

Category	: International Rice Research Conference
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Keyword 1	: Genotype x Environment Interactions
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Title of Entry	: Insight of E. crus-galli genome into its invasiveness and interaction between weed and rice
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Select only one type of presentation	: 15 minute oral presentation

Abstract : *E. crus-galli* is one of the most serious agricultural weeds in the world. Barnyardgrass is similar to rice plant type. That is why, it is very difficult to control Barnyardgrass in the paddy fields via manual weeding. Paddy weeding is currently largely dependent on chemical herbicides. The use of a large number of herbicides not only pollutes the environment, but also increases the cost of production and resistance to Barnyardgrass. Therefore, the selection of "green rice" with inhibition of barnyardgrass is an important way to reduce the use of chemical herbicides. China National Rice Research Institute (CNRRI) of Chinese Academy of Agricultural Sciences (CAAS) with the collaboration of Zhejiang University sequenced the genome of barnyardgrass, and found that the defensive secondary metabolites of barnyard grass were synthesized by clustered genes, which were used to compete with rice and resist rice pathogen, and provide an important genetic resource for rice C4 breeding. An extremely large repertoire of genes encoding cytochrome P450 monooxygenases and glutathione S-transferases associated with detoxification are found. Two gene clusters involved in the biosynthesis of an allelochemical 2,4-dihydroxy-7-methoxy-1,4-benzoxazin-3-one (DIMBOA) and a phytoalexin momilactone A are found in the *E. crus-galli* genome, respectively. The allelochemical DIMBOA gene cluster is activated in response to co cultivation with rice, while the phytoalexin momilactone A gene cluster specifically to infection by pathogenic *Pyricularia oryzae*. The results provide a new understanding of the molecular mechanisms underlying the extreme adaptation of the weed and the interaction between weed and rice.

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