

## SHORT COMMUNICATION

### A DEEPWATER TOLERANT GENE DETECTED IN THE COMMON WILD RICE

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#### INTRODUCTION

Rice is grown under diverse ecological conditions where cultural management practices vary considerably and the adapted cultivars have greatly diverged with distinct characteristics. Rice growing environments have been classified into five categories: (World bank, 1992) irrigated rice (77.5 M. ha), rainfed lowland rice (33 M. ha), deepwater rice (12 M. ha), upland rice (19 M. ha) and tidal wetland rice (5 M. ha)

Deepwater rice is grown in areas flooded deeper than 50 cm for one month or longer during the growing season. Deepwater rice grows under rainfed dryland or shallow flooding conditions for 1-3 months, then subjected to flooding with water depth of over 50 cm for one month or longer. Where water levels are over 100 cm, the crop is usually called floating rice.

Plants utilize environmental signals for *altering the timing of gene expression* so as to respond to change environment. A drastic change in morphology due to changing environments is known as phenotypic plasticity which is particularly important in plants because of their sessile life style. An example of plastic response is deepwater or floating rice whose internodal elongation starts

with increasing water depth to escape submergence, resulting in various changes in morphology.

However, no or little internodal elongation occurs in non-deepwater rice as well as air-grown deepwater rice. A number of recent experiments indicated that deepwater tolerance is related to enhance internodal elongation resulting from the action of the plant hormones ethylene and gibberellin. Gibberellic acid promoted the elongation of all organs while abscisic acid inhibited the elongation of leaves but the inhibition of second internode elongation by abscisic acid was not recognized within the range of 0 ppm to 1 ppm. The response of each variety should be examined again. (Chai Prechachart, Chalit Setabutara and et al, 1989 - Huntra Bangkok Rice Experiment Station, Thailand)

Segregation analysis revealed that the gene responsible for submergence tolerance in FR 13A (typical tolerant deepwater rice) was allelic to one of the two complementary genes governing elongation ability (T D Thach & D Senadhira, 1992)

Although the inheritance of deepwater tolerance seems to be complex. The genetic and developmental regulation gives an excellent opportunity for understanding the mechanisms of phenotypic plasticity in plants.

In the present study, we successfully detected a major gene which is responsible for deepwater tolerance in rice. We report here that responding to flood the gene for deepwater tolerance induces elongation of basal internodes whose intercalary meristem gives no elongation without the genes

**MATERIALS AND METHODS**

The material used were a perennial type of *Oryza sativa* of wide rice namely (W. 120 from India) and a near isogenic line of Taichung 65 with wx (T. 65 wx). Generally, a perennial type of *O. rufipogon* shows tolerance for deepwater since they prefer deepwater and stable habitats while Taichung 65 is a non-deepwater tolerance (susceptible to deepwater)

In order to introduce an allele factor responsible for deepwater tolerance, the

T 65wx /W 120 F1 was successively backcrossed with T 65 used as the recurrent parent. In each generation, F2 plants were grown in a deepwater tank and subjected to flood at 6 weeks of seedling age. The water level was risen 10 cm every other day to maximum depth 100 cm. Under this condition, only 1/5 to 1/4 F2 plants survived and came to flowering which were used for further backcrossing.

The data was subjected to use  $\chi^2$  test to check the theory assumption

**RESULTS AND DISCUSSION**

Segregation data analysis used  $\chi^2$  test in BC5 F1 and BC4 F3 consistency supported the assumption that deepwater tolerance is controlled by a single recessive gene which was designated as dw3 (table 1 and table 2)

Table 1. Segregation pattern for deepwater tolerance in BC5 F2 of T 65wx / W 120

Segregation			$\chi^2$ (3:1)	Degree of freedom (d.f)
<i>Non-resistant</i>	<i>Resistant</i>	<i>Total</i>		
83 (75. 75)	18 (25. 25)	101	2.78ns	1

*ns = shows non-significance*

Table 2. Segregation pattern for deepwater tolerance in BC4 F3 of T 65wx / W120

No. of lines				$\chi^2$	d. f
<i>dw3+/dw3+</i>	<i>dw3+/dw3</i>	<i>dw3/dw3</i>	<i>Total</i>		
6 ( 7. 25)	18 ( 14. 5)	5 ( 7. 25)	29	1.76ns	2

*ns = shows non-significance*

**References**

Chai Precha Chart, Chalit Setabutara et al. Inheritance and Correlation of

Floating Habit with other Characters of Rice. Huntra

Bangkhen Rice Experiment Station in 1975.  
Mitsugu Eiguchi and Yoshio Sana. Rice genetic newsletter Vol. 8 (116-117.p) National institute of genetics, Mishima, 411 Japan.

T. D. Thach and D. Senadhira. MSc. thesis. The genetic association between elongation ability and submergence tolerance in rice

## TÓM TẮT

### Phát hiện một gen kháng ngập ở lúa hoang

Cây trồng nói chung và cây lúa nước sâu nói riêng, chúng tồn tại được đều bị chi phối ảnh hưởng của 2 yếu tố chính là yếu tố di truyền của giống và điều kiện ngoại cảnh mà chúng sinh sống. Tuy nhiên tính chịu ngập của cây lúa nó còn phụ thuộc rất nhiều vào điều kiện ngoại cảnh như: nhiệt độ môi trường, mực nước, độ trong, đục của nước nhất là hàm lượng carbohydrate trong cây có liên quan mật thiết với sự hoạt động của các hormone sinh trưởng như ethylene và gibberellin. Cho nên, cây lúa có thể sử dụng các tín hiệu biến đổi của môi trường bằng cách thay đổi về kiểu hình một cách mềm dẻo theo thời gian dẫn tới có một vài thay đổi về hình thái và kiểu hình. Trong thí nghiệm này cho thấy sự khám phá ra một gen lúa hoang có tên là W 120, nguồn gốc từ Ấn Độ có mang gen chịu ngập đã tạo ra sự vươn lóng ở các lóng gốc. Thí nghiệm lai giữa Taichung 65 (T 65) / W 120 sau đó lai hồi giao lại với T 65 rồi gửi đi thanh lọc ngập theo quy trình IRRI (Viện lúa gạo quốc tế). Qua phép thử  $\chi^2$  test cho thấy gen kiểm soát tính chịu ngập là gen đơn lặn tên là *dw3*.