An Insight of Quinclorac Resistance Mechanism in Early Watergrass (Echinochloa oryzoides)

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Abstract: **Background:** Quinclorac- main herbicide targeting to barnyard grass, has been used for decades in rice fields. *Echinochloa* species have been reported evolving into quinclorac resistance.

Objective: Quinclorac resistance and its mechanism remain undisclosed in *Echinochloa oryzoides* (Ard.) Fritsch that needs to be uncovered.

 $\label{eq:methods: Dose-response assays were performed, followed by ethylene synthesis, and related enzyme activities along with gene transcription were studied.$ $<math display="inline">\beta\text{-CAS}$ activity and its molecular docking were investigated.

Results: *E. oryzoides* evolved into 21 times resistance to quinclorac from Jiangsu province of China. The increment in ethylene levels in this biotype was correlated negatively with the level of resistance and positively with quinclorac-induced growth inhibition. Ethylene response pathway determination showed that resistant biotype decreased

1-aminocyclopropane-1-carboxylic acid (ACC) contents, related enzyme activities, and transcription of ACS and ACO genes. These results indicated that ethylene biosynthesis inhibition and quinclorac resistance possessed a positive correlation. Resistant biotype exhibited ~ 2-fold more β -CAS activity than susceptible ones. Resistant *EcCAS* gene depicted nucleotide changes as compared to susceptible ones, which resulted in two amino acid substitutions (Met-287-Lys and Thr-352-Ala). Consequently, resistant β -CAS enzyme exhibited an increase in binding residue in active site (simulation modelling); that can be the probable reason for higher enzyme activity in the resistant biotype.

Conclusions: The study concludes that variation in response pathway of auxin and potentially improved cyanide degradation were plausible mechanisms endowing quinclorac resistance in *E. oryzoides*.

Keywords: ACS and ACO genes; auxin response pathway; β -cyanoalanine synthase; Ethylene biosynthesis.

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1. Introduction

The history of chemical weed control dates back to 1945 when 2,4-D {2,4-dichlorophenoxyacetic acid (synthetic auxin)} was first made available commercially. Multiple herbicide-resistant weed populations were selected owing to the long history of herbicidal weed control (Heap, 2021). Ultimately, the choices for alternative and effective herbicides are reduced. A 30 years long history of herbicidal control of *Echinochloa* weeds gave rise to herbicide resistance. *Echinochloa oryzoides* (Ard.) Fritsch is considered to be a noxious rice weed (Damalas et al., 2008). The herbicide resistance is swiftly evolving owing to the insistent herbicide usage. A study reported the first herbicide resistance case in *E. oryzoides* against lipid inhibitors in 2000 (Fischer et al., 2000). Furthermore, multiple herbicide resistance was reported in the same species against ALS (cyhalofobbutyl, bispyribac sodium) and ACCase (penoxsulam) inhibitors (Altop et al., 2014).

The widespread usage of quinclorac upsurged the herbicide resistance in *Echinochloa* species such as *E. colona*, *E. crus-galli* (Malik et al., 2010), *E. crus-galli* var. *zelayensis* and -var. *mitis* (Xu et al., 2013: Zia Ul Haq et al., 2020), *E. crus-pavonis* (Yang et al., 2021), *E. phyllopogon*, *E. oryzicola* and *E. hispidula* (Heap, 2021).

TIR1/AFB has been revealed as auxin co-receptors with Aux/IAA protein; hence the same are receptors for quinclorac (LeClere et al., 2018). It fits well in the auxin binding site of the TIR1 receptor, hence proving that target sites for quinclorac are auxin receptors. Quinclorac application contributes to the activation of auxinresponsive genes {1-aminocyclopropane-1-carboxylic acid (ACC) synthase}: hence, persuading the de novo synthesis of ACC synthase (ACS). In susceptible plants, ACS activity increases ACC contents; furthermore, ACC is oxidized by ACC oxidase (ACO) activity into ethylene and hydrogen cyanide (HCN). Higher HCN levels can impair several metabolic enzymes, eventually leading to plant death (Gao et al., 2017). HCN inhibits one of the essential respiratory chain enzymes- cytochrome c oxidase (Ikegaya et al., 2001). A multigene family encodes the ACS and ACO enzymes in the ethylene biosynthesis pathway. Varied transcript levels of *ACS* and *ACO* genes were observed in quinclorac susceptible and resistant *E. crus-galli* var. *zalayensis* and -var. *mitis* (Gao et al., 2018; Zia Ul Haq et al., 2020).

β-cyanoalanine synthase (β-CAS) degrades the HCN produced during ethylene biosynthesis (Lai et al., 2009). Several studies have indicated that resistance to quinclorac could be instigated by high β-CAS activity (Gao et al., 2017). Defiantly, a study revealed that quinclorac resistance solely depended on ethylene biosynthesis inhibition instead of cyanide degradation in *E. phylopogan* (Chayapakdee et al., 2019). Though, mutations may increase the activity of the enzymes (Mdodana et al., 2019). Quinclorac resistant *E. crus-galli* var. *zelayensis* and -var. *mitis* were found to develop single and three nucleotides mutations in β-CAS, respectively (Gao et al., 2017; Zia Ul Haq et al., 2020).

A study recently reported differential herbicide translocation and metabolism in quinclorac resistant and susceptible *E. crus-pavonis* (Yang et al., 2021), contradictory to previous studies-those stating that in resistant and susceptible plants, the quinclorac absorption/uptake, transport, and metabolism were found indifferent. The resistant populations of *E. crus-galli* var. *zelayensis* and -var. *mitis* did not express a notable rise in ethylene level post quinclorac application. In resistant biotypes, the low level of ACS activity is caused by less susceptibility in the auxin receptor level or the modified auxin signal transduction pathway. As well as degradation of cyanide by β -CAS can offer an extra benefit to resistant biotypes in coping with quinclorac sensitivity (Xu et al., 2013; Zia Ul Haq et al., 2020)

Although *E. oryzoides*, as one of the main weeds in rice fields, has been subjected to decades of' quinclorac application, its quinclorac resistance has not been reported so far. One *E. oryzoides* biotype from Jiangsu province of China was found to develop quinclorac resistance. To elucidate the possible mechanism of quinclorac-resistance, ethylene production, ACC accumulation, related enzymes, and β -CAS activity and enzyme binding with cofactor- PLP (molecular simulation), along with gene transcript levels, were relatively assessed among one resistant and two susceptible biotypes of *E. oryzoides*.

2. Material and Methods

2.1 Collection of Plant Material

Seeds of *E. oryzoides* were collected from paddy fields of Jiangsu (Shuyang 33.97 N/118.89 E) in China during autumn 2016. This site from Jiangsu province was under quinclorac usage for over 15 years. At the same time, four more biotypes were collected from rice fields of Ningxia province {(Tongfu, 38.78 N/106.59 E; NX1-S), (Guanqu, 38.55 N/106.47 E; NX2-S), (Zhangzheng, 38.42 N/106.44 E; NX3-S), (Zhongning, 37.67 N/106.88 E; NX4-S)} and one biotype from Liaoning province (Dawa, 41.93 N/ 122.00 E; LN1-S). Two quinclorac susceptible biotypes (which were not exposed to quinclorac herbicide before), one from Heilongjiang province (Suihua, 46.73 N/126.98 E) and another from Zhejiang province (Jinhua, 29.17 N/119.88 E), were collected for comparative analysis. The collected seeds were screened against varying levels of quinclorac in Petri plates. These eight biotypes were sown in the field (30 and 60 plants for R and S biotypes, individually). At 3-4 leaf stage, the seedlings were sprayed with quinclorac (field rate: 300 g a.i. ha⁻¹); half of the S seedlings were left without spray (seeds from half un-treated plants were used in further studies). Cross-pollination was avoided by covering the inflorescence with a butter paper bag (35 days after emergence). Seeds of surviving biotype of quinclorac field dose were employed in further study.

2.2 Quinclorac Resistance Confirmation (Screening in Petri Plates and Pot Assay)

Quinclorac was used in 5 varied concentrations (1200, 600, 300, 150, 75 mg L⁻¹), besides quinclorac free control was also maintained to screen seeds of R and S biotypes in Petri plate (9 cm diameter) bioassay using filter papers (Whatman no.1) and 15 seeds were incubated in each Petri plate. 5 mL herbicide solution or distilled water was applied to each Petri plate, and further rehydration was accomplished with the application of distilled water when required. The study was conducted in a growth chamber with 600 μ mol photon m⁻² s⁻¹ PAR, 26/18 °C temperature, relative humidity at 60%, and a day/night period set at 14/10 h. Five random seedlings from each Petri plate were selected for shoot length measurement (9 days after incubation).

Five seedlings of individual biotypes were maintained in plastic pot having a diameter of 12 cm diameter for whole-plant bioassay. Pots were filled with organic soil and sand with 1:2 ratio. A laboratory sprayer (280 L ha⁻¹ delivering capacity at 230 kPa) furnished with a flat fan nozzle (3WPSH-500D, Nanjing, China) was used to spray quinclorac at 3-4 leaf stage. For R biotype quinclorac was applied at 0, 75, 150, 300, 600, 1200 g a.i. ha⁻¹ and for S biotypes the dose was 0, 37.5, 75, 150, 300 and 600 g a.i. ha⁻¹. The seedlings of S biotypes were treated only with the double field dose as it was understood that these seedlings would not survive on four-times field dose. Three weeks after quinclorac application, the above-ground plant parts were harvested for fresh weight measurement. Percent fresh weight reduction is the percent change in dry biomass at every dose with respect to un-treated control. The percent survival rate was calculated by subtracting the values of percent fresh weight reduction from 100.

2.3 Determination of Ethylene Production

Quinclorac was sprayed on all biotypes at 3-4 leaf stage with different concentrations (0, 150, 300, 600 g $\,$

a.i. ha⁻¹). At various time periods (0, 12, 24, 48, 96 h post spray), shoots from each treatment were harvested and incubated at 25 °C for five hours in 15 mL tared screw-neck vial. Abdallah's method was employed for the quantitative determination of ethylene using a GC system 7890A (Agilent Technologies). The injector, detector, and column were set at temperature of 70, 200, 250 °C, respectively. The flow rates of N₂, air, and H₂ were 30, 300, 30 mL min⁻¹, respectively. The ethylene contents were calculated in nmol g⁻¹fresh weight h⁻¹ of incubation.

2.4 Endogenous ACC Levels Determination

Quinclorac-induced differential ACC levels in R and S biotypes were found in an experiment. Growth conditions, quinclorac application time and dose, as well as sampling times, were the same as ethylene determination. Shoot tissue (0.2 g) was powdered in liquid N2, and 5% sulfosalicylic acid (0.4 mL) was used for extraction. Chemical conversion of ACC into ethylene in samples was carried out by $HgCl_2$ (Bulens et al., 2011). The reaction was carried out in 5 mL tared screw neck vials. The escaped ethylene gas from the reaction was quantitatively determined by using a GC system 7890A (Agilent Technologies). ACC contents were calculated from ethylene by using the formula of Bulens et al. (2011).

2.5 ACS and ACO and β-CAS activities determination

Varying quinclorac doses (0, 150, 300, 600 g a.i. ha⁻¹) were applied to plants at 3-4 leaf stage. Root tissues were collected 24 h after quinclorac application for ACS activity (pmol g⁻¹ root fresh weight h⁻¹ of incubation) determination. ACC levels in extracted samples were monitored by their conversion into ethylene to find out ACS activity. Shoot samples from the same experiment were collected 24 h after quinclorac application for ACO activity (pmol g⁻¹ root fresh weight h-1 of incubation) determination. Crushed frozen sample (0.5 g) was extracted by 1 mL MOPS extraction buffer {add MOPS (8.37 g) + 10 mL glycerol + ascorbic acid sodium salt (0.594 g) and make final volume to 100 mL by adding distilled water}. The samples were vortexed and incubated at 4 °C for 10 min at thermo mixer. After incubation, the samples were centrifuged for 30 min at 22000 × g and 4 °C. The supernatants (400 µl) were permitted to react with 3.6 mL of MOPS reaction buffer {add MOPS (1.046 g) + 10 mL glycerol + ascorbic acid sodium salt (0.099 g) + sodium bicarbonate (0.168 g) + iron sulphate (0.3 mg) + ACC (0.01 g) + DDT (0.015 g) and make final volume to 100 mL by adding distilled water}. After incubation for 1 h, the headspace gas was withdrawn to measure ethylene levels by GC system (Bulens et al., 2011).

Potential cyanide degradation by β -CAS activity in R and S biotypes was determined. Kasugai nutrient solution was prepared by adding (NH₄)₂ So₄ (188.7 mg), Na₂HPO₄ (40 mg), CaCl₂ (7.9 mg), Fe-EDTA (27.4 mg), MnCl₂ (0.75

mg), KCl (47.5), SiO₂ (137.3 mg), N (40 mg), P₂O₅ (20 mg), CaO (4 mg), MgO (6 mg), K₂O (30 mg) in 1 L of distilled water. Seedlings were grown till 3-4 leaf stage in Kasugai nutrient solution. Plant sample collection time was 1, 12, and 24 h after addition of quinclorac {50 μ mol L⁻¹ (μ M)} in growth medium. Enzyme extract was incubated for 30 min at 35 °C after extracting with 0.1 M Tris-HCl buffer. Absorbance was recorded at 650 nm using Na₂S as standard (Chon et al., 2008).

2.6 EcCAS Gene Sequence

Primers sequence (F-CCGTCCTTCAGCGTCAAA, R-ATGCCAACCAAAAGACCCT, TM = 55°C) was employed to amplify partial sequence of EcCAS in E. oryzoides. PrimeScript[™] RT Reagent Kit with gDNA Eraser (TaKaRa, Otsu, Japan) was used to synthesize cDNA from RNA of samples that was extracted by using Plant Easy Spin RNA Miniprep Kit (Biomiga, San Diego, USA). TaKaRa PCR Thermal Cycler (TaKaRa, Otsu, Japan) was used for amplification in 50 µl total volume that consisted of TaKaRa ExTaqTM 0.4 µl, 10X Taq Buffer 5 µl, 4 µl of MgCl2 and dNTP each, forward and reverse primers 2 µl (10 µM) each, ddH2O 30.6 µl, and cDNA (2.5 ng). Gel/ PCR Extraction Kit (Biomiga, San Diego, USA) was used to gel-purify PCR product. pMDTM 19-T Vector Cloning Kit (Clontech, USA) was employed to clone purified cDNA into E. coli DH5 α Competent Cells (Clontech, USA), and then further sequencing was carried out by Sangon Biotech (Shanghai, China).

of Rapid Amplification cDNA Ends (RACE) was accomplished by SMARTer® RACE 5'/'3' Kit (Clontech, USA) with the use of primers (5'-RACE-CCCTCCTCTCAAGACTGGTGTATGACGGCA, 3'-RACE-CTGAAGCAAATGTTCTGAATGGTGGAAAGCC, TM= <70°C). After gel purification, PCR product was sequenced from the company. BioEdit Sequence Alignment Editor was used to align the obtained sequences. NCBI website's ORF Finder Function (https://www.ncbi.nlm.nih.gov/orffinder/) was employed to find EcCAS gene open reading frame (ORF). The ORF amplification was done by the primers (F-ATGGAGAGGATGCTGGCG, R- TTAGTCTACTGGCACTGGT

TCC, TM = 57° C) and sent to Sangon Biotech, Shanghai, China, for sequencing (4 individual plants and 6 clones from each replicate).

2.7 Computational Simulation of $\beta\text{-CAS}$ Binding with its cofactor- PLP

Quinclorac resistant and susceptible β -CAS structures underwent homology modelling. 3D structure of β -CAS was constructed by Protein Homology/analogY Recognition Engine (Phyre2) (Kelley et al., 2015). Energy minimization of the structure was carried out using YASARA, and further structure validation was carried out by ProSA. The structure of PLP was obtained from PubChem (CID: 1051). Both structures were prepared for docking by AutoDock Tools v. 1.5.6. and further AutoDock Vina v. 1.1.2. was used for docking of β -CAS and PLP. Docking grid box size (Å) was X:40, Y:60, and Z:44 and X:43, Y:51, and Z:44 for quinclorac susceptible and resistant β -CAS enzymes, respectively. Results obtained from docking were visualized and mined by PyMOL v. 2.3.3.

2.8 Transcriptional studies of ACS, ACO, and CAS Genes by Real-time PCR

Seedlings of R and S biotypes were grown, and samples were collected following the same procedure for β -CAS activity determination. Primers for EcACS7, EcACS-like, EcACO-like, EcACO homolog 4, EcACO1, and EcACO5-like (Table 1) were designed by using Primer Premier 5. EcActin {HQ395760; Table 1} was used as reference gene (Li et al., 2013). cDNA was synthesized as described earlier. Gene expression analysis of three biotypes of E. oryzoides was carried out on real-time PCR (Eppendorf Metercycler® Realplex2) with SYBR® Premix Ex TaqTM (Tli RNAaseH Plus; TaKaRa, Otsu, Japan). The volume of the reaction mixture was 10 µl, containing 5 µl SYBR® Premix Ex TaqTM, 0.4 μ l primers (10 μ M), 0.8 μ l cDNA (2.5 ng), and 3.8 µl ddH₂O. PCR profile was as follows; 95°C for 30 s, 40 cycles at 95°C for 5 s, and 60°C for 30 s. A standard curve (Ct value-based) against cDNA template serial dilution was constructed to evaluate each primer set's PCR amplification efficiency. Target and internal control were confirmed for approximately equal amplification efficiencies. $\Delta\Delta Ct$ method was employed to calculate relative mRNA levels (3 biological and 4 technical replicates). Up- or downregulation of gene expressions was carried out by the t-test (P < 0.05) and fold change.

2.9 Statistical Analysis

Dose-response bioassays were conducted in triplicate. The concentration of ethylene, ACC contents, ACS, ACO, and β -CAS activity-related experiments were carried out in quadruplicate. All the experiments were repeated twice by

using a completely randomized design. Percent reduction of fresh weight/shoot length related to untreated control was calculated. Dose-response function (growth/sigmoidal) of Origin Pro 8 SR0 {v 8.0724 (B724), Origin Labs Corporations. MA 01060. USA.} was used to calculate EC50 and GR50 (effective concentration to inhibit growth by 50%). Primer Premier 5 (PREMIER Biosoft International, Canada) was used to design primers. Graphs were drawn by Microsoft Excel 2019 and Sigma Plot. Correlation analysis and ANOVA construction were accomplished by SPSS version 24 (SPSS, Chicago, IL, USA).

3. Results and Discussion

3.1 Dose-response Analysis Confirmed Quinclorac Resistance in *Echinochloa oryzoides*

Biotypes from Ningxia and Liaoning viz; NX1-S, NX2-S, NX3-S, NX4-S, and LN1-S, respectively, exhibited quinclorac sensitivity after Petri plate bioassay (Table 2). Hence, these five biotypes were not used in further study. HLJ-S and ZJ-S depicted lower values of EC50, GR50, and RI, as on increased quinclorac rates, both biotypes were not able to survive (Figure 1; Table 3). However, JS-R biotype was able to survive at higher dose of quinclorac field rates, and it showed 21-32-fold increase in RI compared to HLJ-S- proving this biotype was resistant to quinclorac. The quinclorac resistance outbreak in Echinochloa species in Chinese rice fields mainly occurred by an exaggerated use of this herbicide as *E. oryzoides* biotype exhibited quinclorac resistance from Jiangsu province of China. Resistance evolution in this biotype was caused by the continuous use of quinclorac. As per earlier projections, those stated that continuous use of herbicide with the same mode of action could lead to resistant weed species (Malik et al., 2010).

3.2 Effect of Quinclorac Application on Ethylene Biosynthesis

In susceptible plants, ethylene biosynthesis is induced by the application of quinclorac (Zia Ul Haq et al., 2020). Therefore, to determine the relationship between quinclorac

Table 1 - Primers set for ACS, ACO and CAS genes amplification in Echinochloa oryzoides.							
Gene Forward primer Reserve		Reserve Primer	Annealing Temperature (°C)	Length of Product			
EcActin	5'-TACTCCTTCACCACAACCGC-3'	5´-TGATGACCTGTCCATCAGGC-3´	60	154			
EcACS7	5´-TCGCGAGGATGAGCAGATTC-3´	5´-ACCCAAGGTAGTATTATTTACCCTC-3´	60	124			
EcACS-like	5'-GATGCTGTCGGACCACGAG-3'	5'-GTCCATCCACGAGAAGAGCC-3	60	148			
EcACO homolog 4	5'-CATCTTCCCGCACACGGAC-3'	5´-GATGGAAACCCTTGGCTCGT-3´	60	250			
EcACO1	5´-AGTCCCAGGTTTGGAGTTTCTG-3´	5´-ATTATGGCGTCAGCACCAGG-3´	60	207			
EcACO-like	5´-CCGGAGTTCAAGGAGACCAT-3´	5´-TGACCTTGGTGCCGAAGAAG-3´	60	163			
EcACO5-like	5´-GCACATGGCGGTGAACTACT-3´	5'-CACGCTCTTGTAGCGGTCAT-3'	60	229			
EcCAS	5 ⁻ ATGCCGTCATACACCAGTCTT-3 ⁻	5'- CAGCAGGTTCAACTCCATAGAT-3'	57	253			

resistance and ethylene biosynthesis, three biotypes were subjected to the measurement of the ethylene levels. Ethylene levels increased more rapidly and exhibited higher values in susceptible biotypes. However, the resistant biotype showed a little increase in ethylene levels even at 2 times of quinclorac field dose (Figure 2a, b). This biotype showed 4 times higher ethylene levels than the untreated control at a quinclorac dose of 600 g a.i. ha⁻¹, verifying that ethylene production correlated negatively with resistance

Table 2 - EC ₅₀ , and RI of quinclorac sensitive biotypes of <i>Echinochloa oryzoides</i> from Ningxia and Liaoning Provinces.						
-	Dose-Response Analysis					
Populations	EC ₅₀ (mg L ⁻¹)	٢	RI (EC ₅₀ Ratio)			
NX1-S	401.18 (3.32)	0.97	3.57			
NX2-S	282.93 (7.33)	0.99	2.52			
NX3-S	197.71 (1.63)	0.99	1.76			
NX4-S	196.62 (0.46)	0.98	1.75			
LN1-S	196.71 (0.55)	0.99	1.75			

 EC_{50} = effective dose causing 50 % inhibition, RI (Resistance Index) = ratio of EC_{50} R over EC_{50} S, r^2 = Coefficient of determination, P < 0.05, Standard errors are in parenthesis. Biotypes showing RI less than 10 are considered as herbicide sensitive.

against quinclorac (Figure 3a). 24 h after quinclorac application, a peak in ethylene production was observed; afterward, a gradual decrease was evident in three biotypes at the quinclorac rate of 300 g a.i. ha^{-1} (Figure 2a, b).

Nevertheless, HLJ-S and ZJ-S biotypes showed nearly 2 times increment in ethylene levels measured at 96 h after guinclorac application than their respective controls. Additionally, the quinclorac-induced ethylene level increment triggered toxicity in plants and reduced fresh weight in both susceptible biotypes. Stimulation of ethylene biosynthesis and quinclorac-induced growth inhibition were found to possess a positive correlation. JS-R biotype exhibited a relatively slight increase (0.5 times compared to untreated control) after quinclorac spray, hereafter verifying that quinclorac resistance levels and ethylene biosynthesis correlated negatively. In susceptible plants, an increase in ethylene and cyanide contents due to de novo synthesis of ACS are evident from the application of quinclorac- as it is an auxin herbicide (Abdallah et al., 2006; Xu et al., 2013). Senescence and plant death are governed by a major plant hormone- ethylene. Several studies reported that ethylene biosynthesis inhibition in barnyard grass could be a possible mechanism endowing quinclorac resistance (Abdallah et al., 2006; Xu et al., 2013; Gao et al., 2018).

This study showed distinct levels of ethylene in resistant and susceptible biotypes post quinclorac



Figure 1 - Dose-response curve of Echinochloa oryzoides possessing varied levels of quinclorac sensitivity.

Table 3 - EC ₅₀ , GR ₅₀ , and RI of <i>Echinochloa oryzoide</i> s possessing varied levels of quinclorac sensitivity.						
Deculations	Dose-Response Assay					
Populations	EC ₅₀ (mg L⁻¹)	٢²	RI (EC ₅₀ Ratio)	GR ₅₀ (g a.i. ha⁻¹)	۲ ²	RI (GR ₅₀ Ratio)
HLJ-S	112.46(16.24)	0.99	1	29.54(4.60)	0.99	1
ZJ-S	177.95(18.56)	0.99	1.58	47.61(5.28)	0.99	1.61
JS-R	3570.21(290.84)	0.97	32	625.86(70.04)	0.99	21

 EC_{50} = effective dose causing 50 % inhibition, GR_{50} = effective dose causing 50% growth inhibition, RI (Resistance Index) = ratio between R and S (EC_{50} or GR_{50}), r^2 = Coefficient of determination, P < 0.05, Values in parenthesis are standard errors.



Figure 2 - Ethylene concentration (a, b; % of mean untreated plant in same biotype) and ACC contents (c, d; % of mean control) depicted by *Echinochloa oryzoides* biotypes (quinclorac resistant and susceptible) effected by various quinclorac doses (0, 150, 300, 600 g a.i. ha⁻¹) at 24 HAT and sampling times (0, 12, 24, 48, 96 HAT) at quinclorac dose of 300 g a.i. ha⁻¹.

application, which validates the link between ethylene biosynthesis inhibition and quinclorac resistance (Xu et al., 2013; Gao et al., 2018). In this study, quinclorac-induced hormone homeostasis imbalance resulted in phytotoxic growth inhibition confirming the positive relationship among ethylene biosynthesis and growth inhibition. Hereby, this validates the protagonist of ethylene in quinclorac phytotoxicity (Abdallah et al., 2006; Xu et al., 2013; Zia Ul Haq et al., 2020).

3.3 Differential Effect of Quinclorac Application on ACC, ACS, and ACO enzymes activities

ACC accumulation was studied in all three biotypes of *E.* oryzoides at 24 h after treatment with different quinclorac rates (0, 150, 300, 600 g a.i. ha⁻¹; Figure 2c, d). A slight ACC contents increase (1.5-1.9 fold) was observed in JS-R biotype at 150 and 300 g a.i. ha⁻¹, while at 600 g a.i ha⁻¹, this biotype exhibited 2.8-fold increase in ACC contents. HLJ-S and ZJ-S being quinclorac susceptible biotypes, recorded

the highest ACC contents (5 times more as compared to untreated control and 2 times more than resistant biotype) at quinclorac dose of 600 g a.i. ha^{-1} (Figure 2c, d). ACC contents spiked in all biotypes till 24 h after quinclorac application (300 g a.i. ha^{-1}), while a downward trend in ACC contents was observed beyond 24 h (Figure 4). The application of 300 g a.i. ha^{-1} quinclorac caused a slight increment of ACC contents in resistant biotype irrespective of sampling times. While ACC contents in susceptible biotypes, the ACC contents were around 4 times higher than control (0 h after spray) at 24 h after quinclorac application. A negative correlation was found between ACC contents and resistance levels of all biotypes, the same as found in ethylene levels.

Ethylene production rate is controlled by two important enzymes (ACS and ACO) in its biosynthesis pathway. Differential ACS and ACO enzymes activities induced by quinclorac application in resistant and susceptible biotypes of *E. oryzoides* were investigated under varying quinclorac doses. Results revealed that the ACS and ACO activities were



Figure 3 - The ACS (EcACS7, EcACS-like) and ACO (EcACO-like, EcACO homolog 4, EcACO, EcACO5-like) genes relative transcription in Echinochloa oryzoides biotypes calculated at 0-, 6-, 12-, and 24-hours post quinclorac treatment.

EOCAS(Q.Sensitive)	MERMLARLMRRRSSLLHQGAA	PPIPLGASSSLFSTTQQQQADPGVTPGLKIRD	53
EOCAS(Q.Resistant)	MERMLARLMRRRSSLLHQGAA	PPIPLGASSSLFSTTQQQQADPGVTPGLKIRD	53
OSCAS	MFRALMSLMRRRSLLQSGGRA	PPAMAAAAGGSPFFSTLQQAAAADPVQSPGILPGLKIRD	60
EOCAS(0.Sensitive)	SASOL IGRTPMVYLNKVTEGC	GARTAAKLEELOPSESVKDRPATSMLEDAENKGLTTPGK	113
FOCAS(0, Resistant)	SASOL TORTPMVYL NKVTEGC	GARTAAKI EEL OPSESVKDRPATSMI EDAENKGI TTPGK	113
OSCAS	SASQLIGRTPMVYLNKVTEGC	GARIAAKLEFLQPSFSVKDRPAISMLEDAEKKGLITPGK	120
FOCAS (O Sansitiva)			172
EOCAS(Q. Sensicize)	TTL TEDTS GNMGTGLAFMAAL		173
EUCAS(Q.RESISCANC)	TTL TEDTS GNMGTGLAFMAAL		175
USCAS	TILIEPISONMOIOLAPMAAL	KOTELIL IMPSTISLERRV IMRAFOAKLVLIDPIKOMOG	100
EOCAS(Q.Sensitive)	TVRKAAELYEKHPSAYMLQQF	QNPANVKIHYETTGPEIWEDTLGQVDIFVMGIGSGGTVT	233
EOCAS(Q.Resistant)	TVRKAAELYEKHPSAYMLQQF	QNPANVKIHYETTGPEIWEDTLGQVDIFVMGIGSGGTVT	233
OSCAS	TVRKAAELYENHPSAFMLQQF	ENPANVKVHYETTGPEIWEDTLGQVDIFVMGIGSGGTVT	240
FOCAS(0 Sensitive)	GVGKYLKEKNPNTKTYGVEPA		293
EOCAS(O Resistant)	GVGKYLKEKNPNTKTYGVEPA		293
OSCAS	GVGKYLKEKNPNAKIYGVEPA	EANVLNGGKPGPHLITGNGVGFKPEILNMDIMEKVLEVK	300
		0	
EOCAS(Q.Sensitive)	SEDAVKMARELAVKEGLLVGI	SSGANTVAALELAKKPENKGKLIVTVLPSLGERYLSSTL	353
EOCAS(Q.Resistant)	SEDAVKMARELAVKEGLLVGI	SSGANTVAALELAKKPENKGKLIVTVLPSLGERYLSSAL	353
OSCAS	GEDAVKMARELALKEGLLVGI	SSGANTVAALELAKKPENKGKLIVTVLPSLGERYLS	360
EOCAS(Q.Sensitive)	FEELRKEAEAMEPVPVD	370	
EOCAS(Q.Resistant)	FEELRKEAEAMEPVPVD	370	
OSCAS	FEELRAEAEAMOPVPVD	377	

OSCAS: Oryza sativa CAS

Figure 4 - Amino acid sequence (ORF generated) of *EcCAS* gene from quinclorac resistant {EOCAS (Q. Resistant)} and susceptible {EOCAS (Q. Sensitive)} *Echinochloa oryzoides*. Two nucleotide mutations (Met-287-Lys and Thr-352-Ala) between both biotypes are specified by boxed codon.

negatively correlated with quinclorac resistance. ACS activity was the same in three biotypes understudy at 0 and 150 g a.i. ha-1 herbicide dose (Table 4). However, the difference between ACS activity extended between quinclorac resistant and susceptible biotypes with increased quinclorac dose. Nearly 2 times higher ACS activity was observed in HLJ-S and ZJ-S biotypes as compared to JS-R at 600 g a.i. ha-1 quinclorac dose. ACO activity was higher in HLJ-S and ZJ-S biotypes as compared to JS-R before treatment with quinclorac. JS-R biotype depicted the slightest increase (77% higher than control) in ACO activity at guinclorac rate of 600 g a.i. ha⁻¹. Whereas HLJ-S and ZJ-S being quinclorac susceptible biotypes, exhibited much higher ACO activity, as ~60, 120, and 230% increment in ACO activity was found at quinclorac doses of 150, 300, and 600 g a.i. ha⁻¹ (Table 4). A reasonable upsurge in ACC contents, ACS, and ACO activities were recorded in a susceptible biotype of *E*. oryzoides after quinclorac application. While increment of these parameters was relatively low in the resistant biotype. Subsequently, resistant biotype produced a lower level of ethylene as compared to susceptible ones. These results follow previous studies where susceptible biotypes showed a high increase in ACC, ACS, and ACO activities than resistant biotypes (Xu et al., 2013; Zia Ul Haq et al., 2020).

3.4 ACS and ACO Genes Transcription Varied among Resistant and Susceptible Biotypes

The relative transcript levels of ACS and ACO genes were calculated at 0, 6, 12, 24 HAT in all biotypes under study. The data exhibited that the susceptible biotypes expressed a significant upsurge in relative transcript levels of ACS and ACO genes post quinclorac application (Figure 3). The relative transcript levels of six genes (EcACS7, EcACS-like, EcACO-like, EcACO homolog4, EcACO1, and EcACO5-like) under study were upregulated by 39, 12, 18, 8, 67, and 24 folds, respectively at 6 HAT in HLJ-S. Expression levels of *EcACS7* and *EcACO5-like* increased at 12 HAT in HLJ-S, with a decreasing trend till 24 HAT. *EcACS-like* maintained its expression levels at 12 HAT in the same biotype. The remaining genes under study depicted a decreasing trend afterward in HLJ-S (Figure 3). Relative transcription of *EcACS7*, *EcACS-like*, *EcACO-like*, *EcACO homolog4*, *EcACO-like*, *EcACO homolog4*, *EcACO-like*, *EcACO homolog4*, *EcACO homolog4*, *EcACO homolog4*, *EcACO homolog4*, *EcACO homolog4*, *EcACO homolog4*, *EcACO-like*, *EcACO homolog4*, *EcACO homolog4*,

EcACO1, and *EcACO5-like* were amplified to some extent in JS-R; nevertheless, it was significantly lower than the increment in HLJ-S. Except for *EcACO1*, all other genes exhibited 10-folds upregulation in gene transcription level at either calculation time. Less inducible expressions for *ACS* and *ACO* genes triggered a diminution in ACS and ACO enzyme activities in quinclorac-resistant *E. oryzoides*. These expression levels correlated negatively with quinclorac resistance.

Quinclorac susceptible E. crus-galli var. mitis and -var. *zelayensis* exhibited the increment in ethylene production due to ACS and ACO genes upregulation (Gao et al., 2018; Zia Ul Haq et al., 2020). In this study, quinclorac susceptible and resistant E. oryzoides showed the differential relative transcript levels of EcACO5-like, EcACO1, EcACO homolog4, EcACO-like, EcACS-like, and EcACS7 genes. Quinclorac susceptible biotypes of E. oryzoides in the present study exhibited > 10-fold increase in transcript levels of EcACO5-like, EcACO homolog4, EcACO-like, EcACS-like and *EcACS7*. Contrarily, the resistant biotype did not show any remarkable increment in transcript levels of the abovementioned genes. Alteration in ACS and ACO activity induction can be correlated to quinclorac resistance in the present study. As it is clear from ACS and ACO genes transcription data, increased ACS and ACO (~2-3 times, respectively) activity levels in susceptible than resistant biotype of E. oryzoides can reinforce the protagonism of ethylene biosynthesis inhibition causing quinclorac resistance in the resistant biotype.

3.5 Sequence Description, Evaluation, and Mutation Verification of *EcCAS* gene

EcCAS gene ORFs in all biotypes were comprised of 1113 bp, encoding 370 amino acids polypeptide. The sequences were submitted to NCBI website (MT007245, MT007246). *Echinochloa oryzoides EcCAS* gene was found to be highly similar (>90%) with *EcCAS* gene of *E. crus-galli* var. *mitis* (MN815009-10) and -var. *zelayensis* (KY922855.1). Four copies of *EcCAS* gene were found from all biotypes of *E. oryzoides* (data not presented). Nucleotide sequences depicted two-point mutations found in all copies of resistant biotype as compared to susceptible ones. The

Table 4 - ACS and ACO activities by Echinochloa oryzoides biotypes possessing varied quinclorac sensitivity after 24 hoursunder various quinclorac doses.							
Dose (g a.i. ha ⁻¹)	ACS activity (pmol. g ⁻¹ fresh weight h ⁻¹)			ACO activity (pmol. g ⁻¹ fresh weight h ⁻¹)			
	HLJ-S	ZJ-S	JS-R	HLJ-S	ZJ-S	JS-R	
0	50.58±0.65 ^{d NS}	48.08±2.99°NS	44.03±1.44°NS	290.66±6.27 ^{dA}	289.16±10.92dA	207.52±15.44°B	
150	64.78±2.71°NS	60.28±6.87°NS	50.72±1.87 ^{bc NS}	490.54±21.65°A	500.54±31.22°A	263.08±8.09 ^{bc B}	
300	81.92±1.35 ^{bA}	84.67±3.77 ^{bA}	55.59±1.75 ^{ab B}	652.05±18.78 ^{bA}	667.05±30.97 ^{bA}	303.74±21.71 ^{b B}	
600	113.55±2.65ªA	117.80±6.77 ^{a A}	61.34±2.15 ^a ^B	981.19±20.54ªA	1006.19±36.95°A	367.59±11.35°B	

Data are four replicate's means ± standard error. Significant difference among various doses in one biotype, and among various biotypes under the same dose are represented by ^{a-d} and ^{A-B}, respectively, ^{NS} = non-significant under the same quinclorac dose. ACS = 1-Aminocyclopropane-1-carboxylic acid synthese, ACO = 1-Aminocyclopropane-1-carboxylic acid oxidase

mutations of ATG to AAG and TAC to TGC caused amino acid substitutions of Met-287-Lys and Thr-352-Ala, respectively (Figure 4). Non-target enzyme activity can be instigated by gene mutations and alteration in their expression levels (Iwakami et al., 2014).

3.6 Enhanced β -CAS Activity, Expression Pattern of EcCAS Gene, Effect of Mutations on β -CAS Docking with Cofactor- PLP

The β -CAS activity in susceptible biotypes was significantly lower than the resistant one prior to quinclorac treatment (Figure 5a). A decreasing trend in β -CAS was observed in susceptible biotypes post quinclorac treatment, as 24 hours after treatment (HAT), around 25% decline was recorded in β-CAS activity. The resistant biotype exhibited significantly (P < 0.05) higher enzyme activity than susceptible biotypes regardless of the sampling time under study (Figure 5a). Untreated resistant biotype of *E. oryzoides* depicted higher (P < 0.05) relative transcript levels of EcCAS gene than susceptible ones, as it was 1.8-fold higher than susceptible ones (Figure 5b). *EcCAS* transcript levels were declined post quinclorac application in susceptible biotypes, as at 24 HAT, it decreased 0.70-fold in the untreated plants. Resistant biotype was succeeded to maintain EcCAS transcript levels; nevertheless, no significant increase was observed in its transcript levels than untreated plants. An increment of 2.6-fold was observed in EcCAS transcript levels of resistant biotype than susceptible ones at 24 HAT (Figure 5b). Resistant and susceptible biotypes varied regarding β -CAS activity in this study. The higher β -CAS activity was observed in quinclorac-resistant *E*. oryzoides than in susceptible ones, so this biotype was potentially capable of detoxifying produced cyanides due to the quinclorac application. The increased β-CAS activity in quinclorac-resistant *E. crus-galli* var. *zelayensis* and -var. mitis has been documented already (Gao et al., 2017; Zia Ul Haq et al., 2020). Increased cyanides accumulated in susceptible biotypes led to cyanide poisoning. Elevated cyanides in plants disrupted cytochrome c oxidase (Ikegaya et al., 2001). On the other hand, ACS activity can be triggered by cyanides produced, ultimately intensifying the ethylene and cyanide levels in plants (Grossmann and Scheltrup, 1997). Therefore, resistant biotype was escaped from more ethylene production because cyanides were potentially degraded by β -CAS activity. Maintenance of EcCAS relative expression levels in quinclorac resistant E. oryzoides and downregulation in susceptible ones post quinclorac application proved that β -CAS activity and quinclorac resistance were correlated positively. It can be inferred that quinclorac resistance in E. oryzoides was instigated by variation in ethylene response pathway and potential cyanide degradation by β -CAS activity, as found earlier in E. crus-galli var. zelayensis and -var. mitis (Xu et al., 2013; Gao et al., 2018; Zia Ul Haq et al., 2020).

Figure 6a, b shows the 3D structures of β -CAS, and active sites in the structure are shown at the point of binding of PLP (Figure 6c, d). The PLP binding with β -CAS was affected due to point mutations as in susceptible β -CAS, Ser-121, Gln-193, Gly-271, and Asn-272 amino acids bounded the PLP, though it was bound to Ser-121, Gln-193, Ile-269, Gly-271, and Asn-272 in resistant one. Molecular docking was carried out around nine modes (Table 5) in both resistant and susceptible β -CAS 3D enzyme structures. Results depicted a slight decrease in binding free energy (-0.61 to -0.62 kcal mol⁻¹; Table 5), making resistant β -CAS to bind with PLP further conveniently. β -CAS binds with cysteine with the help of a cofactor. CN- attachment with cysteine



Figure 5 - β-CAS activity (a), and *EcCAS* gene relative transcription (b) depicted by *Echinochloa oryzoides* biotypes (quinclorac resistant and susceptible) at various time intervals post quinclorac treatment.



Figure 6 - Ribbon diagram demonstrating the β -CAS structure of *Echinochloa oryzoides* (a) quinclorac susceptible, and (b) resistant. Molecular simulation of active sites of (c) quinclorac susceptible, and (d) resistant β -CAS docked with PLP.

Table 5 - Molecular docking carried out around different modes in quinclorac-resistant and susceptible β-CAS enzyme 3D structure.*						
	Quinclorac-susceptible β-CAS enzyme			Quinclorac-resistant β-CAS enzyme		
Modes	Affinity	Distance from best mode (Å)		Affinity	Distance from best mode (Å)	
	(kcal mol ⁻¹)	RMSD lb	RMSD ub	(kcal mol ⁻¹)	RMSD lb	RMSD ub
1	-6.1	0.000	0.000	-6.2	0.000	0.000
2	-6.0	4.126	6.617	-5.8	2.077	2.903
3	-5.9	2.898	5.553	-5.8	5.317	7.857
4	-5.7	1.984	2.840	-5.7	4.231	6.560
5	-5.6	5.659	7.559	-5.5	2.650	3.958
6	-5.5	5.842	7.115	-5.5	3.480	5.697
7	-5.5	5.886	6.498	-5.4	3.530	5.418
8	-5.4	6.444	7.669	-5.2	5.615	7.375
9	-5.3	4.383	6.317	-5.1	5.037	6.399

RMSD = root mean square deviation, Ib = lower bound, ub = upper bound, Å = Angstrom

*Auto-generated table from AutoDock Vina v. 1.1.2 during molecular docking.

is completed due to the repositioning of amino acid; this binding initiates the β cyanoalanine production (Yi et al., 2012). The understanding of binding variation between quinclorac susceptible and resistant β -CAS enzymes was accomplished by molecular docking studies of PLP and β -CAS. In the active site, five amino acid subunits made polar bonds with resistant β -CAS; this led to a slight decline in binding free energy. This provided a base for easier and firm binding of β -CAS with PLP. Resultingly efficient β -CAS-PLP binding ultimately led to the increased overall efficiency of β -CAS to degrade cyanides produced in plants during the ethylene biosynthesis pathway in response to quinclorac application (Zia Ul Haq et al., 2020). Proteinprotein interactions are responsible for governing cell biological processes.

 β -CAS gene in quinclorac-resistant *E. phyllopogon* showed single nucleotide polymorphism (SNP) in the intron region of the gene, and there was no link between quinclorac resistance and β -CAS mutation (Chayapakdee et al., 2019). Consequently, the translated amino acid sequence did not depict any change due to SNP. Recently, a study on *E. cruspavonis* excluded the role of β -CAS in endowing quinclorac resistance (Yang et al., 2021).

Though, in the present study, *EcCAS* gene of *E. oryzoides* depicted two-point mutation that led to amino acid substitutions. Recently three point-mutations in EcCAS gene have already been reported in E. crus-galli var. mitis (Zia Ul Haq et al., 2020). It is a well-known fact that β -CAS enzyme is responsible for HCN degradation that is produced during ethylene synthesis (Lai et al., 2009). Subsequently, the enzymatic activity was possibly maintained due to mutation in β -CAS gene post quinclorac application. Hence, maintenance of β -CAS activity levels still played a role in endowing resistance against quinclorac. Increased enzymatic activity due to mutation in gene is evident in various studies (Mdodana et al., 2019; Zia Ul Haq et al., 2020). Molecular simulation study revealed the positive role of these mutations in enzyme and cofactor binding by various means such as binding site residues increment, the decline in binding free energy, and structural stability. The affinity of an enzyme and substrate proved to be enhanced by mutations (Wu et al., 2017). Hence, it can be concluded that maintenance in β -CAS enzyme activity post quinclorac application was endowed by said mutations.

Therefore, in light of the above-mentioned results, a decline in ACO and ACS activities was instigated by the decrease in transcript levels of *EcACO1*, *EcACO* homolog4, *EcACO-like*, *EcACO5-like*, *EcACS-like*, and *EcACS7* genes. Besides, *EcCAS* gene mutations endowed varied transcript levels between resistant and susceptible *E. oryzoides*, which led to the maintenance of β -CAS activity. Resultingly, a reduction in ethylene biosynthesis combined with potentially enhanced cyanide degradation caused quinclorac resistance.

4. Conclusions

ACS and ACO activities were enhanced post herbicide treatment in quinclorac susceptible E. oryzoides due to the transcription induction of respective genes. Consequently, ethylene biosynthesis was increased in these plants. Contrarily, quinclorac treatment did not lead to a rise in relative transcript levels of ACS and ACO genes in quinclorac resistant E. oryzoides; hence, ACS and ACO activities kept at low levels that commanded less ethylene production. The auxin-induced genes need further study to find the underlying mechanism; those studies might include gene-specific response and Aux/IAA protein sequencing. Quinclorac susceptible E. oryzoides showed a decline of EcCAS gene expression and ultimately lower β -CAS activity after herbicide treatment. Whereas quinclorac-resistant E. oryzoides exhibited higher β-CAS activity, facilitated HCN degradation. In addition, molecular simulations revealed that two-point mutations in *EcCAS* gene altered the enzyme structure that helped to improve its binding ability with HCN substrate, ultimately resulting in efficient cyanide degradation. Nevertheless, further study is needed to explore whether quinclorac acts as a signalling compound to induce the transcription of ACS and ACO genes or it induces a minute ethylene production.

Author's contributions

Conceptualization of the manuscript and development of the methodology: M.Z.U.H., S.Q.; data collection and curation: M.Z.U.H., Z.Z., R.M.A., D.A., and M.F.; data analysis: M.Z.U.H, Z.Z., R.M.A., D.A., and M.F.; data interpretation: M.Z.U.H., Z.Z., and R.M.A.; funding acquisition and resources: S.Q.; project administration: S.Q., and M.Z.U.H; supervision: S.Q.; writing the original draft of the manuscript: M.Z.U.H., D.A., and M.F.; writing, review, and editing: S.Q. All authors read and agreed to the published version of the manuscript.

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Conflict of Interest

The authors declare no conflict of interest.

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