DETERMINATION OF RESISTANCE OF F1 COTTON HYBRIDS BY INOCULATION WITH DIFFERENT VIRULENT ISOLATES OF THE VERTICILLIUM DÀHLIAE KLEBHAN

Abboskhon Marupov
Uzbek Scientific – Research Institute of Crop Protection
Tashkent, Uzbekistan
Robert Kim
Institute of Cotton Seed Breeding and Seed Production
Tashkent, Uzbekistan
Michael Kim
Uzbek Scientific – Research Institute of Crop Protection
Tashkent, Uzbekistan

Abstract

The plant pathogen *Verticillium dahliae* causes severe cotton losses in Uzbekistan. To create cotton varieties that are resistant to the more virulent races of *V. dahliae* we wanted to determine genotypic resistance of varieties and lines of cotton to more virulent isolates of different geographic populations of the fungus *V. dahliae* isolated from different cotton varieties in Uzbekistan and determine the inheritance of wilt resistance with hybrids of the first generation to various isolates of *V. dahliae*. We found that the highest wilt resistance was observed in the variety Omad and lines L-44, L-408, L-155 and L-1708 to the isolates 28, 30, 32, 36, 40 and 44. These varieties and lines exhibit hypersensitivity when the pathogen is inoculated into the plant, but they do not display external symptoms of wilt. Wilt resistance of hybrids of the first generation as determined by inoculation with the isolates of *V. dahliae* is inherited according the type of super dominance and dominance toward the resistant or susceptible parent independent from the method used to determine the disease index. Also intermediate inheritance is observed. The degree of dominance depends on the combinational ability of parents and genotype reaction of F_1 hybrids when pathogens are introduced into the plant, and also on the virulence of the isolates found in different varieties of cotton from different soil-climatic regions of the Republic of Uzbekistan. The varieties with the highest phenotypic wilt resistance (i.e., tolerance) are Omad, C-5621 and lines L-162, L-842, L-44 and L-1708. Among hybrids, the hybrid combinations L-162 x C-5621, L-162 x L-44, L-155 x C-5621 and L-1708 x C-5621 had the highest phenotypic wilt resistance. The degree of tolerant resistance to wilt varied from 50 to 80%. Genetic control of inheritance of tolerant resistance to *V. dahliae* isolates and F_1 hybrids was characterized by negative and positive super dominance, dominance toward the best or the worst parent and intermediate inheritance. The hybrid combinations L-155 x C-5621 and L-155 x L-44 have the best combinational wilt resistance toward the *V. dahliae* isolates studied, as compared to other hybrid combinations with the maternal forms Omad, C-8284, L-162 and L-408.

Introduction

Verticillium wilt is one the most harmful diseases of cotton and distributed in all cotton growing regions of the world. Different species, forms, and varieties of cotton exhibit different wilt resistance. The degree of wilting depends on a number of factors including plant development, aggressiveness of the pathogen, and ecological and cultural conditions that affect both the plant and parasite. Pathogenicity also can change depending upon external factors such as environment and agricultural techniques of cultivation.

Academician S. M. Mirakhmedov (1974) studied the character of wilt resistant with ecologically distant hybrids of cotton obtained from crossing the wild form of *G. hirsutum* ssp. *mexicanum* with susceptible, medium resistant and resistant varieties of *G. hirsutum*. He found that the uniformity of resistance to wilt in F_1, and in F_2 progeny, was close to that theoretically expected for a monogenic correlation of 3:1 (three parts resistant and one susceptible). Wilhelm et al. observed a similar correlation to wilt resistance (1974).

F. V. Voytenok (1971), while studying inheritance of wilt resistance with inter-varietal crossings observed intermediate resistance to wilt with F_1 and incomplete dominance of susceptibility in F_2, with a correlation of 1:78; with ecologically distant hybridization the dominance of resistance in F_1 and complex cleavage in F_2 showed a correlation of 263:1.

N. G. Simongulyan (1971) proposed that resistance to Verticillium wilt is controlled by several genes. However, others have concluded that the number of genes related to Verticillium wilt resistance is not high, since the genes controlling these high-polymeric characteristics are inherited coherently.
S. Y. Krayevoy and A. E. Egamberdiyev (1975), and R. G. Kim (1985) also reported on the polygenic inheritance of wilt resistance with distant intraspecific and interspecific hybridization of cotton. Academician S. S. Sadykov (1972) suggested that wilt resistance of cotton is defined by the action of two or more dominant genes (R_1, R_2).

Academician A. A. Abdullayev (1974) proposed that resistance of cotton to wilt is characterized by allel interaction of complimentary genes and gene - modifiers. While R. G. Kim (1977, 1985; Kim and Marupov, 2004) proposed that wilt resistance is defined by the genetic nature of the variety's resistance and the wild species of cotton from which it is derived, and that it exhibits field or horizontal, tolerant and vertical resistance.

Thus, to develop cotton varieties that are resistant to the more virulent races, strains and isolates of the pathogen *Verticillium dahliae* Kleb. it is necessary to:

- determine genotypic resistance of varieties and lines of cotton to more virulent isolates of different geographic populations of the fungus *V. dahliae* isolated from different cotton varieties;
- determine the inheritance of wilt resistance with hybrids of the first generation to various isolates of *V. dahliae* by inoculating the host plant with isolates of the pathogen.

Materials and Methods

Inheritance of wilt resistance of the hybrids of the first generation was found to depend on the susceptibility to wilt after inoculation with virulent isolates of the fungus *V. dahliae*. We define inheritance of wilt resistance as the degree of dominance as calculated according to the equation:

$$h = (F_1 - MP)/(HP - MP),$$

where h = coefficient of dominance, F_1 = average value of hybrid characteristic, MP = average value of parental characteristic, and HP = average value of characteristics of the best parent.

Experiments were conducted with the varieties Omad, C-5621 and C-8284, and also with lines L-162, L-842, L-408, L-155, L-44 and L-1708, and F_1 hybrids. The experiment was replicated 3 times, with 20 plants per row in 4 rows for each hybrid combination.

Wilt resistance of F_1 hybrids were recorded according to the phenotypic appearance of the disease on June 15, July 15, and August 15 after inoculation by stem injection in early June at the beginning of anthesis with *V. dahliae* isolates. The degree of disease symptomology of the plant was determined by cutting and examining the main stalk. Plants were scored at the end of September as: 0 = no necrosis, 1 = faint staining, 2 = medium staining, 3 = strong staining and 4 = extensive staining. Plants were also evaluated for wilt symptoms in leaves on June 15, July 15 and August 15.

Results and Discussion

The results showed that the isolates 28, 30, 32, 36, 40 and 44 of *V. dahliae* have different virulence as demonstrated by the degree of disease symptomology exhibited by F_1 hybrid plants. The degree of disease symptomology exhibited in the main stalk and the distribution of the organism in the plant, as well as its genotypic reaction to the isolates exhibited by leaf wilting depends on the heritable analogs received from their parents. For example, on June 15 20% of the hybrid combination Omad x C-6521 showed wilting when inoculated with isolates 28, 30 and 36. On this date, 40% of plants inoculated with isolates 32 and 44 showed wilting. There were no symptoms of wilt in the Omad x C-6521 plants infected with isolate 40. The number of affected Omad x C-6521 plants on July 15 for isolates 28, 30, 32, and 44 was equal to 60, 80, 40, and 60%, respectively. There were no changes in wilt symptoms for plants inoculated with isolates 36 and 40 during the entire study. The highest virulence for hybrid combination Omad x C-5621 was with isolates 28, 30, 32, 44, which were isolated from the varieties C-6524 and C-2609 from the variety Akkurgan-2 in the Fergana valley.

A complete analysis of all of the data (Table 1) shows that the degree of inheritance of wilt resistance of the hybrids Omad x C-5621 to the isolates under investigation is characterized by dominance and super dominance toward the susceptible parent independently of the method of assessment for wilt resistance. The exception was isolate 36. Here there was dominance toward resistant from hybrids derived from the parent C-5621.
A different picture was observed in hybrid combination C-8284 x C-5621 where coefficients of dominance based on phenotypic performance of disease symptoms showed intermediate inheritance of resistance to isolate 30, with dominance and super dominance of wilt resistance to isolates 28, 32, 36 and 40. In the case of C-8284, super dominance of resistance to isolate 44 was evident with both parental forms having a high wilt resistance to isolate 44. Isolate 44 was found in the cotton variety Akkurgan-2 from the Fergana valley. This indicates that *V. dahliae* isolate 44 is more virulent to the C-8284 x C-5621 hybrid combination than other isolates.

Alternatively, wilt resistance can be measured more reliability by observation of necrosis after cutting the main stalk (see Table 1). For example, dominance is observed for hybrids derived from the more susceptible parent C-8284 when it is inoculated with isolate 28 (h = -1.0), while with all hybrids infected with isolates 40 and 44 there is super dominance. Note that inheritance of wilt resistance in the C-8284 x C-5621 hybrid combination depends upon genotypic reaction of hybrids towards isolates and upon the genetic nature of wilt resistance of parents (i.e., the degree of tolerance of the parents) and the virulence of the *V. dahliae* isolates.

Inheritance of wilt resistance in hybrid combinations Omad x L-44 and C-8284 x L-44 is characterized by super dominance on susceptibility in phenotypic wilt resistance after inoculation of these two hybrids with isolate 28. Inoculation of hybrids Omad x L-44 with isolates 30, 32, 36, 40 and 44 demonstrate dominance toward the wilt resistant parent L-44, and when plants are inoculated with isolate 32, there is dominance of the more susceptible parent L-44. The latter shows less wilt resistance than the variety Omad to isolate 32.

The inheritance of wilt resistance with F_1 hybrids by phenotypic response when plants were inoculated with isolates 36 and 40 is characterized by intermediate wilting. Furthermore, dominance toward the more susceptible variety Omad and super dominance to susceptibility after inoculation of hybrids is observed with isolate 44 (h = 60.0). Isolate 44 isolated from the variety Akkurgan-2 in Fergana valley, is more virulent for the Omad x L-44 hybrid. Furthermore, isolate 44 is highly aggressive toward the hybrid Omad x C-5621.

In hybrids between paternal parents C-5621 and L-44, and the maternal varieties Omad and C-8284, the degree of susceptibility of the F_1 hybrids to isolate 36 is at the level of the parents and exhibits intermediate inheritance to isolate-30. The analysis of these results based on the degree of susceptibility of the hybrids and the susceptibility of maternal parents L-162, L-842, L-408, L-155 and L-1708 to all isolates of the fungus, shows they have different genotypical reaction in phenotypic inheritance as indicated by the degree of wilt resistance. Coefficients of dominance in hybrid combination L-162 x C-5621 show, that inheritance of resistance to wilt is characterized by super dominance towards wilt resistance, except for isolate-44 where there is super dominance on susceptibility to wilt. Similar results were obtained by observing the cut stalk, but with some differences according to the degree of dominance. Similar results on inheritance of the degree of wilt resistance to all isolates were found in all hybrids derived from parent L-44, both as regards to plant phenotype as well as that exhibited by cutting the stalk.

The degree of inheritance of wilt resistance in hybrid combinations, where the maternal parent is L-842, there is intermediate dominance and super dominance toward wilt resistance to all isolates, except isolate-32 in the combination L-842 x C-5621. Here there was super dominance towards susceptibility.

With hybrids obtained by crossing L-408 x C-5621 and L-408 x L-44 after inoculation of plants with isolates 28,30, 32, 36, 40 and 44, there was super dominance in phenotypic wilt performance towards isolate-28, and according to the staining observed after cutting the main stalk there is dominance toward the wilt resistant parent. Phenotypic dominance on susceptibility to wilt as measured by cutting the main stalk has been observed also with hybrids which were inoculated with isolates 30 and 32. By this measure there was judged to be intermediate inheritance to isolate 32 and dominance of susceptibility with hybrids infected by isolate-30. Hybrids infected with more virulent isolates-36 and 40 have a high degree of dominance to susceptibility towards the less resistant parent to those isolates. A high degree of inheritance of wilt resistance was observed with hybrids inoculated with isolate-44 independently by observing wilt. With the L-408 x C-5621 and L-408 x L-44 hybrids the isolates with the highest virulence are 36 and

40, which were isolated from the varieties Akkurgan-2 and C-6524 in Fergana valley. Similar results were obtained while evaluating resistance by observing the cut stalk.

Inheritance of wilt resistance in hybrid combination L-408 x L-44 is characterized by dominance of susceptibility in phenotypic wilt performance controlled by parent L-408 when plants were inoculated with isolate 28. Similar inheritance also was observed by the cut stalk. This verifies that L-408 possesses high wilt resistance and a high degree of tolerance towards isolate-28. A high degree of susceptibility to wilt has been obtained with F_1 hybrids by inoculation of plants with isolates 30, 32, 40 and 44 independently of the methods of assessing wilt resistance. According to the degree of dominance, they are characterized by intermediate inheritance, dominance on susceptibility at a level of the parents and super dominance toward the less resistant parent; here coefficients of dominance vary from 0 to 60. Thus, we conclude that for these two hybrids the most virulent isolates of the fungus are isolates 30, 32, and 40. Isolates 30 and 32 were isolated from diseased cotton plants from the Fergana valley from the varieties C-6524 and C-2609, and isolate 40 was found in the Namangan province of the Fergana valley from the variety C-6524. Note, that in hybrid combinations L-408 x C-5621 and L-408 x L-44 there was a relatively weak tolerance to all isolates in the study, and is probably due to the genetic reaction of the initial parents and their hybrids when other microorganisms attack the plant which has been inoculated with the virulent isolates of *V. dahliae.* In hybrids obtained by crossing L-408 with parents C-5621 and L-44 there is a very weak reaction in phenotypic wilt performance after inoculation with isolates 28, 30, 32, 36, 40 and 44 when these were analyzed on August 15, and they are practically absent on June 15 and July 15. The one exception was with the hybrid combination L-408 x C-5621 towards isolate 32 on July 15. The degree of wilt resistance in hybrid combinations with the participation of resistant to wilt maternal form L-155, the F_1 hybrids have high phenotypic resistance to wilt to all of the studied isolates. The number of infected plants in the combinations L-155 x C-5621 and L-155 x L-44 on August 15 varied from 0 to 60% depending upon virulence of the isolates. No plants were affected with wilt on June 15 and July 15 except the hybrid combination L-155 x L-44 to isolate 44. The degree of tolerance varied from 0 to 80 %, depending on genotype reaction of hybrids to the introduction of other pathogenic fungal organisms when the isolates of the pathogen were studied. The hybrid combination L-155 x C-5621 is characterized by phenotypic dominance to susceptibility to isolate-28 at the level of the parents, and as observed by the degree of staining in the cut stalk with super dominance toward the more resistant parent C-5621. Similar results were obtained by inoculation of F_1 hybrids with isolates 30, 32, 36, and 44, which had shown dominance and super dominance as observed by resistance to wilt. Similar results were obtained by observing the cut stalk. Hybrids inoculated with isolate-40 have a dominant character of inheritance toward the more susceptible parent L-155. For the hybrid combination, isolates 30 and 36 are the most virulent, and the L-155 x C-5621 hybrid shows a high degree of tolerance.

Wilt resistance of hybrid combination L-1708 x C-5621 to virulent isolates of the fungus is characterized by higher resistance in phenotypic wilt performance when hybrids were inoculated with isolates 32, 36, 40 and 44 as observed on June 15 and July 15. The number of plants exhibiting wilt in the hybrid combination L-1708 x L-44 on July 15, with all fungal isolates except 32, varied from 20 to 40%; on August 15, the wilt of hybrids L-1708 x C-5621 and L-1708 x L-44 varied from 0 to 40% depending upon the virulence of the isolates of the fungus. The highest virulence for hybrids L-1708 x C-5621 were isolates 28, 30 and 40 (as determined by cutting the stalk), and for hybrids L-1708 x L-44 the most virulent isolates were isolates 28 and 30; isolates 28 and 30 were equally virulent for both hybrid combinations. The degree of tolerance varied from 0 to 60%, and only in one case was it 100% (i.e., isolate 40). Wilt resistance of F_1 hybrids to the isolates of the fungus is inherited according to the principle of super dominance and dominance toward the resistant or more susceptible parent. Intermediate inheritance is observed in hybrid combination L-1708 x C-5621 and to isolates 30 (as determined by cutting the stalk), and also with hybrids L-1708 x L-44 to isolate 28, and in four cases at the level of the parents, and in hybrid combinations L-1708 x C-5621 and L-1708 x L-44 to isolates 28, 36, 30 and 40, respectively.

Summary

These observations on inheritance of wilt resistance of the hybrids of the first generation to the virulent isolates 28, 30, 32, 36, 40 and 44 of the fungus *V. dahliae* show that:

1) The highest wilt resistance was observed in the variety Omad and lines L-44, L-408, L-155 and L-1708 to the isolates 28, 30, 32, 36, 40 and 44. These varieties and lines exhibit hypersensitivity when the pathogen is inoculated into the plant, but they do not display external symptoms of wilt. The pathogen spores do not penetrate beyond the point of inoculation, but some penetrate beyond the first several cells of the host. There they interact with the cells of the host, and the pathogen coexist with the plant for an extended period of time. The necrotic tissue is enclosed in a cyst and is actively extruded by healthy tissues with the necrotic tissue excluded by a mechanical barrier from the periderm. The authors note that the more intensive the hypersensitivity reaction expressed within plants, the faster the infected cells die and visa versa. The higher degree of compatibility of the parasite with the host, the longer they coexist (i.e., the higher the degree of resistance), and fewer cells die. Sometimes there are one or two darkened cells at the point of inoculation.
2) Wilt resistance of hybrids of the first generation as determined by inoculation with the isolates of *V. dahliae* is inherited according the type of super dominance and dominance toward the resistant or susceptible parent independent from the method used to determine the disease index. Also intermediate inheritance is observed. The degree of dominance depends on the combinational ability of parents and genotype reaction of F_1 hybrids when pathogens are introduced into the plant, and also on the virulence of the isolates found in different varieties of cotton from different soil-climatic regions of the Republic of Uzbekistan;
3) The phenotypic degree of wilt performance with parents and F_1 hybrids depends upon the genotypic nature of their resistance to isolates of *V. dahliae* after inoculation with the pathogen, and their exhibition of external phenotypic symptoms of the disease. The varieties with the highest phenotypic wilt resistance (i.e., tolerance) are Omad, C-5621 and lines L-162, L-842, L-44 and L-1708. Among hybrids, the hybrid combinations L-162 x C-5621, L-162 x L-44, L-155 x C-5621 and L-1708 x C-5621 had the highest phenotypic wilt resistance. The degree of tolerant resistance to wilt varied from 50 to 80%.
4) Genetic control of inheritance of tolerant resistance to *V. dahliae* isolates and F_1 hybrids is characterized by negative and positive super dominance, dominance toward the best or the worst parent and intermediate inheritance;
5) The hybrid combinations L-155 x C-5621 and L-155 x L-44 have the best combinational wilt resistance toward the *V. dahliae* isolates studied, as compared to other hybrid combinations with the maternal forms Omad, C-8284, L-162 and L-408.

Acknowledgements

This research was supported by a grant from the USDA, Agricultural Research Service - Former Soviet Union Scientific Cooperation Program, Project, P-105.

References

Abdullayev, A. A. 1974. Evolution and Systematic of Polyploid Species of Cotton. Fan Publishing, Tashkent, Uzbekistan, 260 pp.

Kim, R. G. 1977. Wilt Resistance of Some Hybrids of Cotton on Various Backgrounds of Infection with Verticillium Fungus. Collected tractates of VNIIH, Genetics, Cotton and Alfalfa Breeding and Seed Breeding, Tashkent, pp. 49 – 54.

Kim, R. G. 1985. Wilt Resistance of Distant Hybrids of Cotton and Its Interrelation with the Type of Embranchment, Prematureness and Other Economically – Valuable Characteristics. Abstract on Competition for PhD of Agricultural Sciences Scientific Degree, Tashkent, 21 pages.

Kim, R.G., and A. Marupov. 2004. Wilt Resistance of Varieties and Lines of Cotton of the Species *Gossypium hirsutum L.* After Inoculation with Various Strains of *Verticillium dahliae Kleb.* Fungus. Material of International Scientific – Practical Conference "Problems of Cotton and Grain Growing Development", Tashkent, , pp. 294 – 296.

Krayevoy, S.A., and A. E. Egamberdiyev. 1975. On Polygenic Nature of Cotton Wilt Resistance, VASHNIL (All-Union Academy of Agricultural Sciences named after Lenin), No 5, pp. 22 – 23.

Mirakhmedov S. M. 1974. Intraspecific Distant Hybridization of Cotton of the Species *Gossypium hirsutum L.* for Wilt Resistance. Fan Publishing, Tashkent, Uzbekistan, pp 188.

Sadykov S. S. 1972. Increase of Prematureness and Yields of Cotton. Fan Publishing, Tashkent, Uzbekistan, pp. 322.

Simongulyan N. G. 1971. Problems of Prematureness and Breeding of Cotton. Fan Publishing, Tashkent, Uzbekistan, pp. 207.

Voitenok, F.V. 1971. Breeding of Cotton for Wilt Resistance. Scientific Thesis. Kolos Publishing, Moscow, Russia, p. 133.

Wilheim S., T. S. Cames, and T. Hilga. 1974. *Gossypium hirsutum* subsp. *mexicanum* var. *nervosum. heningrad starain* – a Source of Resistance to Verticillium Wilt" – Phytopathology, V. 64, No 7, pp. 931 – 939.

Table 1. Inheritance of wilt resistance F_1 hybrids depending upon methods of disease assessment

Varieties, lines and hybrids	Isolate Number	Quantitative difference between phenotypic assessment and cut stalk in %					
		Phenotypic wilt observation		Degree of stalk affected (based on the cut stalk for 14.09)		Degree of tolerance observed in %	
		Total (%)	h	Total (%)	h	Total (%)	h
mad	28	0.0		60.0		100.0	
	30	40.0		40.0		0.0	
	32	-		60.0		100.0	
	36	40.0		80.0		50.0	
	40	20.0		60.0		60.7	
	44	00.0		80.0		100	
C-5621	28	20.0		80.0		75.0	
	30	-		80.0		100.0	
	32	20.0		80.0		75.0	
	36	20.0		80.0		75.0	
	40	-		80.0		100	
	44	-		100.0		100.0	
L-44	28	-		80.0		100.0	
	30	20.0		20.0		0	
	32	20.0		100.0		80.0	
	36	20.0		80.0		75.0	
	40	20.0		100.0		80.0	
	44	-		40.0		100.0	
Omad x C-5621	28	20.0	-1.0	100.0	-3.0	80.0	-0.60
	30	80.0	-3.0	100.0	-2.0	20.0	-0.60
	32	60.0	-5.0	100.0	-3.0	40.0	-3.80
	36	20.0	1.0	80.0	0.0	75.0	1.00
	40	60.0	-5.0	60.0	1.0	0	-5.17
	44	60,0	0.0(-60)	100,0	-1.0	40.0	0.0 (-60.0)
Omad x L-44	28	20,0	0.0(-20)	60.0	1.0	66.7	0.0 (-23.3)
	30	20.0	1.0	80.0	-5.0	75.0	0.0 (75.0)
	32	20.0	-1.0	100.0	-1.0	80.0	-1.0
	36	40.0	-1.0	60.0	0.0	33.3	-2.34
	40	20.0	0.0	60.0	1.0	66.7	-0.37

	44	60.0	0.0(60.0)	100.0	-2.0	40.0	0.0 (-40)
C-8284	28	20.0		100.0		80.0	
	30	40.0		100.0		60.0	
	32	40.0		100.0		60.0	
	36	60.0		60.0		0	
	40	20.0		60.0		66.7	
	44	-		60.0		100.0	
C-8284 x C5621	28	20.0	0.0	100.0	-1.0	80.0	-1.0
	30	20.0	0.0	60.0	3.0	66.7	-0.60
	32	20.0	1.0	60.0	3.0	66.7	-0.11
	36	20.0	1.0	60.0	1.0	66.7	0.77
	40	0.0	1.0	100.0	-3.0	100.0	1.00
	44	20.0	0.0(20.0)	100.0	-1.0	80.0	0.00
C-8284 x L-44	28	20.0	-1.0	60	1.0	66.7	-2.33
	30	40.0	0.0	80.0	1.0	50.0	0.67
	32	20.0	1.0	100.0	0.0	80.0	1.00
	36	0.0	2.0	60.0	0.0	100.0	1.67
	40	20.0	0.0	100.0	-1.0	80.0	1.00
	44	40.0	0.0(40.0)	60.0	-1.0	33.3	0.0 (-33.3)
L-408	28	20.0		60.0		66.7	
	30	20.0		60.0		66.7	
	32	0.0		20.0		100.0	
	36	60.0		80.0		25.0	
	40	80.0		80.0		0	
	44	0.0		40.0		100.0	
L-408 x C-5621	28	40.0	0.0(20.0)	60.0	1.0	33.3	-8.92
	30	20.0	1.0	60.0	1.0	66.7	-0.99
	32	20.0	1.0	60.0	0.33	66.7	-1.66
	36	20.0	1.0	40.0	0.0(-40.0)	50.0	0.0
	40	60.0	-0.5	60.0	0.0	0	-1.0
	44	40.0	0.0	100.0	0.0	60.0	0.0 (-40.0)
L-408 x L-44	28	20.0	-1.0	60.0	1.0	66.7	-0.99
	30	80.0	0.0(60.0)	100.0	-3.0	20.0	-0.39
	32	60.0	-5.0	80.0	-0.5	25.0	-6.5
	36	40.0	0.0	40.0	0.0(-40.0)	0	-5.0
	40	60.0	-0.33	80.0	1.0	25.0	-0.38
	44	20.0	0.0(20.0)	60.0	0.0(-20.0)	66.7	-0.66
L-155	28	20.0		100.0		80.0	
	30	60.0		100.0		40.0	
	32	20.0		60.0		66.7	
	36	60.0		80.0		25.0	
	40	20.0		20.0		0	
	44	0.0		60.0		100.0	
L-155 x C-5621	28	20.0	0.0	60.0	3.0	66.7	-4.32
	30	0.0	1.0	80.0	1.0	100.0	1.0
	32	20.0	0.0	80.0	-1.0	60.7	-2.40
	36	20.0	1.0	60.0	0.0(-20.0)	75.0	1.0
	40	20.0	-1.0	40.0	0.33	50.0	0.0 (50.0)
	44	0.0	0.0	60.0	1.0	100.0	0.0
L-155 x L-44	28	20.0	-1.0	40.0	5.0	50.0	-1.0
	30	20.0	1.0	60.0	0.0(-40.0)	66.7	2.33
	32	20.0	0.0	80.0	0.0(-20.0)	75.0	0.24

	36	60.0	-1.0	80.0	0.0	25.0	-1.0
	40	60.0	0.0(40.0)	60.0	0.0(-40.0)	0	-1.0
	44	40.0	0.0(40.0)	60.0	-1.0	33.3	0.0 (-66.7)
L-1708	28	20.0		20.0		0	
	30	60.0		60.0		0	
	32	20.0		20.0		0	
	36	20.0		40.0		50.0	
	40	60.0		80.0		25.0	
	44	20.0		60.0		66.7	
L-1708 x C-5621	28	20.0	0.0	80.0	-1.0	75.0	1.0
	30	20.0	-0.33	80.0	-1.0	75.0	0.50
	32	40.0	0.0(20.0)	40.0	-0.3	0	-1.0
	36	20.0	0.0	40.0	1.0	50.0	-1.0
	40	0.0	1.0	80.0	0.0	100.0	1.0
	44	40.0	-3.0	60.0	1.0	33.3	-.2.99
L-1708 x L-44	28	40	-3.0	80.0	-1.0	50.0	0.0 (50.0)
	30	40	0.0(20.0)	80.0	-2.0	50.0	0.0 (50.0)
	32	40	0.0(20.0)	60.0	0.0	33.3	-0.16
	36	40	0.0(20.0)	60	0.0	33.3	-2.33
	40	20	1.0	40	5.0	50.0	-0.09
	44	20	-1.0	60	-1.0	66.7	-0.99