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SHORT NOTE [NOTA CORTA]

COMBINING ABILITY IN MAIZE LINES USING A DIALLEL CROSS

[APTITUD COMBINATORIA EN LÍNEAS DE MAÍZ USANDO UN CRUZAMIENTO DIALÉLICO]

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SUMMARY

The objective was to select maize (*Zea mays* L.) lines, based on the effects of general combining ability (GCA), specific combining ability (SCA) and heterosis, for the formation of single crosses. During the spring-summer 2008 cycle, 120 single crosses with the combination of 16 lines of white grain maize were evaluated. To estimate the GCA and SCA effects, the method IV, model I of Griffing's method, was used, in an alpha lattice design with two 16 x 8 repetitions. The results revealed that there are lines with good GCA: LRB-14RC2-1-1, LT-154RC2-1-2, LT-155RC2-1-1, VS-536RC2-1-1, VS-536RC2-1-1, CML-264Q and CML-159. The crosses LT-155RC2-1-1xVS-536RC2-1-1, CABGRC2-1-3xD-539RC2-1-1 and D-539RC2-1-1xCML-159 showed the greatest effects of SCA. Of the inbred lines evaluated, LRB-14RC2-1-1, LT-154RC2-1-2, LT-155RC2-1-1, VS-536RC2-1-1, VS-536RC2-1-1, FAM. V-537C, CML-264Q and CML-159 showed the greatest varietal effect values, considering that there is greater additive gene action and that formation of synthetic varieties is possible. The crosses LT155RC2-1-1xVS536RC2-1-1, CABGRC2-1-3xD-539RC2-1-1 and D-539RC2-1-1xCML-159 showed high ACE effects and high heterosis levels, adequate for the formation of maize hybrids. The use of diallel designs to estimate GCA and SCA in inbred lines and their crosses allowed knowing the most efficient breeding method.

Key words: *Zea mays*; diallel cross; combining ability.

RESUMEN

El objetivo fue seleccionar líneas de maíz (*Zea mays* L.), con base en los efectos de aptitud combinatoria general (ACG), aptitud combinatoria específica (ACE) y heterosis, para la formación de cruzas simples. Durante el ciclo primavera-verano 2008 se evaluaron 120 cruzas simples con la combinación de 16 líneas de maíz de grano blanco. Para estimar los efectos de ACG y ACE se empleó el método IV, modelo I del método de Griffing, en un diseño alfa látice 16 x 8 con dos repeticiones. Los resultados indicaron que existen líneas con buena ACG: LRB-14RC2-1-1, LT-154RC2-1-2, LT-155RC2-1-1, VS-536RC2-1-1, VS-536RC2-1-1, CML-264Q y CML-159. Las cruzas LT-155RC2-1-1xVS-536RC2-1-1, CABGRC2-1-3xD-539RC2-1-1 y D-539RC2-1-1xCML-159 mostraron los mayores efectos de ACE. De las líneas evaluadas, LRB-14RC2-1-1, LT-154RC2-1-2, LT-155RC2-1-1, VS-536RC2-1-1, VS-536RC2-1-1, FAM. V-537C, CML-264Q y CML-159 presentaron los mayores valores de efecto varietal, considerando que existe mayor acción aditiva de genes y que es factible la formación de sintéticos. Las cruzas LT155RC2-1-1xVS536RC2-1-1 y CABGRC2-1-3xD-539RC2-1-1, D-539RC2-1-1xCML-159 mostraron altos efectos de ACE y niveles altos de heterosis, adecuadas para la formación de híbridos de maíz. El uso de los diseños dialélicos para estimar ACG y ACE en líneas y cruzas, permitió conocer el método de mejoramiento más eficiente.

Palabras clave: *Zea mays*; cruzas dialélicas; aptitud combinatoria.

INTRODUCTION

In the year 2009, worldwide maize (*Zea mays* L.) production reached 792 million tons harvested in more than 160 million ha. Main maize-producing countries were the USA, China, Brazil, Argentina and Mexico; together, accounted for > 81 % in grain volume of the world total (WASDE, 2009). Maize is the main grain produced in Mexico, with 18 million tons representing 60 % of the total grain production. It provides 59 % of the energy and 39 % of the protein required by the average person. However, 31 million people presents some degree of undernutrition, and 18 million suffer a severe form (Chávez and Chávez, 2004; Espinosa *et al*., 2006), mainly in the southeastern region of Mexico. This is partially caused by low levels of lysine and tryptophan in maize consumed, essential amino acids for human growth and development. This is a serious problem of low nutritional level on maize-based diet, since the apparent *per capita* consumption is 209.8 kg (Morris and López, 2000).

Mexican tropical region includes the states of Veracruz, Tabasco, Yucatan, Quintana Roo, Chiapas, Campeche, Oaxaca and Guerrero, where 2.8 million ha are planted with maize. There, the average maize yield is 2.3 ton ha^{-1}, accounting for 3.3 million ton (SIAP, 2009). Since its beginnings in the XX century, Mexican maize breeding programs were led by the Special Studies Office (OEE, Spanish acronym of Oficina de Estudios Especiales), currently the National Institute for Forest, Agriculture and Livestock Research (INIFAP, Spanish acronym of Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias). This institution has worked on the identification of the base germplasm, which has allowed the incorporation of desirable genes that simultaneously improve adaptability, stability, yield and pests and diseases resistance (Sierra *et al*., 2004).

With the rise in population and recurring economic crisis the access to food and other basic goods has decreased, increasing poverty, hunger and undernutrition (FAO, 2009). Since 1997 INIFAP, in collaboration with the International Center for the Improvement of Maize and Wheat (CIMMYT, Spanish acronym for Centro Internacional de Mejoramiento de Maíz y Trigo), started selecting and deriving lines with the Opaque-2 gene (*o2o2*) or Quality Protein Maize (QPM), emphasizing those lines with high levels of lysine and tryptophan. It is estimated that in the next years the consumption of QPM maize could contribute to fight undernutrition in over 27 million people from rural and social excluded urban regions of Mexico (FAO, 2009).

Planning of a genetic improvement program allows capitalization of the desirable traits in a group of lines (parents). A group of these maize lines with a broad genetic base can be combined, exceeding quality, yield and agronomic characteristics of the commercial varieties currently available. With good behavior *per se* and combining ability of the parental lines, greater efficiency can be achieved, since it allows to select parental lines with an acceptable average behavior (Guillen-de la Cruz *et al*., 2009). It is necessary to discriminate these maize lines based on their behavior *per se*, good general combining ability (GCA) and specific combining ability (SCA) (Sierra *et al*., 1991).

One analysis method currently available to know the type of gene action from the parent lines is the diallel design proposed by Griffin (1956). It involves all the possible crosses among different parents, and identifies the best superior combinations and the best parents, to design the most efficient improvement methods (Gutiérrez *et al*., 2002). Sprague and Tatum (1942) proposed a method that includes diallel crosses and that gave origin to the concepts of GCA and SCA. The value of a line can be determined through two main aspects: *per se* characteristics of the lines, in which yield, adaptation and seed production are considered, and the GCA, or the ability a line shows to combine or cross with other lines to produce the best averages (Rojas and Sprague, 1952; Quemé *et al*., 1991; Espinosa *et al*., 1998; Sierra *et al*., 2000).

Genetic diversity and combining ability of lines are important to obtain high heterosis values in the formation of maize hybrids (Sierra *et al*., 2005). Quemé *et al*. (1990) mentioned that the GCA gives information on pure lines that should produce the best hybrids when crossed with other lines. However, it is also important to consider the behavior *per se* of the line and the SCA (Vega and Bejarano, 1975; Vasal and Cordova, 1996).

Therefore, the objective was to determine the behavior of high-quality protein maize lines, based on the effects of GCA and SCA, for their use in the formation of hybrids or synthetic varieties.

MATERIALS AND METHODS

Study location

The study was carried out at Cotaxtla Experimental Station, INIFAP, located in the Central region of the state of Veracruz, Mexico (Lat. 18º 56' N, Long. 96º 11' W, at 15 m altitude), with a AW$_1$ (w) climate, mean annual rainfall of 1350 mm, distributed from

June to November, and a dry season from December to May (García, 1981).

Germplasm used

Genetic material used were regular lines derived from germplasm of Tuxpeño breed adapted to the tropical region in southeastern Mexico, which were converted to the high-quality protein trait using crosses with line CML 144 as trait donor. During Autumn-Winter 2007/2008 irrigation cycle, in a plot with controlled pollination, diallel crosses were formed using a group of lines converted to the high-quality protein trait. Crosses were evaluated during Spring-Summer 2008 cycle. A total of 16 parents of white-grain maize converted to high-quality protein (QPM) were evaluated, along with their 120 diallel crosses n(n – 1)/2, as well as some regular grain controls (Table 1).

Table 1. Lines of high-quality protein maize included in the Cotaxtla diallel. Spring-Summer 2008.

No.	Genealogy	Origin
1	(LRB-14XCML-144)LRB-14RC2-1-1	Lines from Cotaxtla Experimental Station maize program, INIFAP.
2	(LT-154XCML-144)F2XLT-154RC2-1-2	
3	(LT-155XCML-144)F2XLT-155RC2-1-1	
4	(LT-155XCML-144)F2XLT-155RC2-1-1	
5	(D-539XCML-144)F2XD-539RC2-1-1	
6	(VS-536XV-537C)VS-536RC2-1-1	Recycled lines of VS-536, commercial use variety.
7	(VS-536XV-537C)VS-536RC2-1-1	
8	(VS-536XV-537C)VS-536RC2-1-1	
9	(VS-536XV-537C)VS-536RC2-1-1	
10	(CABGXCML-144)CABGRC2-1-1	Germplasm compound with broad genetic base (GCBGB).
11	(CABGXCML-144)CABGRC2-1-3	
12	CML-264Q	Lines derived from populations of regular CIMMYT and with Opaque-2 gene (*o2o2*).
13	CML-159	
14	CML-491	
15	CML-150	
16	FAM. V-537C-1-2	Recycled lines of V-537C, commercially used variety

Procedure

Maize was planted on a 16 x 8 alpha lattice design with 128 treatments and two replicates, in plots with a 5 m long furrow and separation of 80 cm, placing two seeds every 20 cm and clearing to leave one plant and a density of 62,500 plants ha^{-1}. Plants were fertilized with 161-46-00 (N-P-K), using urea as nitrogen source and tricalcium superphosphate as phosphorus source, applied two times: no later than 10 days after sowing all the phosphorus and half nitrogen were applied, the rest nitrogen was applied 30 days after sowing.

Agronomic variables

For each genotype the following variables were recorded: days to male and female flowering; height of plant and ear; aspect and health of plant and ear assessed using a scale of 1 to 5, where 1 is the best expression, vigorous and healthy plants, well-formed ears without rotting, and 5 is for sick and malformed plants and ears; and percentage of lodging, husk cover and stunting. During harvest number of ears was counted, percentage of rotten ears calculated, and field weight recorded. Grain yield was obtained in ton ha^{-1}, adjusted at 14 % moisture.

Statistical design

An analysis of variance was carried out based on the lattice design proposed by Barreto (1999), with the following statistical model:

$$Y_{ijk} = \mu + R_i + (B/R)_{ij} + T_k + E_{ijk}$$

Where:
Y_{ijk}: effect of the i-th repetition of the j-th block, of the k-th treatment

μ: overall mean
R_i: effect of the i-th repetition
$(B/R)_{ij}$: effect of the j-th block, within the i-th repetition
T_k: effect of the k-th treatment
E_{ijk}: effect of the experimental error

Genetic design

After obtaining the adjusted data from the analysis of variance, which was corrected based on the lattice design, the diallel was analyzed using Griffing's method (1956), modified by Reyes (1985), with the following model:

$Y_{ijk} = \mu + g_i + g_j + S_{ij} + C_{ijk}$

where:
Y_{ijk}: phenotypic value observed for the cross with parents i and j in block k
μ: effect common to all the observations
g_i: effect of the general combining ability of parent i
S_{ij}: effect of the specific combining ability of the cross (i, j)
C_{ijk}: random environmental effect corresponding to the observation (i, j, k).

Heterosis percentage was calculated based on the average of two parents (*Hx*) and with respect to the best parent (*Hμ*), according to the formula proposed by Griffing (1956), modified by Reyes (1985). To estimate the global and specific variance of GCA and SCA for each parent, the formula of Griffing's model (1956), modified by Reyes (1985), were used:

$$\sigma_g^{\,2}(a) = \frac{p-1}{p(p-2)}\left[\left(\frac{\left(\frac{p}{2}Ta - T\bar{x}\right)^2}{\frac{p(p-1)(p-2)}{4}}\right) - \frac{E'}{r}\right]$$

where:
$\sigma_g^2(a)$ = estimator of the variance for GCA of parent a
p = number of parents included
Ta = sum of the values or total of the crosses of parent a with the others, adding up means
E' = mean square of the error calculated from the global analysis
r = number or repetitions
$T\bar{x} =$ total of means

$$Adjustment(ab) = (p-2)(ab) - Ta - Tb + \frac{2}{p-1}T\bar{x}...$$

where:
ab = mean yield of the cross between parents a and b
Ta = total of row a
Tb = total of row b
$T\bar{x} =$ total of means of the single crosses $\frac{p(p-1)}{2}$
p = number of parents

RESULTS AND DISCUSSION

Yield and agronomic characteristics

Results of the analysis of variance for maize crosses are presented in Table 2. Statistical difference was found in 11 variables ($P \leq 0.01$) and two variables ($P \leq 0.05$). This result agreed with the report of Sierra *et al*. (2000, 2005), where the best crosses formed with outstanding lines were identified, showing the existence of genetic variability. For grain yield, 5.0 ton ha^{-1} were obtained as overall mean, and were good plant and ear archetype, having intermediate cycle, and low values for aspect and health of plant and ear. It can be inferred that these crosses show a high degree of heterosis or hybrid vigor resulting from crossbreeding parents with a relative genetic divergence (Sierra *et al*., 2000, 2005). The relative efficiency of the lattice design with respect to the random block design is shown in most values greater than one (> 1), indicating efficiency in the evaluation of those materials (Quemé *et al*., 1991).

Genetic design

Mean squares and significance for the source of variation of the diallel analysis are shown in Table 3. Statistical differences ($P \leq 0.01$) were found in blocks and crosses, which value ranged between 6.6 and 2.4 ton ha^{-1}. Gutiérrez *et al*. (2002) mentioned that as genetic diversity of the lines increases, the differences among their hybrids also increase. The sources of variation of parents against crosses and among parents showed no statistical difference ($P \leq 0.05$), suggesting that their genetic variation is minimal. This can also be understood as the absence of maternal effect or any other female influence (Reyes, 1985).

Table 2. Significance for treatments, coefficient of variation, mean values and relative efficacy of maize crosses. Cotaxtla Experimental Station. Spring-Summer 2008.

F.V.	GY† ton ha^{-1}	Height		Flowering††		Aspect		Health		%			
		Plant	Ear	Plant	Ear	Plant	Ear	Plant	Ear	HC	RE	ST	LG
MS	1.9*	543.4NS	252.8NS	3.4*	3.4*	0.2*	0.4*	0.2*	0.4*	3.0*	1.3*	1.8*	6.8*
CV	13.8	8.9	12.9	1.9	2.0	15.5	18.1	14.5	13.7	48.1	37.9	38.4	31.2
Mean	5.03	212	108	53	54	2.2	2.3	2.1	2.1	2.12	2.2	2.5	5.09
REF	1.0	5.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.1	0.9	1.1	1.2

*P ≤ 0.01; NS: not significant; †Grain yield; ††Days to male and female flowering; Husk cover (HC), rotten ears (RE), stunting (ST) and lodging (LG); MS: mean squares; CV: coefficient of variation; Mean: mean values; REF: relative efficiency.

Table 3. Mean squares and significance of diallel analysis for grain yield (ton ha^{-1}) in maize lines. Cotaxtla Experimental Station. Spring-Summer 2008.

Source of variation	DF	MS	Fc
Blocks	1	36.89	24.59**
Crosses	135	2.11	1.41*
Parents and crosses	1	2.74	1.83NS
Among parents	15	2.20	1.47NS
Error	119	1.50	
Total	271		

*P ≤ 0.05; **P ≤ 0.01; NS: not significant; DF: degrees of freedom; MS: mean square.

The analysis of variance made to determine GCA and SCA (Table 4), showed no significant difference for GCA and SCA, since some lines are related. Although no differences were found for these two sources of variation, variance for GCA was greater (1.89), indicating a greater additive gene action from parents t participating in the cross (Reyes, 1985).

Effects of GCA and SCA were obtained with the mean values of grain yield (Table 5). All parents showed negative effects on GCA, but only the parents LRB-14RC2-1-1, LT-154RC2-1-2, LT-155RC2-1-1, VS-536RC2-1-1, VS-536RC2-1-1, FAM. V-537C, CML-264Q and CML-159 obtained the highest effects, indicating a high contribution in the expression of yield in their corresponding progenies, and the importance of the additive effects (Guillen-de la Cruz *et al*., 2009). Relevance of the GCA effects in parents LT-154RC2-1-2 and LT-155RC2-1-1 was as expected, since they are the parents of the hybrid H-513 that showed adaptation to the tropical areas of Veracruz and Chiapas. To this respect, Sierra *et al*. (2000) suggested that when greater effects of GCA are detected, exploitation of the additive proportion of genetic variance available is possible through the formation of synthetic varieties.

Table 4. Mean squares and significance for the global estimation of general combining ability (GCA) and specific combining ability (SCA), in maize lines. Cotaxtla Experimental Station. Spring-Summer 2008.

Source of variation	DF	MS	Fc
Block	1	44.12	0.85 NS
GCA	15	1.89	0.04 NS
SCA	104	1.41	0.03 NS
Error	119	51.80	
Total	239		

NS: not significant; DF: degrees of freedom; MS: mean square.

Greater yield of crosses LT155RC2-1-1xVS536RC2-1-1 and CABGRC2-1-3xD-539RC2-1-1, D-539RC2-1-1xCML-159 indicates the best effects of SCA; thus, the non-additive gene action is involved in these crosses and grain yield can increase through hybridization (Sierra *et al*., 1991). Guillen-de la Cruz *et al*. (2009) studied eight tropical maize populations in a diallel system, and found that populations 23 and 43 had the greatest effects in GCA, whereas for SCA the crosses VS536xPob32, Pob22xPob43, Pob25xPob49 and Pob43xPob49 showed the greatest effects, which suggests that populations 23 and 43 have a potential to be used in a maize hybridization program.

Table 5. Effects of general combining ability (GCA) and specific combining ability (SCA) of 120 crosses and 16 parents, using the model IV by Griffing (1956) modified by Reyes (1985). Cotaxtla Experimental Station. Spring-Summer 2008.

No.	Parents	Parents															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	LRB-14RC2-1-1	-1.73	92.0	82.1	77.1	95.4	68.5	73.9	71.2	90.4	80.8	85.4	60.4	77.2	98.5	78.8	80.8
2	CABGRC2-1-3		-1.66	68.9	70.5	69.3	86.5	67.4	95.0	72.8	61.3	101.8	89.0	62.5	85.9	74.8	71.8
3	LT-154RC2-1-2			-1.70	92.4	97.3	76.1	87.2	86.5	84.7	93.9	82.0	75.8	77.9	84.7	90.2	91.4
4	LT-155RC2-1-1				-1.73	82.2	85.4	69.8	79.3	105.0	71.2	67.7	80.2	79.5	96.1	88.5	78.3
5	LT-155RC2-1-1					-1.73	68.4	84.7	83.2	83.4	88.6	77.0	78.9	89.7	81.9	84.1	83.2
6	VS-536RC2-1-1						-1.62	83.6	79.2	41.5	80.6	75.1	91.4	63.7	82.9	69.9	95.2
7	VS-536RC2-1-1							-1.69	88.3	99.0	85.4	80.5	83.8	94.6	70.0	86.3	81.6
8	VS-536RC2-1-1								-1.72	93.0	73.8	69.6	92.4	85.1	68.2	84.1	88.6
9	VS-536RC2-1-1									-1.72	82.5	79.1	85.2	82.5	61.0	97.3	82.5
10	CABGRC2-1-1										-1.71	86.2	88.2	76.9	81.4	79.6	85.7
11	D-539RC2-1-1											-1.72	81.6	100.1	80.6	80.8	71.2
12	CML-264Q												-1.70	85.9	70.0	81.5	83.7
13	CML-159													-1.73	83.1	82.1	78.8
14	CML-491														-1.73	85.8	64.1
15	CML-150															-1.67	85.3
16	FAM. V-537C																-1.73

Degrees of heterosis with respect to parents average (H*x*) and the best parent ($H\mu$) are presented in Table 6. Maximum and minimum values of heterosis with respect to parents average were 350.2 and 2.9 %, respectively, corresponding to crosses (LT-155xCML-144)F_2xLT-155RC2-1-2xFAM.V-537C-1-2 (4x16) and (LRB-14xCML-144)LRB-14RC2-1-1x(VS-536xV-537C)VS-536RC2-1-4 (1x9). In heterosis regarding the best parent, the maximum and minimum values were 298.3 % for (LT-154xCML-144)F_2xLT-154RC2-1-2x(CABGxCML-144)CABGRC2-1-3 (2x11) and -21.2 % for CML-264QxCML-150 (12x15), respectively. According to Vasal and Cordova (1996), a desirable level for taking full advantage of heterosis in a cross is at least 20 %; heterosis exhibited by crosses in the present study was over the minimum recommended level, which indicates genetic diversity among parental groups.

CONCLUSION

Of the inbred lines evaluated, LRB-14RC2-1-1, LT-154RC2-1-2, LT-155RC2-1-1, VS-536RC2-1-1, VS-536RC2-1-1, FAM.V-537C, CML-264Q and CML-159 had the greatest values of variety effect, considering the existence of greater additive gene action and that formation of synthetic varieties is possible. Crosses LT155RC2-1-1xVS536RC2-1-1 and CABGRC2-1-3xD-539RC2-1-1, D-539RC2-1-1xCML-159 had high effects of SCA and high heterosis levels, adequate for high-yielding maize hybrids formation. The best triple-cross hybrid would be formed through the single cross with the greatest SCA effect and a third line that showed the best GCA value. Use of diallel designs to estimate GCA and SCA in lines and crosses allowed knowing the most efficient method for plant breeding.

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Table 6. Single cross, grain yield (GY) ton ha^{-1}, heterosis based on parents average (H*x*) and the best parent (H*μ*). Cotaxtla Experimental Station. Spring-Summer 2008.

Crosses	GY	H*x*	H*μ*	Crosses	GY	H*x*	H*μ*	Crosses	GY	H*x*	H*μ*	Crosses	GY	H*x*	H*μ*
4x9	6.60	97.5	28.7	6x14	5.50	28.3	2.6	5x16	5.10	166.8	128.6	2x15	4.60	99.1	74.1
11x13	6.60	72.9	60.8	11x12	5.50	92.7	85.4	6x8	5.10	10.2	9.4	4x16	4.60	350.2	298.3
7x9	6.35	46.4	5.3	1x2	5.45	62.4	43.2	3x12	5.05	40.3	30.9	5x6	4.60	76.4	22.1
1x14	6.25	91.0	62.1	8x15	5.45	97.1	46.3	4x6	5.05	104.2	38.2	4x10	4.55	163.1	106.7
9x15	6.25	61.0	14.4	12x15	5.45	78.5	48.0	5x14	5.05	187.2	135.3	10x13	4.55	93.7	72.0
3x5	6.20	103.3	47.0	15x16	5.45	194.0	128.8	8x13	5.05	33.4	19.5	5x11	4.50	131.7	80.5
2x8	6.15	45.6	20.2	9x12	5.40	46.7	20.2	10x11	5.05	91.0	81.6	5x12	4.50	3.9	-21.2
6x16	6.15	93.9	23.5	12x16	5.40	119.7	50.4	11x14	5.05	56.9	46.8	7x14	4.50	115.3	99.1
2x11	6.05	91.6	87.3	6x7	5.35	57.4	18.9	1x10	5.00	66.7	43.4	12x14	4.50	97.4	78.3
3x15	6.05	109.2	64.2	3x8	5.30	42.9	32.3	1x16	5.00	111.4	39.4	1x8	4.45	35.4	25.5
2x12	5.95	75.0	64.7	5x13	5.30	160.3	92.7	11x15	5.00	122.7	90.6	2x16	4.45	164.9	88.2
1x9	5.85	3.0	-10.5	10x16	5.30	167.5	93.0	4x5	4.95	244.2	257.7	8x11	4.45	44.0	21.0
4x14	5.85	125.5	79.1	1x3	5.25	5.6	5.7	4x12	4.95	125.5	66.3	8x10	4.40	54.1	24.3
8x9	5.85	26.4	17.9	5x15	5.25	115.2	91.5	1x4	4.90	149.9	76.3	8x14	4.35	40.0	11.5
8x12	5.85	21.2	5.2	6x10	5.25	82.2	47.7	1x7	4.90	100.7	59.9	2x3	4.30	56.2	37.9
1x5	5.80	89.6	37.1	13x15	5.25	105.0	65.3	1x13	4.90	25.2	20.9	2x4	4.25	181.2	116.7
7x10	5.80	133.6	112.9	3x9	5.20	17.1	1.9	5x10	4.90	220.1	159.2	6x11	4.25	35.2	14.2
3x4	5.75	73.0	22.1	3x14	5.20	77.8	50.9	7x16	4.90	310.0	215.0	6x13	4.25	20.6	8.6
7x15	5.75	104.8	100.6	7x11	5.20	130.6	100.8	10x14	4.90	84.2	81.3	6x15	4.25	58.4	18.1
8x16	5.70	115.1	36.6	7x12	5.20	113.7	80.1	10x15	4.90	170.5	142.2	2x13	4.20	30.5	18.8
10x12	5.70	58.0	44.9	9x10	5.20	43.4	9.9	1x15	4.85	64.6	29.2	11x16	4.15	140.6	68.2
2x14	5.65	96.9	88.5	9x13	5.20	34.3	13.2	4x13	4.85	134.4	69.1	2x7	4.10	157.4	128.9
3x16	5.65	121.9	46.4	9x16	5.20	77.2	9.5	4x8	4.80	58.5	6.9	14x16	4.05	225.9	137.3
4x15	5.65	157.8	121.5	13x14	5.20	58.6	38.8	9x11	4.80	12.5	-10.5	4x11	3.95	124.0	69.6
6x12	5.65	10.7	-3.5	14x15	5.15	118.3	98.1	13x16	4.75	122.3	49.3	1x6	3.90	43.2	33.4
7x13	5.65	67.1	36.9	1x11	5.10	46.9	32.2	3x6	4.70	48.1	38.0	9x14	3.85	72.6	30.8
12x13	5.65	27.4	23.0	2x6	5.10	6.7	-11.5	3x11	4.65	75.2	57.7	1x12	3.70	49.2	39.1
3x7	5.60	50.2	19.8	3x10	5.10	35.3	16.4	3x13	4.65	61.7	56.0	2x5	3.65	171.4	115.2
5x7	5.55	136.7	107.3	5x8	5.10	103.4	40.2	4x7	4.65	151.5	112.8	2x10	3.60	70.9	66.3
7x8	5.55	90.9	43.6	5x9	5.10	44.2	-4.2	2x9	4.60	46.1	14.2	6x9	2.40	10.1	2.1

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