

Genetic analysis of salinity tolerance in japonica rice

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1. Objective

To determine the order of dominance and the genetic components of variation for salinity tolerance

2. Materials and Methods

The materials consisted of a complete diallel(including reciprocals) of nine japonicas, F₁ seeds were grown in a salinized solution for 12 days and treated initially at an EC of 6 dSm⁻¹ for four days followed by an EC of 12 dSm⁻¹ for 20 days. Samples were analyzed for Na⁺ concentration in the shoot. The diallel analysis procedure of Hayman(1954) was used.

3. Results

- Covariance-variance analysis satisfied simple additive-dominance model and detected partial dominance of the trait.
- Genetic components analysis revealed significant additive, dominance, and environmental effects and confirmed incomplete dominance of the trait
- Number of gene groups governing Na⁺ uptake was found to be 4.
- Narrow-sense heritability was estimated at 0.49.

Table . Origin, plant type, height, and tolerance parameters of varieties selected for 9x9 diallel cross.

				TOLERANCE PARAMETER					
VARIETY DESIGNATION CODE	ORIGIN	PLANT TYPE ¹	SEEDLING HEIGHT (CM)	VISUAL SCORE (1-9)	SHOOT Na ⁺ (%)	SHOOT K ⁺ (%)	SHOOT Na-K RATIO	OVERALL GROUPING ²	
Agami M1	P1	Egypt	TR	52±4.9	3.9±0.42	1.48±0.14	1.67±0.06	0.89±0.11	T
Geori	P2	Korea	TR	43±1.5	4.2±0.57	1.69±0.08	1.56±0.13	1.09±0.10	T
Namyang 7	P3	Korea	IM	30±3.1	3.8±0.57	1.39±0.09	1.87±0.19	0.75±0.11	T
Yunlee 11	P4	China	IM	45±5.5	5.4±0.52	1.89±0.10	1.44±0.04	1.31±0.08	MT
Yunlee 12	P5	China	IM	54±4.0	6.4±0.48	1.88±0.06	1.64±0.10	1.15±0.10	MT
Akihikari	P6	Japan	IM	45±5.0	6.0±1.14	1.81±0.19	1.50±0.20	1.24±0.3	MT
Yeosudo	P7	Korea	TR	52±1.9	8.0±0.67	2.26±0.21	1.61±0.11	1.41±0.20	S
Daegudo	P8	Korea	TR	52±4.0	7.3±0.67	2.32±0.14	1.32±0.05	1.77±0.16	S
Jinling 78-2	P9	China	IM	52±5.0	8.6±0.52	2.76±0.29	1.79±0.15	1.55±0.16	S

¹TR = Traditional, IM = Improved, ²T = Tolerant, MT = Moderately tolerant, S = Susceptible

Table . Estimates of genetic parameters for shoot Na⁺ concentration in a 9x9 diallel cross.

GENETIC PARAMETER		ESTIMATE±S.E.
(D) Additive effect		0.07176±0.0432*
(H) Dominance effect		
H ₁		0.03853±0.00953*
H ₂		0.02487±0.00819*
h ²		0.08150±0.00549*
(F) Gene distribution		0.06054±0.01007*
(E) Environmental effects		0.00664±0.00137*
Proportional Values		
(H ₁ /D) ^{1/2}	Mean degree of dominance	0.73276
(H ₂ /4H ₁)	Proportion of genes with + or - effects on parent	0.16136
(KD/KR) ¹	Proportion of dominance and recessive genes in the parent	3.71281
r	Correlation between (W _r +V _r) and Y _r	0.89411
r ²	Prediction for measurement of completely dominant and recessive parents	0.79943
(h ² /H ₂)	No. of gene groups that control tolerance and exhibit dominance	3.27677
(h _{ns})	Heritability (narrow-sense)	0.49178
(h _{bs})	Heritability (broad-sense)	0.74460

* = Significant at P<0.05

¹KD/KR = [(4DH₁)^{1/2}+1/2FY]/[(4DH₁)^{1/2}-1/2F]

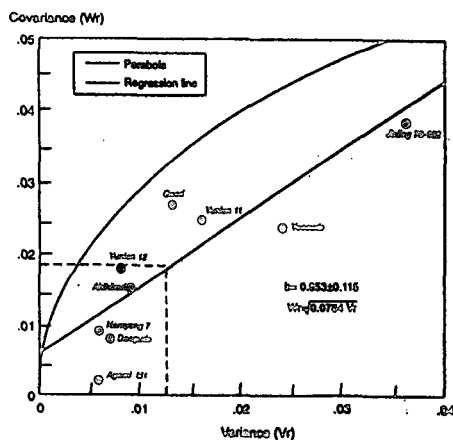


Fig. Covariance and variance (Wt-Vt) regression graph of the 9x9 diallel analysis for shoot Na⁺ concentration.