Due to the low genetic correlations estimated, genetic mechanisms involved in determining the grade of severity of the disease MRC may not be the same for different environments (Table 1). This complicates selection of genotypes from these RILs.

However, estimated h^2 showed high values (Table 2), which indicates that the grade of the disease is controlled by a high proportion of genes with additive effect and some independence with the medium. Since the E had values <1 (Table 1), the direct selection strategy in each environment represents the best alternative and the indirect selection strategy may not have good prospects.

Table 2. Heritability (h^2) in five environments of evaluation for the grade of severity of MRC in 111 RILs of maize.

| Parameter | Environment [a] | | | | |
	R4	S4	R5	S5	R6
Heritability [b]	0.70	0.45	0.56	0.60	0.66

[a]R4 = Río Cuarto 2004, S4 = Sampacho 2004, R5 = Río Cuarto 2005, S5 = Sampacho 2005 and R6 = Río Cuarto 2006
[b]$h^2 = (\sigma^2_g)/[(\sigma^2_g)+(\sigma^2_e/r)]$

Diallel analysis of Mal de Río Cuarto tolerance and yield components in maize

--Borghi, ML; Ibañez, MA; Bonamico, NC; Dallo, MD; Kandus, MV; Salerno, JC; Di Renzo, MA

Mal de Río Cuarto (MRC) is a devastating disease of maize in Argentina. The disease reduces grain yield (GY) and causes several symptoms, such as enations, reduced root systems, shortened superior internodes, flattened stems, leaves with small leaf areas, atrophic tassels, "hokey pole" ears and small ears with few or no kernels. The identification of heterotic patterns plays an important role in the selection of germplasm to develop hybrids. Analysis of diallel crosses provides preliminary data about heterotic relationships (Hallauer and Miranda Filho, Quantitative Genetics in Maize Breeding. Iowa State Univ. Press, Ames, IA, 1981; Hallauer and Miranda, Quantitative Genetics in Maize Breeding, 2nd Edition. Iowa State Univ. Press, Ames, IA, 1988). Our objective for this study was to estimate general (GCA) and specific combining ability (SCA) (Sprague and Tatum, J. Am. Soc. Agron. 34:923-932, 1942) in twelve lines of maize evaluated through diallel crosses, without reciprocals, for tolerance to MRC, grain yield and its components. The maize lines were BLS14, BLS1, BLS16, BLS61, BLS76, BLS91, BLS96, BLS101, BLS104, LP109, LP521 and LP125R.

The lines and their 66 crosses were planted on 21 November 2007 through a complete randomized block experimental design with two replications at Río Cuarto, Argentina (33°8′S 64°20′W). All plants were artificially infested with viruliferous insect vectors of MRC (*Delphacodes kuscheli* Fennah). Data were collected for the grade of severity of MRC disease (GS), number of kernel/m² (KN), unit weight of kernels (WK), and grain yield, standardized to 14.5% moisture (GY). Data were subjected to an ANOVA analysis using Griffing´s method 2 model II (Griffing, Aust. J. Biol. Sci. 9:463-493, 1956), by means of a diallel computer program (Magari and Kang, J. Hered. 85:336, 1994). Significance was estimated with t tests. The relative importance of general and specific combining ability on progeny performance was estimated as the ratio: $2\sigma^2_{ACG}$ / $(2\sigma^2_{ACG} + \sigma^2_{ACE})$ (Baker, Crop Sci. 18:533-536, 1978) where σ^2_{ACG} and σ^2_{ACE} are the variance components for GCA and SCA. A value of 1 indicates that all genetic variance is additive. Analysis

of variance revealed that mean square values for GCA were highly significant ($p \le 0.01$) for the traits studied, with the exception of grain yield. The variations due to SCA were highly significant ($p \le 0.01$) for all traits studied. The ratios $2\sigma^2_{ACG}$ / $(2\sigma^2_{ACG} + \sigma^2_{ACE})$ were 0.15, 0.08, 0.19 and 0 for GS, NK, WK and GY, respectively, indicating that non-additive effects predominated in the expression of these traits. Marino and Teyssandier (Congreso Anual de la Sociedad Argentina de Genética, BuenosAires, 1982) reported the same results for tolerance to MRC, and Bhatnagar et al. (Crop Sci. 44:1997-2005, 2004) and Srdic et al. (Maydica 52:261-264, 2007), indicated that SCA effects were highly significant for GY. In our scoring, negative effects on combining ability are associated with tolerance to disease and positive effects with susceptibility. For GS, the highest GCA values were observed for line BLS1 (-0.39), followed by BLS16 (-0.2), and for WK the highest values were observed for line LP109 (0.03), followed by BLS104 (0.02) (Table 1). These parental lines presented highly significant GCA effects

Table 1. General combining ability (GCA) effects of each parental line for different characters.

Line	GS		NK		WK (g)	
BLS61	0.02	ns	57.85	ns	-0.01	ns
BLS91	0.07	ns	-69.54	ns	0.01	ns
BLS101	0.00	ns	-181.68	ns	0.01	ns
BLS76	-0.09	ns	32.95	ns	-0.01	ns
BLS96	-0.08	ns	-36.04	ns	-0.00	ns
BLS104	0.37	**	-74.64	ns	0.02	**
BLS16	-0.2	**	103.85	ns	-0.03	**
BLS14	0.04	ns	195.38	ns	-0.01	ns
BLS1	-0.39	**	119.1	ns	-0.01	ns
LP109	0.08	ns	-29.68	ns	0.03	**
LP521	0.09	ns	-16.93	ns	0.00	ns
LP125R	0.07	ns	-100.61	ns	0.00	ns

* Significant at 5% and ** significant at 1% probability level. GS=grade of severity of MRC disease, NK=number of kernel/m² and WK=unit weight of kernel.

for GS and WK, while the effects for NK were not significant. The highest SCA effects were observed for hybrids BLS101 x BLS104, LP109 x LP125R, BLS91 x BLS16 and LP109 x LP125R for GS, NK, WK and GY, respectively. The hybrid that manifested the best behavior for GS also presented good performance for the other traits, in contrast to the hybrid that manifested the greatest SCA for GY, which displayed negative effects for GS. We conclude that the lines with high general combining ability would be a valuable source of germplasm to develop hybrids that combine tolerance to MRC and good yield.

RIO CUARTO, ARGENTINA
Universidad Nacional de Río Cuarto
CORDOBA, ARGENTINA
Universidad Nacional de Cordoba
CASTELAR, ARGENTINA
Instituto Nacional de Tecnología Agropecuaria

Discriminant analysis to identify molecular markers associated with Mal de Río Cuarto (MRC) resistance

--Bonamico, NC; Arroyo, AT; Balzarini, MG; Ibañez, MA; Borghi, ML; Díaz, DG; Salerno, JC; Di Renzo, MA

In Argentina, the production of maize for grain is highly affected by MRC-disease, which is caused by a virus of the family *Reoviridae*, genus *Fijivirus* and transmitted by the planthopper