

**Evolution and Spread of Glyphosate Resistant Barnyard Grass  
(*Echinochloa colona* (L.) Link) from Australia**

By  
**Thai Hoan Nguyen**

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School of Agriculture, Food and Wine  
Faculty of Sciences  
The University of Adelaide  
Waite Campus

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## Abbreviations

ACCCase:	Acetyl-CoA carboxylase
AFLP:	Amplified fragment length polymorphism
AGRF:	Australian Genome Research Facility
ALS:	Acetolactate synthase
EPSP:	5-enolpyruvylshikimate-3-phosphate synthase
HAT:	Hour after treatment
LD <sub>50</sub> :	Lethal dosage (dose required to control 50% of individuals in the population)
LSD:	Least significant different
NSW:	New South Wales
PCR:	Polymerase chain reaction
QLD:	Queensland
R/S:	Resistance/susceptibility
RAPD:	Randomly amplified polymorphic DNAs
RFLP:	Restriction fragment length polymorphism
SA:	South Australia
SE:	Standard error
SSR:	Simple sequence repeats
VIC:	Victoria
WA:	Western Australia

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## Abstract

*Echinochloa colona* is an important summer-growing weed species in northern Australian cropping regions. The intensive use of glyphosate in summer fallow operations has led to the appearance of glyphosate resistant *E. colona* populations at a large number of sites. Studies of the genetic diversity, resistance mechanisms, inheritance and spread of resistance were undertaken to better understand the evolution of glyphosate resistance in this species. A survey of 65 barnyard grass populations collected from Queensland and New South Wales determined 34 populations were resistant to glyphosate with resistance levels ranging from 2 to 11-fold. High genetic diversity within three populations and between 62 populations was identified by the AFLP technique. A total of 99.2% of alleles identified within populations were polymorphic with a higher percentage of polymorphic alleles within the two resistant populations compared to the susceptible population. The level of glyphosate resistance in populations was dependent on the ambient temperature. Resistant populations showed a noticeably higher level of resistance at 30°C compared to 20°C whereas there was no effect of temperature on the response of the susceptible population. Experiments were carried out on glyphosate absorption and translocation in resistant and susceptible plants to identify the reason for these differences and the results showed a considerable decrease in glyphosate absorption into leaves at 30°C. Differences were also identified in glyphosate translocation between the treated leaves and the other sections of plants at the different temperatures. There were no differences in glyphosate absorption or translocation between the susceptible population and the resistant populations suggesting that differences in absorption and translocation of the herbicide are not the mechanism of resistance in the studied populations. Studies of *EPSPS* gene copy number showed gene amplification was not the resistance mechanism either. A mutation was detected at codon 106 (proline substituted by serine) of the *EPSPS* gene of the most resistant population, A533.1, indicating the presence of target-site resistance in this population. Gene flow by pollen exchange between the glyphosate resistant

population A533.1 and the susceptible population Echi S occurred at a frequency of 1.38% when progeny from the susceptible parent was tested at 240 g a.e. ha<sup>-1</sup> of glyphosate. The mutation in the *EPSPS* gene was detected in 24 F<sub>1</sub> progenies of this population pair. Segregation of resistance in the gene flow experiment between resistant and susceptible individuals occurred at a 3:1 resistance : susceptibility ratio in the F<sub>2</sub> generation indicating the trait of glyphosate resistance is a single dominant trait of *E. colona*. Sequencing the *EPSPS* cDNA of five parental and F<sub>2</sub> filial individuals revealed at least two *EPSPS* genes present in *E. colona*. Shikimate accumulation of the F<sub>1</sub> hybrid and the glyphosate response of F<sub>2</sub> progenies were intermediate between the two parental populations.

## **Declaration**

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