05$) compared with the $ZnSO_4$ treatment alone (Fig. 2II and III). There was no significant difference ($p > 0.05$) in ITC content or MYR activity under $ZnSO_4$ plus melatonin treatment in 4 day-old broccoli sprouts compared with those treated with $ZnSO_4$ alone.

3.3. Effect of melatonin on total antioxidant capacity and peroxidase activity of broccoli sprouts

T-AOC and POD activity were dramatically increased ($p < 0.05$) in broccoli sprouts exposed to $ZnSO_4$ treatment during germination (Fig. 3). However, the T-AOC and POD activity of 4 day-old broccoli sprouts under $ZnSO_4$ plus melatonin treatment were significantly lower than those treated with $ZnSO_4$ alone ($p < 0.05$).

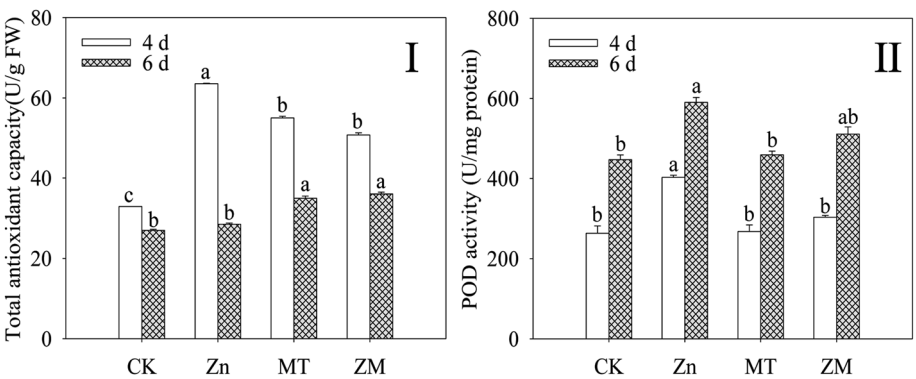

Fig. 3 Effect of exogenous melatonin on T-AOC (I) and POD activity (I) of broccoli sprouts under $ZnSO_4$ treatment during germination. Each data point represents the average of three independent biological replications (average ± SD). Lower case letters reflect the significance of the differences in indexes between treatments at the given germination times ($p < 0.05$). CK: control; Zn: $ZnSO_4$; MT: melatonin; ZM: $ZnSO_4$ + melatonin.

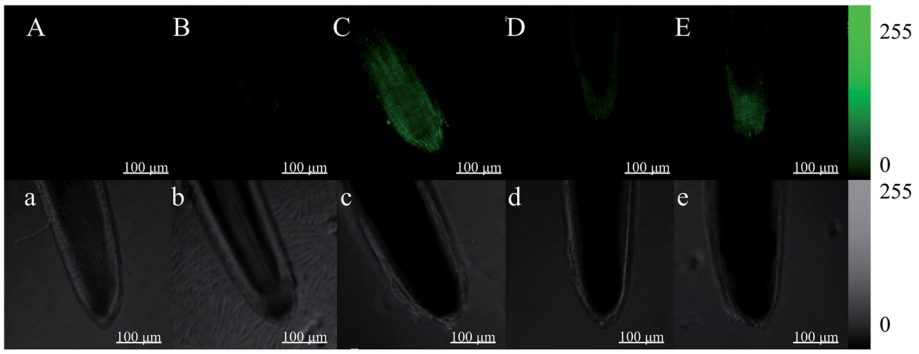

Fig. 4 Changes in the calcium ion content of sprout root tip cells after different treatments for 4 days. (B) Control; (C) $ZnSO_4$; (D) melatonin; (E) $ZnSO_4$ + melatonin. (A) Root tip cells treated with distilled water without the addition of probe before observation under the laser scanning confocal microscope. (A–E) show pseudocolor images of Ca^{2+} in the root tip, and (a–e) show the corresponding pictures taken under a bright field. The color bars on the right side show the minimum (0) and maximum intensities (255). Scale bar = 100 μm.

3.4. Effect of melatonin on intracellular free calcium of broccoli sprouts

Root tips of broccoli sprouts cultured in vermiculite for 4 days were cut into 4 mm lengths and then put into an HBSS buffer solution in the presence (Fig. 4B–E) or absence of Fluo-4 AM (Fig. 4A). The root tips were observed after incubation. The cell wall and cytoplasm of the broccoli sprout root tip without the Fluo-4 AM treatment both showed no spontaneous fluorescence. However, under the $ZnSO_4$ stress and $ZnSO_4$ plus melatonin treatments, the fluorescence intensities of the root tip cell walls treated with Fluo-4 AM were significantly higher than that of the control, exhibiting a brighter green fluorescence.

3.5. Changes in gene expression of key enzymes in ITC synthesis in broccoli sprouts

As shown in Fig. 5, the expression of *OX1* was induced by $ZnSO_4$, melatonin and their combined treatment in 4 day-old broccoli sprouts while the expression of *ST5b* was reduced ($p < 0.05$) (Fig. 5II and III). $ZnSO_4$ treatment also significantly reduced the expression of *UGT74B1*, while the other treatments had no significant effect (Fig. 5I). $ZnSO_4$ plus melatonin treatment significantly increased the expression of *MYB28* compared with the control (Fig. 5V). In $ZnSO_4$ and $ZnSO_4$ plus melatonin treated 4 day-old sprouts, the respective expression levels of *AOP2* were 3.79- and 2.74-fold that of the control, respectively (Fig. 5VIII). $ZnSO_4$ plus melatonin treatment significantly increased the expression of *CYP83A1* and *BOHMT1*, while the other two treatments had no significant effect on them (Fig. 5VI and X). Compared with the control, other treatments all increased the expression of *CYP83A1* (Fig. 5VI). $ZnSO_4$ plus melatonin treatment increased the expression of *BOHMT1* to 1.82 times that of the control (Fig. 5X). Compared with the control, $ZnSO_4$ plus melatonin significantly increased the expression level of *BOSAT1*, while $ZnSO_4$ treatment gave no significant change ($p > 0.05$) (Fig. 5IX).

3.6. iTRAQ analysis and identification of differentially abundant proteins

In the present study, a total of 466 DAPs were identified from all replicates and different treatments used (ESI Table S3†). A total of 152 DAPs were identified in the Zn *vs.* CK samples, consisting of 150 up-regulated and 2 down-regulated proteins, 108 DAPs were identified in the MT *vs.* CK samples with 100 up-regulated and 8 down-regulated, 145 DAPs were identified in the ZM *vs.* Zn samples with 135 up-regulated and 10 down-regulated, and 165 DAPs were identified in the ZM *vs.* MT samples with 117 up-regulated and 48 down-regulated (Fig. 6 and 7). A hierarchical clustering analysis of the DAPs in the four comparison groups revealed different expression patterns. The ZM *vs.* Zn and Zn *vs.* CK groups had nine common DAPs; while 12 DAPs were found in both ZM *vs.* Zn and MT *vs.* CK, and 27 common DAPs were found in Zn *vs.* CK and ZM *vs.* MT. Only one DAP overlapped in all four comparison groups. A total of 92, 56, 115 and 114 DAPs were independently expressed in Zn *vs.* CK, MT *vs.* CK, ZM *vs.* Zn, and ZM *vs.* MT, respectively (Fig. 6).

According to the molecular functions listed on the UniProt and KEGG websites, these DAPs could be divided into 13 functional classes, *i.e.*, defense/stress, protein biosynthesis, carbohydrate metabolism, amino acid metabolism, protein folding and degradation, protein destination and storage, nucleotide metabolism, energy, signal transduction and transcription, transport, lipid metabolism, secondary metabolism, and other (Fig. 7). After germinating for 4 days under $ZnSO_4$ plus melatonin, the abundance of all of the DAPS in the defence/stress, secondary metabolism, signal transduction and transcription, energy, and carbohydrate metabolism classes increased significantly, while the nucleotide metabolism-related DAPs decreased compared with the levels in the sprouts under $ZnSO_4$ stress alone (Fig. 7).

These DAPs were analysed using bioinformatics approaches to obtain relevant pathway information. All of the identified peptides and DAPs under the different treatments were classified into three major gene ontology (GO) categories: biological processes (BP), cellular components (CC), and molecular

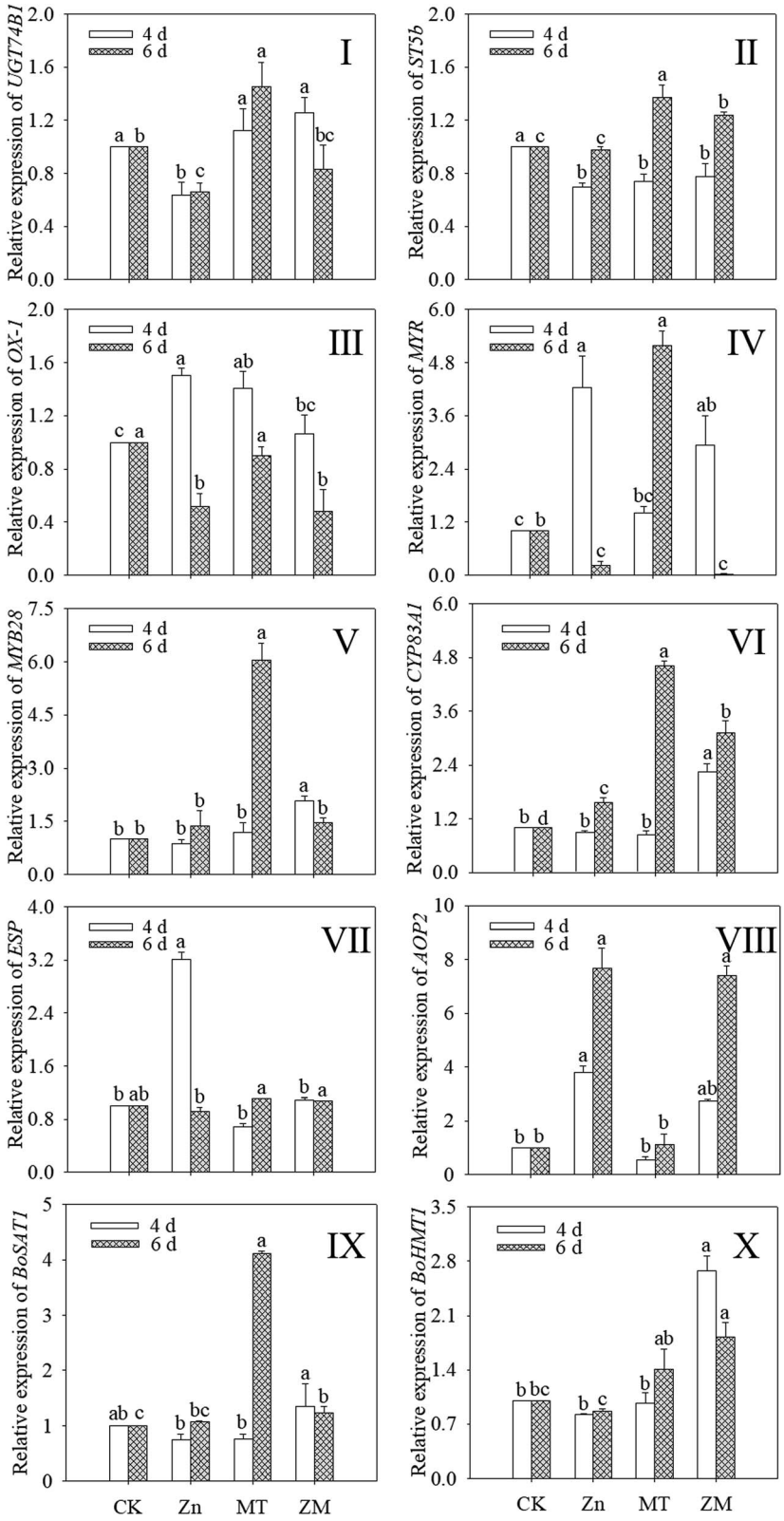

Fig. 5 Changes in relative expression levels of UGT74B1 (I), ST5b (II), OX-1 (III), MYR (IV), MYB28 (V), CYP83A1 (VI), ESP (VII), AOP2 (VIII), BOSAT1 (IX), and BOHMT1 (X) in broccoli sprouts under different treatments during germination. Lower case letters reflect the significance of the differences in indexes between the treatments at the given germination times ($p < 0.05$). CK: control; Zn: $ZnSO_4$; MT: melatonin; ZM: $ZnSO_4$ + melatonin.

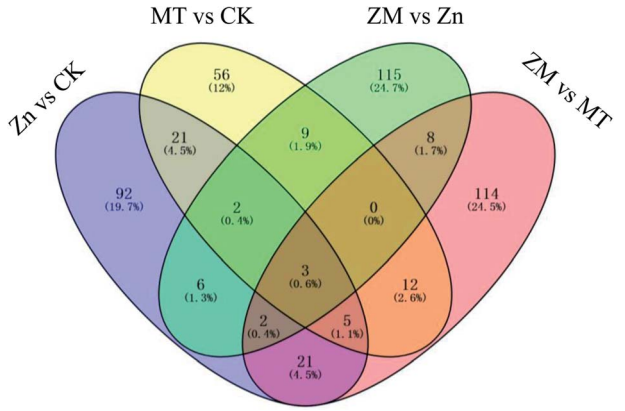

Fig. 6 Venn diagram showing the numbers of DAPs in broccoli sprouts dependent on the different treatments. CK: control; Zn: $ZnSO_4$; MT: melatonin; ZM: $ZnSO_4$ + melatonin.

functions (MF). The most common biological processes were oxidation–reduction processes; the most common molecular functions related to structural constituents of the ribosome and metal ion binding; and the most common cellular components were in the cytosol, cytoplasm and chloroplasts (Fig. 8).

In order to analyse the affected metabolic pathways, the DAPs were further researched using the KEGG database. The pathway enrichment analysis identified 17, 16, 14 and 15 KEGG pathways for the Zn *vs.* CK, MT *vs.* CK, ZM *vs.* Zn and ZM *vs.* MT groups, respectively, taking a *p*-value of less than 0.05 as the threshold (Table 1). They participated in pathways involving for example carbon metabolism, biosynthesis of secondary metabolites and selenocompound metabolism.

3.7. Discussion

Stressful conditions can strongly enhance the ITC content of plants.[34] In the present study, under $ZnSO_4$ treatment, the ITC content in broccoli sprouts significantly increased (Fig. 2I), indicating that broccoli sprouts can be used as a good source of functional health components. However, $ZnSO_4$ stress also inhibited the growth and development of the sprouts (Fig. 1I–III). Stress triggers reactive oxygen species (ROS) accumulation and breaks down the balance between ROS generation and detoxification in plants.[35] The accumulation of ROS can induce lipid peroxidation and chlorophyll degradation, and cause the loss of cell membrane integrity.[36] Compared with the control, electrolyte leakage and MDA content increased markedly in broccoli sprouts under $ZnSO_4$ treatment (Fig. 1IV and V).

As an abiotic anti-stressor, melatonin mediates multiple physiological processes in plants such as growth, development, and enhanced tolerance of abiotic stress.[15] After germinating under $ZnSO_4$ plus melatonin treatment, the sprouts' lengths and fresh weights increased while electrolyte leakage and MDA content decreased significantly ($p < 0.05$) compared to those germinated with $ZnSO_4$ treatment alone (Fig. 1). The results confirmed that exogenous melatonin could not only alleviate the adverse effects of $ZnSO_4$ stress on sprout growth and development, but also increase the sulforaphane content in broccoli sprouts (Fig. 1 and 2).

As a plant cell signaling ion, Ca^{2+} plays a key role in adjusting plant growth and development under biotic and abiotic stress. External stimulation can increase intracellular Ca^{2+}, which moderates transcription through the bioregulation of transcription factors. In the present study, it was observed that

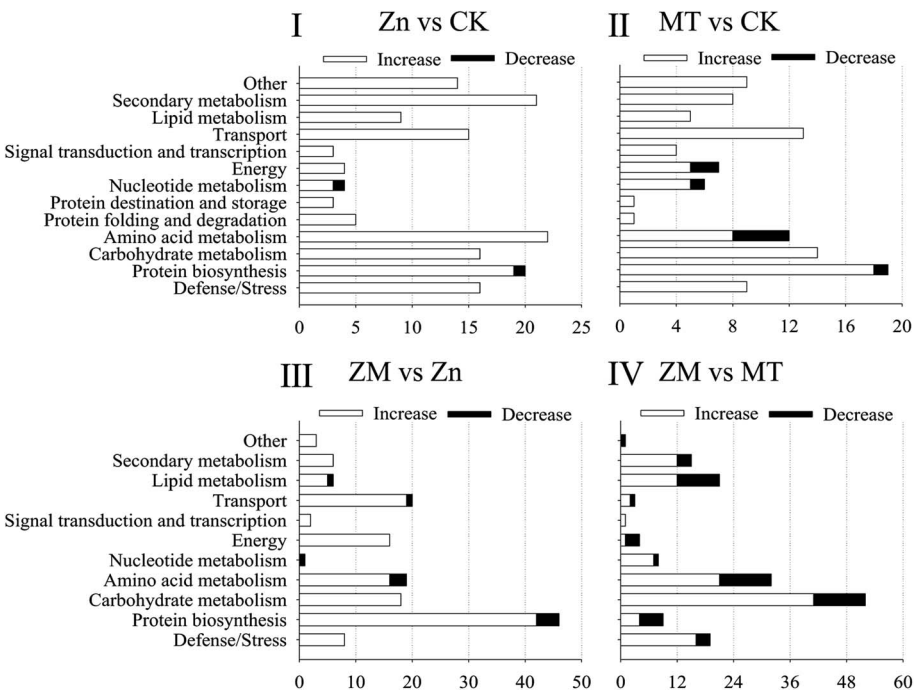

Fig. 7 The abundance of DAPs in each functional classification for the comparison groups. The *x*-axis represents the numbers of DAPs enriched in each functional classification; the *y*-axis specifies the functional classifications. CK: control; Zn: $ZnSO_4$; MT: melatonin; ZM: $ZnSO_4$ + melatonin.

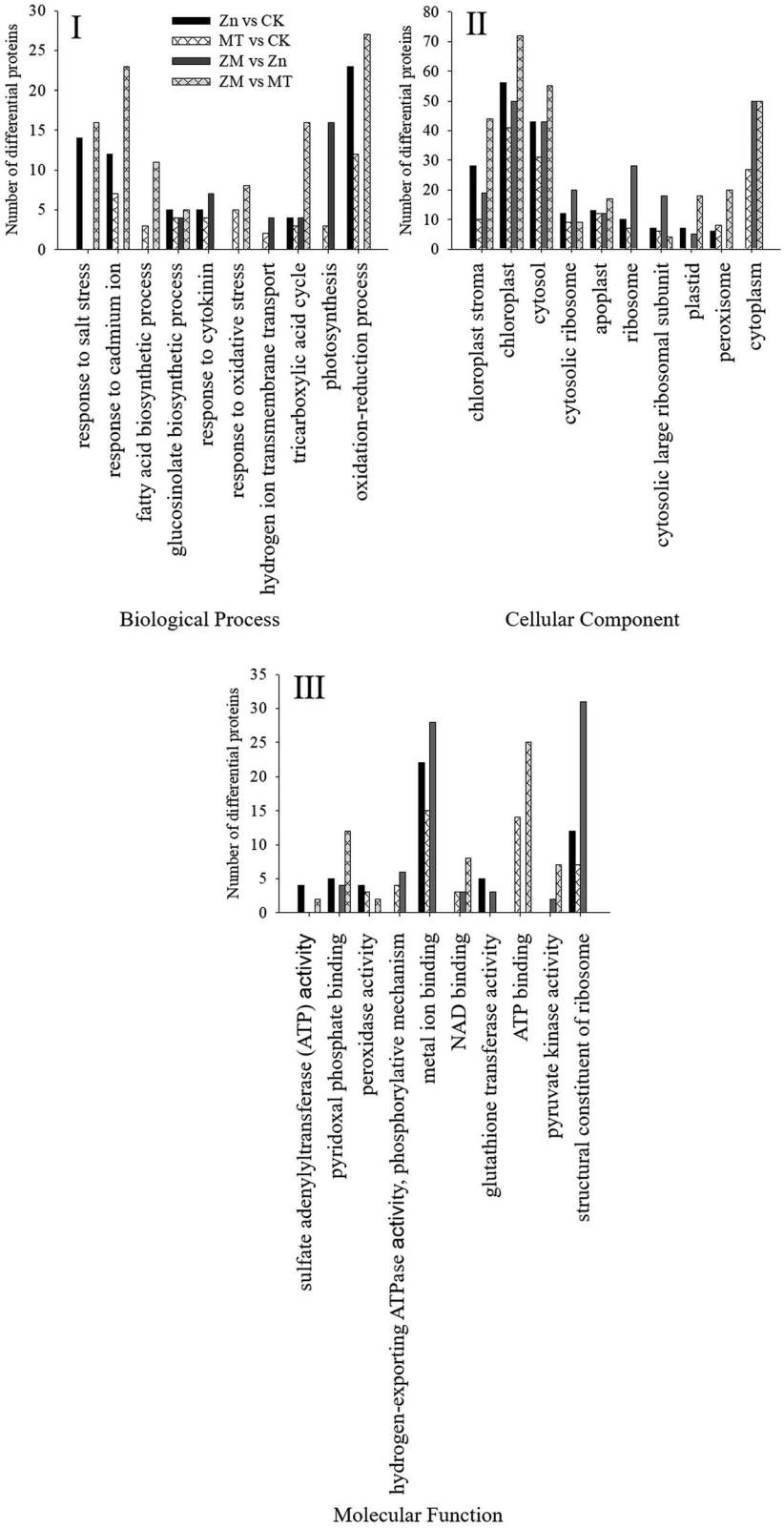

Fig. 8 GO classification of all DAPs found in broccoli sprouts under the different treatments. (I) Number of proteins in pathways of the biological process classification. (II) Number of proteins in different cellular components. (III) Number of proteins in pathways of the molecular function classification. CK: control; Zn: $ZnSO_4$; MT: melatonin; ZM: $ZnSO_4$ + melatonin.

Table 1 Primary reagent pathway enrichment analysis of DAPs in broccoli sprouts

		Input number				*p*-Value			
Pathway ID	Pathway	Zn *vs.* CK	MT *vs.* CK	ZM *vs.* Zn	ZM *vs.* MT	Zn *vs.* CK	MT *vs.* CK	ZM *vs.* Zn	ZM *vs.* MT
ath01100	Metabolic pathways	64	36	61	106	1.70×10^{-43}	2.62×10^{-20}	9.31×10^{-37}	4.79×10^{-101}
ath01110	Biosynthesis of secondary metabolites	36	19	23	88	3.89×10^{-24}	6.92×10^{-11}	1.34×10^{-10}	5.62×10^{-95}
ath00920	Sulfur metabolism	12	2	1	7	7.29×10^{-19}	0.0061	1.0000	1.70×10^{-9}
ath00450	Selenocompound metabolism	9	2	1	4	1.84×10^{-16}	0.0011	1.0000	1.88×10^{-6}
ath01200	Carbon metabolism	16	9	20	61	3.84×10^{-14}	1.09×10^{-7}	1.47×10^{-18}	1.32×10^{-84}
ath01230	Biosynthesis of amino acids	13	3	10	47	3.60×10^{-11}	0.0344	1.75×10^{-7}	6.66×10^{-61}
ath00966	Glucosinolate biosynthesis	6	2	4	5	1.63×10^{-9}	0.0024	5.93×10^{-6}	2.06×10^{-7}
ath00380	Tryptophan metabolism	7	4	2	5	6.78×10^{-9}	2.83×10^{-5}	0.0279	1.13×10^{-5}
ath00190	Oxidative phosphorylation	9	8	10	1	7.09×10^{-8}	6.27×10^{-8}	1.06×10^{-8}	1.0000
ath03010	Ribosome	11	6	28	4	1.56×10^{-6}	0.0015	1.27×10^{-24}	0.1501
ath00020	Citrate cycle (TCA cycle)	4	3	2	20	0.0001	0.0007	0.0306	7.39×10^{-30}
ath01212	Fatty acid metabolism	3	3	1	14	0.0019	0.0007	0.2308	2.21×10^{-19}
ath00195	Photosynthesis	3	3	7	1	0.0055	0.0021	1.54×10^{-7}	1.0000
ath04146	Peroxisome	2	4	1	13	0.0375	7.17×10^{-5}	1.0000	1.59×10^{-16}
ath00620	Pyruvate metabolism	3	2	9	24	0.0057	0.0267	3.32×10^{-10}	4.33×10^{-34}
ath00061	Fatty acid biosynthesis	3	1	1	8	0.0004	0.0952	0.1418	1.55×10^{-11}
ath00710	Carbon fixation in photosynthetic organisms	2	1	8	15	0.0342	1.0000	1.62×10^{-9}	4.52×10^{-20}

$ZnSO_4$ stress treatment and $ZnSO_4$ plus melatonin could significantly induce Ca^{2+} influx into sprout root tip cells (Fig. 4), similar to the increase seen in Ca^{2+} in barley root tip cells under salt stress.[37]

The transcription levels of key genes including *MYB28*, *UGT74B1*, *ST5b*, *OX1*, *MYR*, *ESP*, *CYP83A*, *AOP2*, *BOSAT1* and *BOHMT1* under the different treatments in broccoli sprouts were analysed using qRT-PCR (Fig. 5). *MYB28* is a major gene which regulates aliphatic-glucosinolate synthesis;[38] *UGT74B1* and *ST5b* are involved in the formation of the core glucosinolate biosynthesis;[39] $FMO_{GS\text{-}OX1}$ is involved in side-chain modification of glucosinolate; and *MYR* and *ESP* can regulate the hydrolysis of glucosinolates to ITCs.[13] In the present study, the expression of ITC synthesis-related genes showed different changes under the treatments of $ZnSO_4$ and $ZnSO_4$ plus melatonin. This phenomenon has also been observed in heat shock and hypoxia treatments.[30] $ZnSO_4$ up-regulated the gene expression of *MYR*, *ESP*, $FMO_{GS\text{-}OX1}$, and *AOP2* to increase the content of glucosinolates, thereby enriching ITC content. The increase in MYR activity might be related to its gene expression. Yang *et al.*[13] found that $ZnSO_4$ stimulated the formation of ITCs by enhancing the gene expression and activity of MYR, and the gene expression and glucosinolate content in broccoli sprouts. After germination for 4 days, the reduction of glucosinolate content under melatonin treatment was not related to the expression of *MYR*, *ESP*, *AOP2* or *ST5b*. Moreover, MYR activity was not consistent with its gene expression level.

Methylthioalkylmalate synthase 1 (MAM1), isopropylmalate isomerase 2 (IPMI2), 3-isopropylmalate dehydratase large subunit (IIL1), 3-isopropylmalate dehydrogenase (IMD1), branched-chain-amino-acid aminotransferase 3 (BCAT3), cytosolic sulfotransferase 16 (STO16), cytosolic sulfotransferase 17 (SOT17), cytosolic sulfotransferase 18 (SOT18), cytochrome P450 83B1 (CYP83B1), myrosinase 1 (MYR1), myrosinase 2 (MYR2), epithiospecifier protein (ESP) and nitrile-specifier protein 2 (NSP2) play an important role in the formation of ICTs.[40] In the present study, from the iTRAQ data, IPMI2 (A0A178VZE1), IIL1 (Q94AR8), IMD1 (Q5XF32), STO16 (Q9C9D0), SOT17 (Q9FZ80) and CYP83B1 (O65782) involved in the metabolism of aliphatic glucosinolates differed markedly in abundance under the different treatments, while MAM1 (Q9FG67), BCAT3 (Q9M401) and SOT18 (Q9C9C9) involved in the metabolism of indole glucosinolate metabolism were not significantly changed (ESI Table S1†). The $ZnSO_4$ and $ZnSO_4$ plus melatonin treatments positively regulated the metabolism of aliphatic glucosinolates by increasing the relative abundance of IPMI2, IMD1, STO16 and SOT17. The results indicate that the up-regulation of these proteins had a positive regulatory effect on the metabolism of aliphatic thiocyanates, and thus increased the ITC content. In the present study, some enzymes (CYP79F1, UGT74B1, FMOGS-OX1, AOP2), involved in the formation of the core structure of the aliphatic glucosinolates in broccoli sprouts were not detected. It might be that the abundance of these proteins was too low to be detected in this test, or that these enzymes in broccoli were less compatible with those in the *Arabidopsis thaliana* database; these proteins were also not detected in the previous study.[30] MYR1 (P37702), MYR2

(Q9C5C2), ESP (Q8RY71) and NSP2 (O49326) were detected; Koroleva[41] and Guo *et al.*[30] also detected MYR1 and MYR2. Under $ZnSO_4$ treatment, the abundance of MYR1, MYR2 and ESP in broccoli sprouts increased significantly compared with the control, while the abundance of NSP2 did not change significantly. MYR activity was consistent with protein expression, and the expression of the ESP gene was consistent with that of the protein, showing that $ZnSO_4$ enriches ITCs in broccoli sprouts by increasing the gene expression and protein expression of glucosinolates, and increasing MYR activity and the abundance of MYR1 and MYR2. Compared with $ZnSO_4$ treatment, the abundance of MYR1, MYR2 and ESP did not significantly differ under $ZnSO_4$ plus melatonin treatment, while MYR activity and MYR gene expression increased compared with the control, indicating that $ZnSO_4$ plus melatonin improves MYR activity and induces MYR1 and MYR2 protein abundance, therefore enriching ITCs.

In the present study, under $ZnSO_4$ stress, antioxidant enzyme-related DAPs were stimulated, such as superoxide dismutase (F4J504) and peroxidase (F4IQ05). Compared with $ZnSO_4$ treatment, $ZnSO_4$ plus melatonin treatment enhanced the antioxidant capacity of broccoli sprouts by increasing the F4IQ05 abundance, while the F4J504 protein abundance did not change significantly.

According to the hierarchical clustering analysis of DAPs, the four comparison groups showed different expression patterns (ESI Fig. S1†). Carbohydrate catabolism and amino acid metabolism produce the energy for many processes, and also provide basic carbon skeletons for the biosynthesis of secondary metabolites.[42] In the current study, one of the most remarkable changes associated with melatonin application was the up-regulation of many proteins related to photosynthesis and carbohydrate metabolism in response to $ZnSO_4$ stress. During photosynthesis, the reaction-center subunit of the photosystem serves as the key site in plants that can be damaged by stress such as that of $ZnSO_4$. $ZnSO_4$ stress increased photosynthetic proteins in broccoli sprouts (P56778, Q8HT11), while melatonin treatment decreased photosynthetic proteins (P56778). These results indicate that $ZnSO_4$ stress inhibits photosynthesis in seedlings, whereas melatonin can enhance energy conversion during $ZnSO_4$ stress.

Ribosomes are large macromolecular ribosomal proteins (r-proteins) responsible for catalysing protein synthesis in the cell and play a crucial role in regulating cell growth, differentiation, and development.[43] In the present study, the majority of r-proteins were up-regulated significantly under $ZnSO_4$ stress. However, plants treated with melatonin showed significant increases in r-proteins compared to untreated plants under $ZnSO_4$ stress alone. For instance, nine 40S r-proteins (A0A178UFG0, A0A178VBG6, F4K5C7, P59224, Q8VYK6, Q93VH9, Q9M0E0, Q9SIK2 and Q9SIW5), 14 60S r-proteins (A0A178V6A2, A8MQA1, P38666, P41127, P51420, P59231, P60040, Q42064, Q42347, Q8VZB9, Q93VI3, Q9FF90, Q9M0E2 and Q9SF53), two 30S r-proteins (A0A1B1W4U6, A0A1B1W4X5) and one 50S r-protein (Q9SYL9) were dramatically induced by $ZnSO_4$ stress. A previous study has also shown that melatonin enhances heat resistance by promoting protein biosynthesis in tomato plants.[44] These results indicate that the promotion of protein biosynthesis might be a very important response of broccoli sprouts under melatonin plus $ZnSO_4$ treatment.

4. Conclusions

Physiological and comparative proteomic analyses have revealed the putative molecular mechanism of exogenous melatonin treatment on induced $ZnSO_4$ stress responses (Fig. 9). Exogenous melatonin reduced electrolyte leakage and MDA content, induced the levels of peroxidase, ribosomal and defence-related proteins, and thus improved the growth and development of broccoli sprouts and alleviated the negative effects caused by $ZnSO_4$ stress. Meanwhile, compared with the control, exogenous melatonin contributed to glucoraphanin

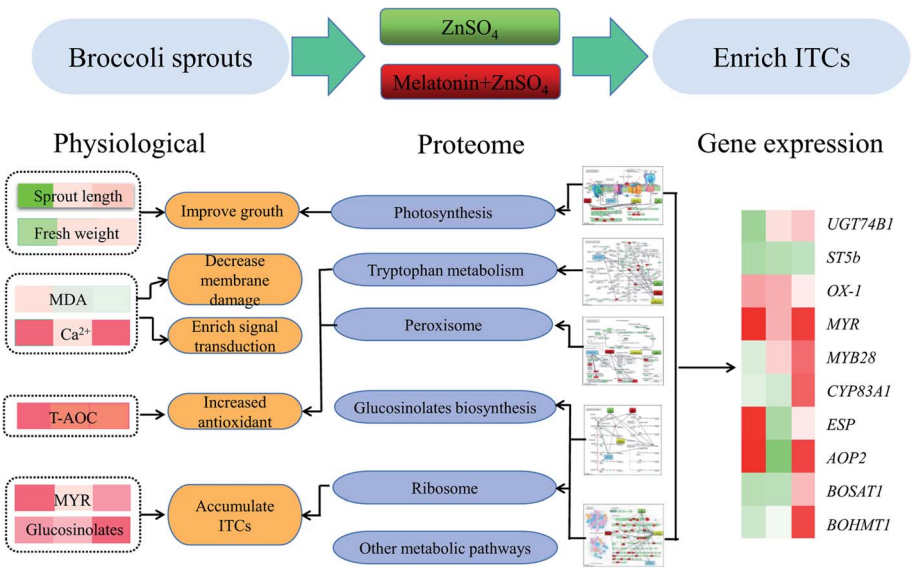

Fig. 9 Putative molecular mechanism of exogenous melatonin treatment on induced $ZnSO_4$ stress responses in 4 day-old broccoli sprouts.

biosynthesis and the hydrolysis of glucoraphanin to form ITCs in broccoli sprouts under $ZnSO_4$ stress *via* up-regulating the expression levels of glucoraphanin biosynthesis genes, increasing glucosinolate content and myrosinase activity, and increasing the abundance of myrosinase and epithiospecifier proteins. These results provide novel insights into the accumulation of ITCs in broccoli sprouts and provide new evidence to support the multiple roles of melatonin in moderating $ZnSO_4$ stress.

Conflicts of interest

There are no conflicts of interest to declare.

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