*International Journal of Bio-resource and Stress Management* https://pphouse.org/ijbsm.php

Crossref

*IJBSM November* 2022, 13(11):1233-1239 Print ISSN 0976-3988 Online ISSN 0976-4038 **Article** AR2813

**Research Article** *Natural Resource Management*

DOI: HTTPS://DOI.ORG/10.23910/1.2022.2813

# Study of Iron Supplementation on Rice Genotypes

**R. Saini[1], A. Dahiya[2], H. S. Saini[3], B. Brar[4], S. Verma[5] and A. Verma[6]**

[1,2]Dept. of Chemistry & Biochemistry, Chaudhury Charan Singh Haryana Agricultural University, Hisar, Haryana (125 004), India.
[1]Dept. of Biotechnology Engineering, Kurukshetra University, Kurukshetra, Haryana (136 119), India.
[2]Dept. of Biotechnology, Lala Lajpat Rai University of Veterinary & Animal Science, Hisar, Haryana (125 004), India.
[3]Dept. of Botany, Christ Church College Kanpur, Uttar Pradesh (208 001), India
[4]Dept. of Crop Improvement, ICAR-Indian Institute of Wheat & Barley Research, Karnal, Haryana (132 001), India

Open Access

**Corresponding** verma.dwr@gmail.com

0000-0001-9255-6134

## ABSTRACT

Promising rice genotypes were evaluated during June to October in the Department of Chemistry and Biochemistry, CCS HAU, Hisar, Haryana, for 2015–2016 and 2016–2017 cropping seasons. Biochemical changes in root tissues were estimated in response to augmentation of iron concentrations during vegetative to reproductive stages. Estimated values of metabolities observed variation in ascorbic acid from 343.3–680.2 among treatments for this study. Values of hydrogen per oxide expressed deviation from 506.8–230.8, while malondialdehyde deviated from 10.9–30.8. Very large deviation had expressed by peroxidase values i.e. 38.1–160.8. Larger values expressed by hydrogen per oxide as varied from 187.3–457.5, and least total deviation from 9.9–24.2 for malondialdehyde values. The first principal component accounted for 73.8% of the total variation among estimated values and larger contribution expressed by peroxidase, catalase, superoxide dismutase of vegetative stage and superoxide dismutase, catalase, ascorbate peroxidase of reproductive stage etc. Total of 22.6% to the total variation contributed by second principal component with major contributors were malondialdehyde, hydrogen peroxide, superoxide radicals of vegetative stages along with malondialdehyde, hydrogen peroxide, superoxide radicals, of reproductive stages. Agronomic biofortification with a proper balance of iron augmentation induce desirable effect on the physiological process of the plants.

**KEYWORDS:** Antioxidative metabolites, ROS related metabolites, synthetic chelated micronutrient

***Citation* (VANCOUVER):** Saini et al., Study of Iron Supplementation on Rice Genotypes. *International Journal of Bio-resource and Stress Management*, 2022; 13(11), 1233-1239. HTTPS://DOI.ORG/10.23910/1.2022.2813.



***Data Availability Statement:*** Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

***Conflict of interests:*** The authors have declared that no conflict of interest exists.

RECEIVED on 05th January 2022 RECEIVED in revised form on 20th October 2022 ACCEPTED in final form on 12th November 2022 PUBLISHED on 23rd November 2022

## 1. INTRODUCTION

Larger proportion of people in developing countries relies on rice as their staple foods for daily consumption (Masuda et al., 2020). Resources poor populations face hardship to afford other micronutrients-rich non staple food for balance diet to ensure good health (Aung et al., 2013; Bouis et al., 2017). Rice the prime source of nutrition of Indian population would be fortified with Iron to overcome the problem of Anemia in children and lactating women (Samtiya et al., 2020). The problem of micronutrient deficiency among human beings has been tackled by biofortification interventions at worldwide (Boonyaves et al., 2017; Masuda et al., 2020). Recently, the biofortified crops have been advocated to cultivate on larger areas to supplement the daily requirement of micronutrients intake on economical basis (Slamet et al., 2015; Jan et al., 2020). Agronomic bio fortification is the application of a micronutrient containing mineral fertilizer to soil and/or plant leaves (foliar) to improve the micronutrient quality of the edible portion of food crops (Bouis & Saltzman, 2017; Garget al., 2018). The predominance of cereal-based diet mostly in Africa and South Asia, approximately 2 billion people has been affected due to Micronutrient deficiency (Trijatmiko et al., 2016; Jalal et al., 2020). Recent food protection policies have emphasized more on Micronutrient Safety, i.e. development and availability of nutrition's rich healthy food (Bharadva et al., 2019). This method is beneficial for ensuring the availability of micronutrients that can be directly absorbed by the plant, such as iron (de Valença et al., 2017; Kumar et al., 2019). Among various approaches chosen to increase the Fe concentration in rice grains, fertilization is considered as a rapid and efficient method (Ramzan et al., 2020). The effectiveness of agronomic biofortification can be enhanced by application of synthetic chelated micronutrient fertilizers and/or organic fertilizers fortified with micronutrients in combination with NPK ensuring proper nourishment of crops with adequate nutrient supply by slow release of nutrients in soil solution (Giordano et al., 2019).

Table 1: Details of treatments consisted of genotypes and augmented level of iron

| Genotype/ iron augmentation | 0 mM EDTA-Fe(II) | 0.1 mM EDTA-Fe(II) | 0.5 mM EDTA-Fe(II) |
|---|---|---|---|
| Govind | C1G1 | C2G1 | C3G1 |
| Super | C1G2 | C2G2 | C3G2 |
| HKR120 | C1G3 | C2G3 | C3G3 |
| PUSA1121 | C1G4 | C2G4 | C3G4 |
| HBC19 | C1G5 | C2G5 | C3G5 |
| Palman | C1G6 | C2G6 | C3G6 |

## 2. MATERIALS AND METHODS

Promising six rice varieties were evaluated under field trials during June to October in the net houses of the Department of Chemistry and Biochemistry, CCS HAU, Hisar, Haryana, India during cropping seasons 2015–2016 and 2016–2017. Seeds of all rice varieties were sown directly in pots at 2–3 cm depth in light textured (loamy) soil with recommended agronomical practices (Sikirou et al., 2006) and the pots were divided in 3 sets after 20 days of sowing for Iron augmentation as : 1st set was given Yoshida nutrient medium without Fe (0 mM EDTA-Fe(II)). 2nd set was given Yoshida nutrient medium with 0.1 mM EDTA-Fe(II) concentration. 3rd set was given Yoshida nutrient medium with high Fe concentration (0.5 mM EDTA-Fe (II)). ROS related metabolites; malondialdehyde (MDA), superoxide radical ($O_2^{\cdot-}$), hydrogen peroxide ($H_2O_2$), antioxidative metabolites viz. ascorbic acid, glutathione (GSH and GSSG), enzymes; superoxide dismutase (SOD), catalase (CAT), peroxidase (POX), ascorbate peroxidase (APX), glutathione reductase (GR) and isozymes of SOD, CAT, APX and GR were estimated in the root tissues of the varieties. Malondialdehyde content (MDA)was estimated according to the method of Heath and Packer (1968). Superoxide radical (SOR) was measured by monitoring the nitrite formation from hydroxylamine following the method of Elstner and Heupel (1976). $H_2O_2$ was estimated by the method of Sinha (1972). Ascorbic acid content was estimated by the method of Mukherjee and Chaudhari (1983), which was based on the reduction of 2, 4-dintrophynel hydrazine. Glutathione was estimated by the method of Griffith (1980). Superoxide dismutase was assayed by measuring its ability to inhibit the photochemical reduction of nitroblue tetrazolium by the method of Giannopolities and Ries (1977). Catalase activity was determined by the procedure of Sinha (1972). The Peroxidase enzyme activity was estimated by the method of Shannon et al. (1966). The data obtained in the present investigation was subjected to analysis of variance (ANOVA) technique and critical differences in values at 5% level of significance was used for making comparisons among the rice genotypes augmented with additional iron levels and changes were studied in metabolites estimation from vegetative to reproductive stages of the genotypes.

## 3. RESULTS AND DISCUSSION

### *3.1. Analysis of yield and contributing traits*

ANOVA analysis had observed highly significant variations among the estimated values among treatment comprises of genotypes as well as doses of iron supplementation at vegetative and reproductive stages (Shi et al., 2016).

### *3.2. Vegetative stage of genotypes*

Variations among the mean of ROS related ten metabolites

at the vegetative stage of genotypes were displayed in table 2. Range of 63.8–233.5 observed for superoxide radicals (SOR) values among genotypes augmented with three doses of iron augmentation. Values of ascorbic acid (AA) varied from 343.3–680.2 among treatment combinations for this study (Yang et al., 2016). Larger values expressed by hydrogen peroxide (HPO) as varied from 506.8–230.8, total deviation from 10.9–30.8 for malondialdehyde (MDA) values. Short range that varied from 4.1–9.9 was seen for the values of total glutathione (TOG) while catalase (CAT) expressed variation from 14.2–33.9 among treatment combinations. Estimated values of superoxide dismutase (SOD) ranged from 28.2–61.5 while deviation from 10.3–42.4 observed for ascorbate peroxidase (APX) values. Very large deviation had expressed by peroxidase (POX) values i.e. 38.1–160.8. Least deviation had observed among values of glutathione reductase (GR) among the treatment combinations (Kabir et al., 2016).

Table 2: Differential pattern in metabolites estimation for treatments at vegetative stages

| Treatments | Superoxide radicals | Ascorbic acid | Hydrogen peroxide | Malondialdehyde | Total Glutathione | Catalase | Superoxide dismutase | Ascorbate peroxidase | Peroxidase | Glutathione reductase |
|---|---|---|---|---|---|---|---|---|---|---|
| C1G1 | 139.29 | 343.33 | 331.80 | 17.17 | 4.43 | 14.17 | 28.25 | 10.30 | 44.83 | 3.83 |
| C1G2 | 132.54 | 355.56 | 350.86 | 18.05 | 4.08 | 15.61 | 31.66 | 11.16 | 38.17 | 4.01 |
| C1G3 | 107.30 | 375.76 | 305.81 | 13.47 | 5.31 | 19.43 | 36.04 | 14.59 | 62.67 | 4.62 |
| C1G4 | 86.30 | 416.16 | 296.64 | 14.98 | 4.78 | 17.43 | 33.11 | 16.79 | 67.50 | 4.27 |
| C1G5 | 69.97 | 458.89 | 230.89 | 10.98 | 5.93 | 22.08 | 42.22 | 18.04 | 93.63 | 5.35 |
| C1G6 | 63.81 | 430.30 | 253.06 | 11.75 | 5.53 | 21.43 | 39.23 | 22.64 | 83.00 | 5.01 |
| C2G1 | 205.73 | 377.98 | 425.20 | 23.15 | 4.99 | 16.39 | 31.73 | 13.35 | 54.67 | 4.26 |
| C2G2 | 198.21 | 386.32 | 465.84 | 24.19 | 4.63 | 17.89 | 36.53 | 14.10 | 43.17 | 4.64 |
| C2G3 | 148.79 | 442.61 | 376.38 | 15.56 | 6.37 | 23.38 | 43.65 | 21.13 | 85.43 | 5.83 |
| C2G4 | 116.05 | 503.95 | 356.15 | 17.95 | 6.09 | 21.67 | 40.60 | 23.43 | 94.17 | 5.43 |
| C2G5 | 89.89 | 618.18 | 259.50 | 12.05 | 8.18 | 29.29 | 55.30 | 29.74 | 133.50 | 7.42 |
| C2G6 | 84.16 | 581.82 | 280.86 | 13.01 | 7.45 | 27.96 | 50.02 | 35.72 | 123.50 | 6.75 |
| C3G1 | 233.49 | 413.33 | 496.16 | 28.35 | 5.60 | 17.95 | 34.50 | 15.81 | 62.50 | 5.36 |
| C3G2 | 226.78 | 421.03 | 506.88 | 30.85 | 5.08 | 20.21 | 38.29 | 16.15 | 55.83 | 5.65 |
| C3G3 | 159.33 | 466.38 | 413.95 | 21.70 | 7.50 | 26.74 | 48.77 | 24.67 | 94.33 | 7.31 |
| C3G4 | 125.08 | 540.10 | 388.53 | 23.74 | 7.22 | 23.73 | 44.18 | 28.06 | 104.83 | 6.90 |
| C3G5 | 96.03 | 680.23 | 284.02 | 15.60 | 9.92 | 33.99 | 61.50 | 34.69 | 160.83 | 9.12 |
| C3G6 | 92.84 | 631.43 | 304.84 | 17.09 | 9.05 | 32.01 | 55.29 | 42.41 | 135.04 | 8.80 |
| CD ($p$=0.05) | 3.99 | 10.34 | 10.68 | 1.14 | 0.80 | 4.31 | 2.48 | 3.04 | 7.13 | 0.48 |

### *3.3. Reproductive stage of genotypes*

Variations in ROS related 10metabolites among the genotypes were displayed at the reproductive stage in the terms of average values of metabolites in table 3. Range of (52.4–173.9) observed for SOR values among genotypes augmented with three doses of iron augmentation at reproductive stage. Values of AA varied from 142.2–421.2 among treatment combinations for this study. Larger values expressed by HPO as varied from 187.3–457.5, and least total deviation from 9.9–24.2 for MDA values. Similarly, short range that varied from 2.8–7.8 was seen for the values of TOG while CAT expressed variation from 8.3–23.9 among treatment combinations (Yadav et al., 2015). Estimated values of SOD ranged from 10.4–28.8 while APX values deviated from 7.7–27.6 as observed in present study. Very large deviation had expressed by POX values i.e. 16.1–82.9. Least deviation had observed among values of GR among the treatment combinations.

### *3.4. Relative change in estimated values*

Changes in ROS related 10 metabolites among the rice genotypes from vegetative to reproductive stages were displayed in the terms of mean values of metabolites in Figure 1. Maximum change on average basis expressed by SOD, POX, AA whereas least change observed in HPO

Table 3: Differential pattern in metabolities estimation for treatments at reproductive stages

| Treatments | Superoxide radicals | Ascorbic acid | Hydrogen peroxide | Malondialdehyde | Total glutathione | Catalase | Superoxide dismutase | Ascorbate peroxidase | Peroxidase | Glutathione reductase |
|---|---|---|---|---|---|---|---|---|---|---|
| C1G1 | 106.98 | 151.58 | 307.28 | 13.79 | 2.89 | 9.87 | 11.09 | 7.70 | 16.10 | 3.08 |
| C1G2 | 101.11 | 142.27 | 288.23 | 13.16 | 3.19 | 8.38 | 10.45 | 8.26 | 21.40 | 2.72 |
| C1G3 | 74.29 | 177.78 | 262.23 | 11.94 | 4.00 | 11.98 | 16.23 | 12.79 | 37.57 | 3.55 |
| C1G4 | 63.02 | 210.10 | 253.06 | 12.39 | 3.58 | 12.06 | 15.72 | 10.85 | 33.63 | 3.42 |
| C1G5 | 52.49 | 258.93 | 187.31 | 9.91 | 4.79 | 16.10 | 19.56 | 15.33 | 46.63 | 4.01 |
| C1G6 | 57.78 | 242.42 | 209.48 | 10.47 | 4.22 | 14.63 | 18.77 | 16.99 | 47.30 | 3.85 |
| C2G1 | 153.62 | 184.34 | 397.03 | 18.37 | 3.19 | 11.14 | 13.19 | 9.03 | 20.60 | 3.65 |
| C2G2 | 144.06 | 169.00 | 384.10 | 17.88 | 3.65 | 9.71 | 12.73 | 10.18 | 28.61 | 3.16 |
| C2G3 | 98.02 | 236.67 | 320.81 | 14.72 | 5.01 | 14.58 | 21.06 | 17.49 | 50.80 | 4.51 |
| C2G4 | 81.70 | 288.99 | 295.23 | 15.67 | 4.57 | 15.02 | 20.45 | 15.16 | 47.07 | 4.30 |
| C2G5 | 64.78 | 392.22 | 206.93 | 11.27 | 6.91 | 21.53 | 27.13 | 23.26 | 66.92 | 5.55 |
| C2G6 | 72.73 | 362.88 | 235.47 | 12.18 | 6.01 | 18.97 | 25.21 | 24.81 | 70.37 | 5.22 |
| C3G1 | 173.95 | 192.41 | 457.58 | 24.25 | 3.41 | 12.22 | 14.09 | 11.04 | 23.05 | 4.10 |
| C3G2 | 166.03 | 182.07 | 436.30 | 22.48 | 3.80 | 10.17 | 13.43 | 11.32 | 31.73 | 3.78 |
| C3G3 | 114.43 | 248.48 | 346.37 | 17.81 | 5.59 | 16.32 | 21.77 | 19.59 | 58.23 | 5.42 |
| C3G4 | 94.19 | 300.12 | 324.95 | 19.41 | 5.11 | 16.40 | 20.60 | 16.10 | 53.52 | 5.03 |
| C3G5 | 73.32 | 421.21 | 225.44 | 13.07 | 7.89 | 23.95 | 28.84 | 26.19 | 82.98 | 6.87 |
| C3G6 | 81.57 | 387.47 | 255.26 | 14.09 | 6.68 | 21.39 | 26.74 | 27.66 | 79.53 | 6.33 |
| CD ($p$=0.05) | 9.89 | 11.52 | 8.51 | 0.974 | 0.40 | 1.12 | 2.60 | 1.16 | 2.85 | 0.39 |

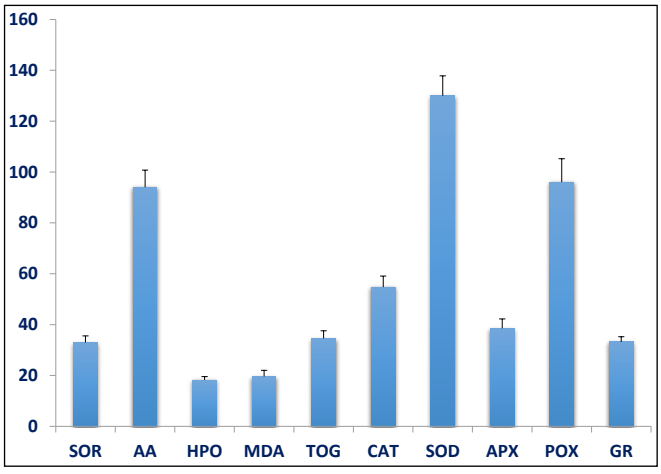


Figure 1: Standard errors in the estimated values

along with MDA estimated values.

Combination C2G3 had expressed maximum change in values for super oxide radicals (SOR) followed by C2G4 and C1G3 in roots while C1G6 achieved minimum value of 10.4 (Figure 2). Estimation in roots observed minimum change in value for C2G5 and maximum value by C1G2, C3G2

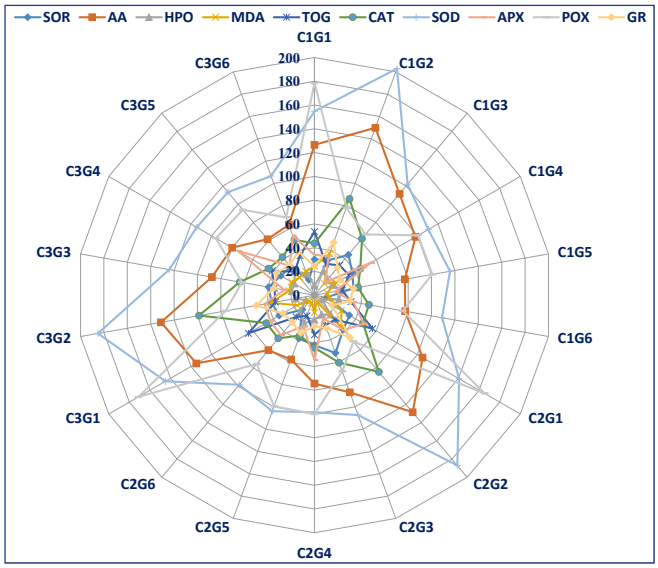


Figure 2: Relative change in values of metabolites with advancement of stages of genotypes

and C2G2 of estimated ascorbic acid (AA). Treatment combination C2G1 had minimum value 7.1 in roots whereas larger estimation exhibited by C3G5, C2G5, C1G5

for hydrogen peroxide (Zhang et al., 2018). MDA observed maximum change for C3G2 followed by C1G2 and C2G2 and minimum value by C2G3 (5.7) as per for estimation.

Larger values of superoxide dismutase (SOD) expressed by the C1G2 (202.9) followed by C2G2 and C3G2 as compared to least value mentioned by 98.4 (C2G6) for roots estimation. Ascorbate peroxidise (APX) values were more in C3G4, C1G4, C2G4 as compared to least value by C1G3(14.1). Lower values had observed for glutathione reductase (GR) in roots estimation for C2G1 as compared to corresponding larger C3G2, C1G2, C2G2. Wide variation observed among values for TOG as ranged from 64.1(C3G1)–18.5(C2G5) as compared to catalase (CAT) values from 98.7(C3G2)–36.1(C2G5) values estimated in roots. peroxidase (POX) values expressed as lower value in roots estimation value i.e. 50.8(C2G2) while maximum observed for C1G1 followed by C3G1 and C2G1 (Bouis et al., 2011).

### 3.5. *Biplot analysis of metabolities versus treatments*

First two principal components explained 96.4% of the total variation among the treatments of the study as evident from (Table 4). The first principal component (PC) accounted for 73.8% of the total variation among estimated values and larger contribution expressed by POX, CAT, SOD of vegetative and SOD, CAT, APX of reproductive stage etc. Principal component two contributed 22.6% to the total variation. Major six contributors were MDA, HPO, SOR, of vegetative and reproductive stages. Out of the 20 traits evaluated, 06 contributed most to the first two principal components (Table 4) and these considered most desirable to summarize variation among the accessions through hierarchical cluster analysis (Figure 3).

Table 4: Contribution of metabolites in principal components

| Traits | PC1 | PC2 |
|---|---|---|
| VSORR | -0.1637 | -0.3535 |
| VAAR | 0.2452 | -0.1091 |
| VHPOR | -0.1543 | -0.3718 |
| VMDAR | -0.1384 | -0.3851 |
| VTOGR | 0.2434 | -0.1482 |
| VCATR | 0.2492 | -0.1154 |
| VSODR | 0.2468 | -0.1207 |
| VAPXR | 0.2438 | -0.0938 |
| VPOXR | 0.2560 | -0.0545 |
| VGRR | 0.2276 | -0.2134 |
| RSORR | -0.1647 | -0.3508 |
| RAAR | 0.2516 | -0.0551 |
| RHPOR | -0.1685 | -0.3546 |
| RMDAR | -0.1165 | -0.4090 |
| RTOGR | 0.2527 | -0.0840 |
| RCATAR | 0.2554 | -0.0481 |
| RSODR | 0.2560 | -0.0417 |
| RAPXR | 0.2525 | -0.0560 |
| RPOXR | 0.2551 | -0.0443 |
| RGRR | 0.2352 | -0.1849 |
| % variance explained | 73.87 | 22.60 |

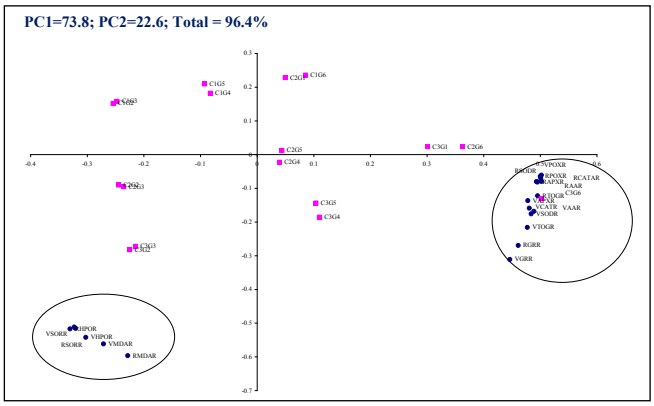


Figure 3: Clustering pattern of metabolites

The biplot analysis is an appropriate method to analyse the association analysis among treatment combinations and estimated values of metabolites and narrowing down the number of metabolites to the ones contributing a major portion to the variability Prity et al. (2021). In the biplot vectors of metabolites showing acute angles are positively correlated whereas those showing obtuse or straight-line angles are negatively correlated and those with right angles have no correlation (Kumar et al., 2020).

POX, HPO, MDA and SOR expressed strong association ship as observed together in one cluster. This showed the estimation of these metabolites at vegetative stage would be appropriate and estimation at reproductive stages may be avoided to reduce the work load (Figure 4). Similar

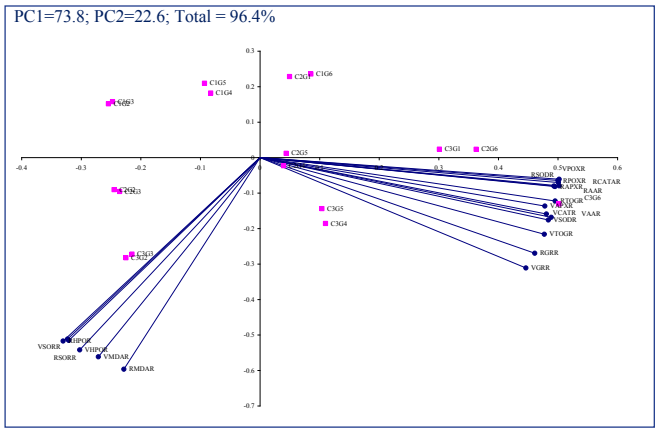


Figure 4: Association analysis among metabolites

type of behaviour exhibited by AA, APX, CAT, POX, SOD, TOG, and GR metabolites as formed large group. Group of these metabolites had maintained distance from earlier group as observed in different cluster. More over these would be not correlated with HPO, MDS and SOR metabolites as nearly right angles observed among the rays connecting to the estimated metabolites values in the biplot analysis.

## 4. CONCLUSION

The less accumulation of reactive oxygen species along with the gradual increase in antioxidative metabolites' contents and enzymes' activities at higher iron augmentation treatments observed a superior ROS scavenging system. Increased the mineral availability in the edible part of the staple crops had proved an effective strategy in alleviating malnutrition economically. This complementary food-based approach would be the safest and cost effective way to ensure bio fortified nutrients on a larger scale to the poor populations.

## 5. REFERENCES

Aung, M.S., Masuda, H., Kobayashi, T., Nakanishi, H., Yamakawa, T., Nishizawa, N.K., 2013. Iron biofortification of Myanmar rice. Frontier in Plant Science 4, 158. DOI 10.3389/fpls.2013.00158

Bharadva, K., Mishra, S., Tiwari, S., Yadav, B., Deshmukh, U., Elizabeth, K.E., Banapurmath, C.R., 2019. Prevention of Micronutrient Deficiencies in Young Children: Consensus Statement from Infant and Young Child Feeding Chapter of Indian Academy of Pediatrics. Indian Pediatrics 56, 577–586.

Boonyaves, K., Wu, Ting-Ying, Gruissem, W., Bhullar, N.K., 2017. Enhanced Grain Iron Levels in Rice Expressing an iron-regulated metal transporter, nicotianamine synthase, and ferritin gene cassette. Frontiers in Plant Science 8. DOI 10.3389/fpls.2017.00130

Bouis, H.E., Saltzman, A., 2017. Improving nutrition through biofortification: A review of evidence from Harvest Plus, 2003 through 2016. Global Food Security 12, 49–58.

de Valença, A.W., Bake, A., Brouwer, I.D., Giller, K.E., 2017. Agronomic biofortification of crops to fight hidden hunger in Sub-Saharan Africa. Global Food Security 12, 8–14.

Garg, M., Sharma, N., Sharma, S., Kapoor, P., Kumar, A., Chunduri, V., 2018. Biofortified crops generated by breeding, agronomy, and transgenic approaches are improving lives of millions of people around the world. Frontiers in Nutriton 5, 12.

Giordano, M., El-Nakhel, C., Pannico, A., Kyriacou, M.C., Stazi, S.R., De Pascale, S., Rouphael, Y., 2019. Iron biofortification of red and green pigmented lettuce in closed soilless cultivation impacts crop performance and modulates mineral and bioactive composition. Agronomy 9, 290.

Jalal, A., Shah, S., Filho, M.C.M.T., Khan, A., Shah, T., Ilyas, M., Rosa, P.A.L., 2020. Agro-Biofortification of zinc and iron in wheat grains. Gesunde Pflanzen 72(3), 227–236. DOI https://doi.org/10.1007/s10343-020-00505-7

Jan, B., Bhat, T.A., Sheikh, T.A., Wani, O.A., Bhat, M.A., Nazir, A., Fayaz, S., Mushtaq, T., Farooq, A., Wani, S., Rashid, A., 2020. Agronomic bio-fortification of rice and maize with iron and zinc: a review. International Research Journal of Pure and Applied Chemistry 21(16), 28–37.

Kabir, A.H., Begum, M.C., Haque, A., Amin, R., Swaraz, A.M., Haider, S.A., Paul, N.K., Hossain, M.M., 2016. Genetic variation in Fe toxicity tolerance is associated with the regulation of translocation and chelation of iron along with antioxidant defence in shoots of rice. Functional Plant Biology 43(11), 1070–1081. DOI 10.1071/FP16068.

Kumar, S., Palve, A., Joshi, C., Srivastava, R.K., Rukhsar, 2019. Crop biofortification for iron (Fe), zinc (Zn) and vitamin A with transgenic approaches. Heliyon 5, e01914.

Masuda, H., Aung, M.S., Kobayashi, T., Nishizawa, N.K., 2020. Iron Biofortification: The gateway to overcoming hidden hunger, In: de Oliveira, A.C., Pegoraro, C., Viana, V.E. (Eds.), The future of rice demand: quality beyond productivity. Springer Nature, Switzerland, 149–177. DOI 10.1007/978-3- 030-37510-2

Prity, S.A., El-Shehawi, A.M., Elseehy, M.M., Tahura, S., Kabir, A.H., 2021. Early-stage iron deficiency alters physiological processes and iron transporter expression, along with photosynthetic and oxidative damage to sorghum. Saudi Journal of Biological Sciences 28(8), 4770–4777.

Ramzan, Y., Hafeez, M.B., Khan, S., 2020. Biofortification with zinc and iron improves the grain quality and yield of wheat crop. International Journal of Plant Production 14(3), 501–510.

Samtiya, M., Aluko, R.E., Dhewa, T., 2020. Plant food anti-nutritional factors and their reduction strategies: an overview. Food Production Process and Nutrition 2, 6.

Shi, Y., Dong, S., Liu, Z., Yi, K., Wang, J., Zhu, C., Wang, F., 2016. Effect of exogenous ferrous sulfate treatment on edible rice. American Journal of Food Science and Technology 11, 165–170.

Sikirou, M., Saito, K., Drame, K.N., Saidou, A., Dieng, I., Ahanchede, A., Venuprasad, R., 2016. Soil-based screening for iron toxicity tolerance in rice using pots. Plant Production Science 19(4), 489–496. DOI 10.1080/1343943X.2016.1186496.

Slamet-Loedin, I.H., Johnson-Beebout, S.E., Impa, S., Tsakirpaloglou, N., 2015. Enriching rice with Zn and Fe while minimizing Cd risk. Frontier of Plant Science 6, 1–9.

Trijatmiko, K., Duenas, C., Tsakirpaloglou, N., 2016. Biofortified indica rice attains iron and zinc nutrition dietary targets in the field. Scientific Reports 6, 19792. DOI https://doi.org/10.1038/srep19792

Yadav, G.S., Shivay, Y.S., Kumar, D., Babu, S., 2015. Agronomic evaluation of mulching and iron nutrition on productivity, nutrient uptake, iron use efficiency and economics of aerobic rice- wheat cropping system. Journal of Plant Nutrition. 39(1), 116–135. DOI 10.1080/01904167.2015.1084323.

Yang, Q.Q., Zhang, C.Q., Chan, M.L., 2016. Biofortification of rice with the essential amino acid lysine: Molecular characterization, nutritional evaluation and field performance. Journal of Experimental Botany 67, 4285–4296.

Zhang, C.M., Zhao, W.Y., Gao, A.X., 2018. How could agronomic biofortification of rice be an alternative strategy with higher cost effectiveness for human iron and zinc deficiency in China? Food Nutrition Bulletin 39, 246–259.