



## Exploring the Role of Bioactive Polyphenolic Antioxidants in Salinity Tolerance of Two Rice Landraces from Coastal Areas of Bangladesh

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### Abstract

The bioactive polyphenolic compounds (BPC), play an important role in the restoration of cellular redox homeostasis but are seldom studied in context of salinity stress tolerance in rice. RP-HPLC based comparative analysis of some important bioactive polyphenolic compounds (gallic acid, protocatechuic acid, para-hydroxy benzoic acid, catechin, chlorogenic acid, vanillic acid, caffeic acid, syringic acid, p-coumaric acid, ferulic acid, sinapic acid, salicylic acid, naringin, rutin, ellagic acid, myricetin, quercetin, naringenin, apigenin and kaempferol) from seedling of two rice landraces (*Oryza sativa* L. landraces Kutepatnai and Charobalam) subjected to post imbibitional salinity stress (PISS) not only exhibited differential landrace specific accumulation but also exhibited strong correlation with salinity tolerance. The landrace Kutepatnai exhibiting the ability to maintain redox homeostasis under PISS (assessed in terms of biomarkers of oxidative stress like the relative reactive oxygen species accumulation, relative total antioxidant competence and relative oxidative membrane damage) showed significantly greater up-regulation of majority of the polyphenolic compounds derived from chalcone synthase, and cinnamic acid dependent pathway as compared to the salt susceptible landrace Charobalam. The positive correlation between bioaccumulation of BPC (protocatechuic acid, ellagic acid, caffeic acid, syringic acid, rutin, catechin, myricetin, quercetin and apigenin) with redox parameters suggests their role in regulation of redox homeostasis necessary for salt tolerance in experimental land races of coastal areas of Bangladesh.

**Keywords:** Rice Landraces; Salinity Tolerance; Bioactive Polyphenolic Compounds; Antioxidants; Redox Homeostasis

### Abbreviations

ROS: Reactive Oxygen Species; DNA: Deoxyribonucleic Acid; BPC: Bioactive Polyphenolic Compounds; HgCl<sub>2</sub>: Mercuric Chloride; PISS: Post Imbibitional Salinity Stress; DPPH: 2, 2'-diphenyl-1-picrylhydrazyl; DCFDA: 2', 7'-dichlorofluoresceindiacetate; TRIS-HCl: Tris (hydroxymethyl) Aminomethane (THAM) Hydrochloric Acid; RRA: Relative ROS Accumulation; TAC: Total Antioxidant Capacity; TBARS: Thiobarbituric Acid Reactive Compounds; TCA: Trichloroacetic Acid; TBA: Thiobarbituric Acid; RLP: Relative Lipid Peroxi-

ation; T<sub>50</sub>: Time (in hour) of 50% Germination of Seeds Sown; RP-HPLC: Reverse Phase High Performance Liquid Chromatography; DAD: Diode Array Detector; NaCl: Sodium Chloride

### Introduction

Salinity is one of the prime abiotic stress factors that affects various metabolic and physiological pathways in plants such as reducing growth, development, and ultimately impacting global crop yield, slowing down growth and development, and ultimately

impacting crop yields globally [1,2]. Plants are basically harmed by ion toxicity, nutritional imbalance, secondary osmotic and oxidative stresses when there is a high salt concentration in the soil and irrigation water [3-6]. Different plant species and genotypes within a species react to salt stress in different ways. In saline environment, certain moderately or highly salt-tolerant plants can survive. In presence of high salt concentrations, these species are able to avoid ion toxicity and maintain water uptake [7]. Furthermore, salt-tolerant varieties have a stronger antioxidant defense system to combat oxidative damages induced by reactive oxygen species (ROS) induced oxidative damages [8]. Rice landraces tolerant to salinity thus play a vital part in local food security in saline coastal areas and agriculture's long-term sustainability, in addition to their usefulness as a genetic resource for rice genetic improvement [9,10].

In general, salinity leads to the accumulation of antioxidant molecules, which are important in counterbalancing oxidative stress [11-13]. Overproduction of ROS is exacerbated by salinity, which causes oxidative damage by oxidizing proteins, lipids, DNA, and other biological macromolecules [14,15]. Plants have evolved an antioxidative system that includes antioxidative enzymes as well as non-enzymatic low-molecular-mass secondary metabolites and bioactive metabolites like phenolic compounds and flavonoids to minimize ROS-induced damage [15-17]. The dynamics of ROS-antioxidant interactions at metabolic interface are crucial not just for decreasing oxidative damage, but also for triggering ROS signaling during saline environment stressful situations [18,19]. Role of polyphenolic compounds in restoration of redox homeostasis, otherwise disturbed by salinity can be vouched by the inhibition of lipid peroxidation and protection of photosynthetic system from photo damage [20,21]. Many studies are being carried out to determine the involvement of different antioxidant metabolites in plant stress tolerance. Because of increased  $H^+$  donating ability and radical stabilization property of phenolic compounds, among other metabolites, have been researched extensively for their antioxidant characteristics [22-26]. The stronger activity of enzymes related to the metabolization of phenolics and the accumulation of phenolic compounds have been linked with the tolerance of cereals to abiotic stress [27]. For example, phenolics are electron donors and hence serve as ideal substrates for antioxidant enzymes such as peroxidases, which may help to reduce the effects of oxidative stress [17].

Plants raised under saline environment, thus exhibit diverse metabolic imprints of non-enzymatic antioxidant based redox regulatory mechanisms and oxidative deterioration. In this context, standardization of parameters of non-enzymatic redox metabolic fingerprints especially BPC and correlating them with redox status of salinity-induced plants are of utmost significance for understanding mechanistic aspect and screening salinity resistant cultivars of rice and hence is explored in present study. Thus the study is aimed to explore and standardize the accumulation of BPC for the assessment of redox health of two contrasting landraces of rice of coastal areas of Sundarban, Bangladesh.

## Materials and Methods

### Plant growth and treatment of NaCl to induce post-imbibitional salinity stress (PISS)

Two landraces of two rice (*Oryza sativa* L.) germplasm (landraces Kutepatnai and Charobalam) that are commonly cultivated in different coastal areas of Bangladesh were selected and their seeds were collected from Bangladesh Resource Center for Indigenous Knowledge (BARCIK). The seeds of two rice germplasm were multiplied and maintained at the Crop Research and Seed Multiplication Farm (CRSMF), University of Burdwan, Burdwan, West Bengal, India.

The seeds were surface sterilized (with 0.2%  $HgCl_2$ ) for 5 min and imbibed in distilled water for 48 h in the dark at  $25 \pm 2^\circ C$ , after which seeds were added in petri plate lined with moist filter paper and placed in standardized conditions of a thermostat-controlled seed germinator cum stability chamber maintained at  $25 \pm 2^\circ C$ . Water imbibed seed lots were treated with 200 mM NaCl for 7 days to induce post-imbibitional salinity stress (PISS). Water imbibed seeds were added directly in petri plates for the untreated control set. All seed lots were grown at a temperature of  $25 \pm 2^\circ C$ , with a 14 h photoperiod (light intensity of  $270 \mu mol m^{-2} s^{-1}$ ) and relative humidity of  $78 \pm 2\%$ . For all biochemical analyses, 7 days old seedlings raised from aforesaid conditions were used.

### Determination of reactive oxygen species (ROS) and total antioxidant capacity (DPPH radical scavenging property)

#### Total ROS generation

For extraction and estimation of total ROS, methodology of [28] was adopted. 30 mg of seedling tissue was incubated for 60 min at  $30^\circ C$  in 100  $\mu M$  solution of 2', 7'-dichlorofluoresceindiacetate (DCF-

DA, Sigma) dissolved in TRIS-HCl (pH-7.0). Excitation at 504 nm and emission at 525 nm were used to detect the fluorescence in the supernatant using spectrofluorometry. To distinguish ROS from other long-lived compounds capable of reacting with DCFDA, the same technique was used without DCFDA in the control set.

#### Assessment of Relative ROS accumulation (RRA)

Relative ROS accumulation (RRA) was calculated from the result of Total ROS, calculated by the following formula:

$$\text{Relative ROS accumulation (RRA)} = \frac{T(\text{TBARS})}{C(\text{TBARS})} \times 100 \%$$

Where, T (ROS) = Total ROS accumulation during the treated condition, C (ROS) = Total ROS accumulation during the untreated condition.

#### Total antioxidant capacity in terms of 2, 2'-diphenyl-1-picrylhydrazyl (DPPH) radical scavenging activity

The extraction of dry seedling tissue was performed by incubation in 80% methanol at 28°C for 24 h in a shaking incubator for the measurement of DPPH free radical scavenging activity, as described by [29]. Extracts were centrifuged at 3500 rpm for 20 min at 4°C. To determine the radical scavenging activity, 1 mL of sample was combined with 3 mL DPPH (0.04 mg mL<sup>-1</sup> ethanol) and incubated in the dark for 30 min before measuring the absorbance at 517 nm.

Finally total antioxidant capacity (TAC) was determined by the following formula:

$$\text{TAC (\%)} = \frac{T(\text{TBARS})}{C(\text{TBARS})} \times 100 \%$$

[A<sub>t</sub> = 1 mL sample + 3 mL DPPH; A<sub>u</sub> = 1 mL sample + 3 mL ethanol; A<sub>c</sub> = 1 mL ethanol + 3 mL DPPH].

#### Assessment of Relative total antioxidant capacity

The result of total antioxidant capacity was used to compute relative total antioxidant capacity (DPPH radical scavenging activity), calculated by the following formula:

$$\text{Relative total antioxidant capacity (RTAC)} = \frac{T(\text{TBARS})}{C(\text{TBARS})} \times 100 \%$$

Where, T (TAC) = Total antioxidant capacity during the treated condition, C (TAC) = Total antioxidant capacity during the untreated condition.

#### Assessment of membrane lipid peroxidation

Heath and Packer's [30] technique was used to test for thiobarbituric acid reactive compounds (TBARS) to determine membrane lipid peroxidation. 200 mg of sample was homogenized in 5 mL 0.1% trichloroacetic acid (TCA) and then centrifuged at 10,000 rpm for 15 min and finally supernatant was taken. To 1 mL of supernatant, 3 mL of 5% TCA containing 1% thiobarbituric acid (TBA) was added and heated in a hot water bath for 30 min and cooled quickly in cold water bath. It was finally centrifuged at 10,000 rpm for 10 min. At 530 nm, the absorbance of the supernatant was measured. The extinction coefficient of TBARS, which is 155 μM cm<sup>-1</sup>, was used to calculate its concentration. By subtracting A<sub>600</sub> from A<sub>530</sub>, the non-specific turbidity was adjusted. The formula employed as:

$$\text{Conc. of unknown} = \frac{T(\text{TBARS})}{C(\text{TBARS})} \times 100 \%$$

The TBARS content was finally expressed in n mol g<sup>-1</sup> dry mass of tissue.

#### Assessment of relative lipid peroxidation

Relative lipid peroxidation was calculated from the result of TBARS content, calculated by following formula:

$$\text{Relative Relative lipid peroxidation (RLP)} = \frac{T(\text{TBARS})}{C(\text{TBARS})} \times 100 \%$$

Where, T (TBARS) = TBARS content during treated condition, C (TBARS) = TBARS content during untreated condition.

#### Determination of early growth performances

- T<sub>50</sub> values were obtained according to [31,32] for analyzing early growth performances.
- T<sub>50</sub> value of germination = Time (in hour) of 50% germination of seeds sown.

#### RP-HPLC based quantitative assessment of redox-sensitive phenolic acids and flavonoids

##### Sample preparation

Samples were prepared by repeating two cycles of soxlet-mediated hydroethanolic extraction of dry powdered tissue (150 mL 80% ethanol for 15 g powder) at 60°C temperature for each sample, followed by rotary vacuum evaporation for concentrating the samples. 20 μL of solution was taken for HPLC study [33].

### RP HPLC analysis of phenolic acids and flavonoids

For HPLC analyses, a Dionex Ultimate 3000 liquid chromatograph with a diode array detector (DAD) and a 5 cm flow cell was employed, along with a Chromeleon system manager as a data processor. Separation was achieved by a reversed-phase Acclaim C18 column (5 micron particle size, 250 x 4.6 mm). All extracted solutions were filtered using an HPLC filter [0.45 mm membrane filter (Millipore)]. The quantification of phenolic acids and flavonoids in the sample extracts was carried out by measuring the integrated peak area. The contents were determined by plotting peak area versus concentration of the relevant standard sample using the calibration curve. Standard stock solutions of twenty-one phenolic acids and flavonoids (protocatechuic acid, gallic acids, naringenin, para hydroxyl benzoic acid, chlorogenic acid, gentisic acid, vanillic acid, ellagic acid, ferulic acid, caffeic acid, synaptic acid, syringic acid, para coumaric acid, salicylic acid, quercetin, rutin, myricetin, apigenin, kaempferol and catechin) were prepared in methanol at a concentration 10 µg mL<sup>-1</sup>.

### Statistical analysis

Each treatment had three replicates, and each experiment was repeated twice at different times. Results are mean of three replicates ± standard error. The data were statistically analyzed using Microsoft Excel 2010, which revealed substantial differences between untreated control and post-imbibitional salinity stress-raised seedlings.

### Results and Discussion

In order to ascertain the metabolic role of polyphenolic compounds particularly phenolic acids and flavonoids in ROS-antioxidant interaction necessary for redox-regulation and their reliability as standard metabolic fingerprints in adjudging salinity tolerance, RP-HPLC based identification and quantification of some important redox-sensitive phenolic acids and flavonoids were done in PISS-raised seedlings of two experimental landraces Kutepatnai and Charobalam vis-a-vis their untreated control (Table 1, 2). Here, we have identified and quantified important redox-sensitive polyphenolic compounds through RP-HPLC, like gallic acid (R<sub>t</sub> 7.69), protocatechuic acid (R<sub>t</sub> 17.56), para-hydroxy benzoic acid (R<sub>t</sub> 36.76), catechin (R<sub>t</sub> 40.50), chlorogenic acid (R<sub>t</sub> 43.37), vanillic acid (R<sub>t</sub> 45.58), caffeic acid (R<sub>t</sub> 47.05), syringic acid (R<sub>t</sub> 49.17), p-coumaric acid (R<sub>t</sub> 55.27), ferulic acid (R<sub>t</sub> 57.88), sinapic acid

(R<sub>t</sub> 62.66), salicylic acid (R<sub>t</sub> 69.53), naringin (R<sub>t</sub> 70.78), rutin (R<sub>t</sub> 72.40), ellagic acid (R<sub>t</sub> 75.41), myricetin (R<sub>t</sub> 77.90), quercetin (R<sub>t</sub> 88.14), naringenin (R<sub>t</sub> 92.76), apigenin (R<sub>t</sub> 93.60) and kaempferol (R<sub>t</sub> 99.42) (Figure 1).

When compared between the untreated control and PISS-raised seedlings, the landrace Kutepatnai exhibited the highest individual level up-regulation of phenolic compounds tested for PISS-raised seedlings over their untreated control. The landrace Kutepatnai showed a significantly greater accumulation of phenolic acids like Proto-catechuic acid (204.282% increment), Ellagic acid (151.129% increment), Chlorogenic acid (30.23% increment), Caffeic acid (67.379% increment), Syringic acid (195.035% increment), p-Coumaric acid (35.016% increment) and Sinapic acid (139.8% increment) over untreated control along with *de-novo* synthesis of the phenolic acid p-Hydroxy benzoic acid and Ferulic acid which were all together absent in untreated control seedlings. Gallic acid on the other hand suffered an only marginal loss (28.823%) in PISS-raised seedlings over their untreated control (Table 1).

The flavonoids like rutin, catechin, myricetin, quercetin, and apigenin, similarly showed an up-regulation by 408.927%, 17.22%, 28.30%, 129.17% and 56.69% respectively for PISS-raised seedlings of landrace Kutepatnai over their untreated control. Kutepatnai showed significant down-regulation in the accumulation of Naringin, Naringenin and Kaempferol by 14%, 92.29%, and 92.61% respectively in PISS-raised seedlings over their untreated control (Table 2).

The landrace Charobalam on the other hand, also showed significant up-regulation in the accumulation of gallic acid, protocatechuic acid, para-hydroxy benzoic acid, chlorogenic acid, caffeic acid, p-coumaric acid and sinapic acid by 39.996%, 105.462%, 373.112%, 51.279%, 7.377%, 61.51% and 175.25% respectively in PISS-raised seedlings over their untreated control. The landrace Charobalam particularly suffers significant loss in the accumulation of ellagic acid, syringic acid and Ferulic acid over untreated control by 27.87%, 52.696% and 59.209% respectively. Vanillic acid, which was present in untreated control of landrace Charobalam in an appreciable amount (29.031 µg/100g dm) got completely disappeared under PISS. Salicylic acid, which was absent in control seedlings showed *de-novo* expression under PISS in an



appreciable amount (165.054  $\mu\text{g}/100\text{g dm}$ ) in the landrace Charobalam.

The landrace Charobalam showed a significantly greater accumulation of flavonoids like Naringin, rutin, quercetin, Naringenin, apigenin and Kaempferol over untreated control by 487.528%, 12.554%, 101.721%, 677.38%, 40.735% and 54.851% respectively. Charobalam particularly suffers significant loss in the accumulation of catechin and myricetin, over untreated control by 43.702% and 47.607% respectively.

The correlative evaluation of Post imbibitional salinity stress-induced changes in the endogenous titer of redox-sensitive phenolic acids and flavonoids with redox health was done in terms of relative ROS accumulation, relative lipid peroxidation, relative total antioxidant capacity and germination performance ( $T_{50}$  value of germination) of the two rice landraces differing in sensitivity towards NaCl salinity stress. The result exhibited significant accumulation of some up-regulated important redox-sensitive individual phenolic acids like protocatechuic acid, ellagic acid, caffeic acid and syringic acid in PISS raised seedlings of Kutepatnai than its counterpart Charobalam (Table 3). Whereas some individual important up-regulated redox-sensitive flavonoids like rutin, catechin, myricetin, quercetin and apigenin have greater elicitation in PISS raised seedlings of Kutepatnai than its counterpart Charobalam (Table 4).

Relative ROS accumulation and relative lipid peroxidation is significantly reduced in Kutepatnai than its counterpart Charobalam. Thus these results indicate the correlation between the capacity for elicitation of phenolic acids and flavonoids with PISS-induced oxidative damages to the germinating tissue.  $T_{50}$  value is significantly reduced in Kutepatnai than its counterpart Charobalam but it is noticeable that the relative total antioxidant capacity is increased in Kutepatnai than Charobalam. Now, when we compared the salinity induced changes in redox health of the PISS – raised seedlings of two experimental land races of rice, we find strong correlation between the ability of the accumulation of BPC tested with the redox health of both the cultivars. The cultivar Kutepatnai, being able to elicit the overall production of flavonoids and phenolic was found to be capable of restoring the redox homeostasis more efficiently than its counterpart i.e. the landraces Charobalam. The redox metabolic shift towards prooxidants was found to be more for the landrace Charobalam which shows significantly lesser ability in elicitation of polyphenolic compounds tested by RP-HPLC.

Several previous works like [19,34,35] strongly vouch the metabolic role of polyphenolic compounds as potent radical scavenger and inhibitor of lipid peroxidation and fenton reaction, necessary for maintenance of redox homeostasis of crops under stress. Lee., *et al.* [36] and Fiorani., *et al.* [34] through their studies also exhibited significant up regulation of the enzymes of flavonoid and phenolic acid biosynthesis, under oxidative threat as potent mechanism of redox regulation. Moreover, other studies also exhibited significant impact of BPC in stabilizing enzymatic redox hub necessary for redox regulation of crops [19,35].

Salinity induced alteration in redox homeostasis due to obligation of secondary oxidative stress is a well-known event that directly influence growth, development and yield performance of the crops [37,38]. Present experiment entitled a strong correlation between PISS-induced changes in biomarkers of redox status (assessed in terms of relative oxidative membrane damage through lipid peroxidation, relative changes in ROS accumulation and antioxidative capacity) and early growth performances of germinating rice seeds. Oxidative membrane lipid peroxidation is one of the major metabolic incident under salinity that possess several adverse and physiological consequences [39,40]. This course of event disturbs not only membrane architecture but also caters production of ROS and other toxic secondary products oxidative stress, further exasperating the oxidative membrane injury causing loss of cellular redox and metabolic homeostasis [41].

Further, for understanding whether PISS-induced oxidative MLP and altered redox status has any impact on germination, sensitive germination phenotype  $T_{50}$  value were assessed and compared between PISS-raised seedlings of two experimental landraces Kutepatnai and Charobalam vis-a-vis their untreated control. The results in general showed significant inverse relationship between relative ROS accumulation and oxidative membrane lipid peroxidation with  $T_{50}$  values (Figure). The greater the magnitude of oxidative lipid peroxidation and relative changes in redox status of germinating tissue under PISS, more was the inhibitory impact on germination ( $T_{50}$  values). So, in the current study, the assessment of redox biomarkers of PISS exhibited strong correlation with the sensitive germination phenotype of the experimental rice cultivars. This result also corroborated by other studies, showing the impact of accumulation of BPCs in restoration of redox homeostasis and improvement of germination phenotypes and stress tolerance [42,43].

Charobalam		Kutepatnai		Rice ( <i>Oryza sativa</i> L.) Landraces	
PISS (200 mM NaCl)	Untreated Control	PISS (200 mM NaCl)	Untreated Control	Treatment	
652.587 (+39.996%)	466.146	555.169 (-28.823%)	779.98	Gallic acid	
199.871 (+105.462%)	97.279	321.909 (+204.282%)	105.793	Proto-catechuic acid	
273.227 (+373.112%)	57.751	218.811	-	p-Hydroxy benzoic acid	
157.655 (-27.87%)	218.569	454.132 (+151.129%)	180.836	Ellagic acid	
106.936 (+51.279%)	70.688	149.158 (+30.23%)	114.534	Chlorogenic acid	
-	29.031	37.820 (+0.484%)	37.638	Vanillic acid	
515.688 (+7.377%)	480.258	225.039 (+67.379%)	134.449	Caffeic acid	
100.877 (-52.696%)	213.253	234.624 (+195.035%)	79.524	Syringic acid	
1817.932 (+ 61.51%)	1125.602	2366.106 (+35.016%)	1752.464	p-Coumaric acid	
141.987 (- 59.209%)	348.085	249.899	-	Ferulic acid	
481.292 (+175.25%)	174.857	519.091 (+139.8%)	216.468	Sinapic acid	
165.054	-	-	-	Salicylic acid	

**Table 1:** Post imbibitional salinity stress (PISS) induced changes in endogenous titer of some important redox sensitive phenolic acids in two rice landraces (*Oryza sativa* L. landraces Kutepatnai and Charobalam) differing in sensitivity towards NaCl salinity stress (200 mM NaCl/ EC 0.18S cm<sup>-1</sup>). Values within parenthesis represent % increment or reduction under PISS over control.

Rice ( <i>Oryza sativa</i> L.) Landraces		Treatment		Accumulation of redox sensitive flavonoids ( $\mu\text{g}\cdot\text{100g}^{-1}\text{dm}$ )
Charobalam	Kutepatnai	PISS (200 mM NaCl)	Untreated Control	
PISS (200 mM NaCl)	Untreated Control	14.175 (-14%)	16.650	Naringin
112.159 (+487.528%)	19.090	1173.677 (+408.927%)	230.618	Rutin
337.040 (+12.554%)	299.448	152.119 (+17.22%)	129.772	Catechin
58.593 (-43.702%)	104.077	131.555 (+28.30%)	102.534	Myricetin
66.207 (-47.607%)	126.365	810.937 (+129.17%)	353.852	Quercetin
517.135 (+101.721%)	256.362	14.136 (-92.29%)	183.306	Naringenin
586.821 (+677.38%)	75.487	462.548 (+56.69%)	295.208	Apigenin
457.233 (+40.735%)	324.889	15.984 (-92.61%)	216.246	Kaempferol
12.577 (+54.851%)	8.122			

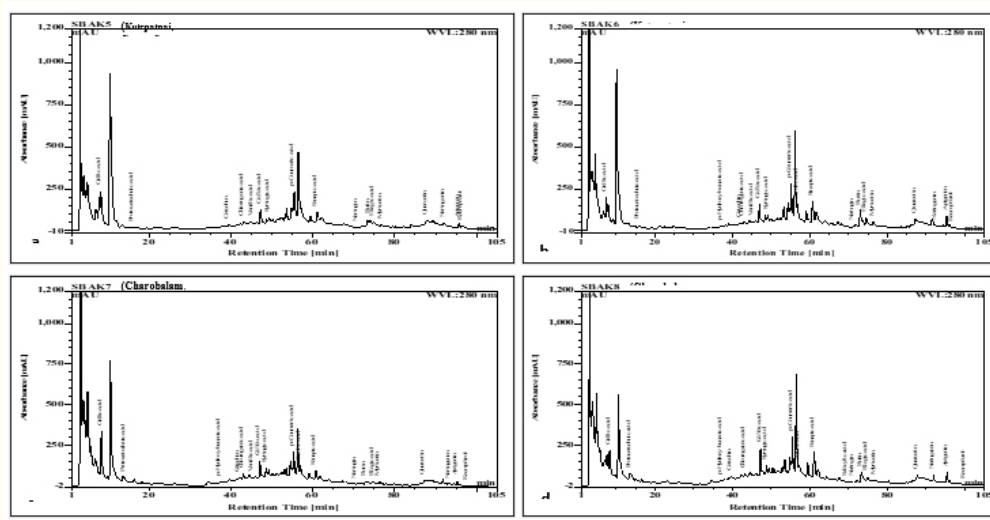
**Table 2:** Post imbibitional salinity stress (PISS) induced changes in endogenous titer of some important redox sensitive flavonoids in two rice landraces (*Oryza sativa* L. landraces Kutepatnai and Charobalam) differing in sensitivity towards NaCl salinity stress (200 mM NaCl/EC 0.18S cm<sup>-1</sup>). Values within parenthesis represent % increment or reduction under PISS over control.





Rice ( <i>Oryza sativa</i> L.) Landraces		Kutepatnai		Redox status
PISS (200 mM NaCl)	Untreated Control	PISS (200 mM NaCl)	Untreated Control	
184.439 ± 0.607	100	130.522 ± 0.510	100	Relative ROS accumulation (%)
100.788 ± 0.158	100	101.972 ± 0.208	100	Relative total antioxidant capacity (%)
188.235 ± 0.587	0	20.898 ± 0.553	100	Relative lipid peroxidation (%)
112.159 (+487.53%)	19.09	-	-	Naringin
337.04 (+12.55%)	299.448	1173.677 (+408.93%)	230.618	Rutin
-	-	152.119 (+17.22%)	129.772	Catechin
-	-	131.555 (+28.30%)	102.534	Myricetin
517.135 (+101.72%)	256.362	810.937 (+129.17%)	353.852	Quercetin
586.821 (+677.38%)	75.487	-	-	Naringenin
457.233 (+40.74%)	324.889	462.548 (+56.69%)	295.208	Apigenin
12.577 (+54.85%)	8.122	-	-	Kaempferol
60.83 ± 0.079	20.83 ± 0.157	24.67 ± 0.208	20.5 ± 0.136	T <sub>50</sub> (hrs)
				Major Flavonoids enhanced
				Germination Performance

**Table 4:** Correlative evaluation of up-regulated major flavonoid compounds with redox status and germination performance of two rice landraces (*Oryza sativa* L. landraces Kutepatnai and Charobalam) of Sundarban, Bangladesh raised from PISS (200 mM NaCl/EC 0.18S cm<sup>-1</sup>). Values are mean of three independent replicates ± standard error and values with in parenthesis represents % increment or reduction under PISS over control.



**Figure 1:** RP-HPLC based Chromatograms of polyphenolic compounds extracted from PISS (200 mM NaCl/EC 0.18S cm<sup>-1</sup>) raised seedlings of two landraces of Rice (*Oryza sativa* L. landraces Kutepatnai and Charobalam).

## Conclusion

Taken as a whole, the present investigation suggests the significance of bioactive polyphenolic compounds derived from Phenylpropanoid pathway in restoration of redox homeostasis under salinity in rice landraces of Sundarbans, Bangladesh. Further, the vulnerability of newly assembled membrane system towards oxidative deterioration through peroxidation and alteration of redox homeostasis at metabolic interface under PISS in experimental rice cultivars and elicitation of redox-sensitive BPCs to combat such deteriorative event found to regulate the germination performance under salinity.

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## Conflict of Interest

The authors have no conflict of interest in preparing of this research article.

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