

Greenhouse screening for Fusarium wilt resistance in lupine

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Abstract

Fusarium wilt can cause total crop failure. Evaluation of Fusarium resistance in heavily infected soil were performed in a greenhouse where the dominant fusarium species in the soil in descending order was *F. oxysporum* then *F. avenaceum*, *F. culmorum*, *F. solani*, *F. gibbosum*. Large fusarium wilt pressure was observed and fully susceptible lines were completely destroyed by Fusarium wilt caused by *F. oxysporum*. Segregation in F2 and F3 in *L. angustifolius* showed that resistant genotypes have two dominant non-allelic resistance genes to wilt. We call this gene Relation to fusarium oxysporum (Rfo1,Rfo2). Susceptible genotypes have either two wild genes (++ ++) or one wild and one dominant resistant gene (++ Rfo2 Rfo2, or Rfo1Rfo1 ++). Crossing '++ Rfo2Rfo2' to 'Rfo1Rfo1 ++' segregates in 9:7 resistant to susceptible in F2, respectively. The same segregation was observed by crossing 'Rfo1Rfo1 Rfo2Rfo2' to '++ ++'. We recommend the use of these resistant genes in breeding in areas with potential Fusarium wilt problems.

Keywords

Fusarium resistance, Lupin angustifolius, albus and luteus, inheritance.

Introduction

Fusarium problems has been reported from all major lupin growing areas (Debelyi et al 1991; Lewartowska et al 1994; Sweetingham et al 1998). The interest in growing *L. angustifolius* is increasing in humid maritime areas in northern Europe due to new earlier and higher yielding varieties. However, these conditions favor Fusarium root rot and Fusarium late wilt development, which could be accentuated by a short rotation of grain legumes in organic fields. Thus fusarium resistance is also highly important in these conditions. Breeding resistant lines for different environment has been reported (Kurlovich et al 1995; Kuptsov 2000), however, only little information about genetics has been provided. For successful breeding the understanding of the genetic control of the Fusarium wilt resistance is highly important, and for this purpose this experiment was carried out.

Material and methods

To evaluate the resistance, susceptible and resistant genotypes and F2 and F3 populations were grown in greenhouse in a sandy soil which 2 years before was taken from a lupin field. Where the resistant genotypes yielded a low frequency of susceptible scores the segregation ratio in of their F2 and F3 were corrected for this error (table1). The precedent crop in the greenhouse was also lupin. The dominant fusarium species in the soil was in descending order *F. oxysporum* then *F. avenaceum*, *F. culmorum*, *F. solani*, *F. gibbosum*. Irrigation was frequent and the soil was kept near field capacity. The day temperature ranged from 18°C to 24°C and the minimum night temperature varied from 8°C to 12°C. Large Fusarium wilt pressure was observed and fully susceptible lines were completely destroyed by fusarium wilt caused by *F. oxisporum*. Suceptible plants did not formed pods and had typical stem symptoms. The susceptible *angustifolius* variety Prima was used as a control of the homogeneity of Fusarium fungi pressure.

Results and Discussion

In *L. angustifolius* total resistance to wilt was among others observed in Crystal (Russia), Mitan (Belarus), Rose, E104, E105, E106 (Denmark), Tanjil (Australia). In *L. albus* Giza (Egypt) and MA (Denmark). All tested *L. luteus* were resistant in these conditions, Mortiv-369, WAL-196 etc.

Very susceptible *L. angustifolius* lines were Prima (Denmark), Sonet (Poland), Borweta (Belarus), Kalya (Australia). The larger part of the *L. albus* lines was 100 % destroyed eg. Lublanch (France), E1 and P1 (Denmark). These results correlate well to known resistance under field conditions in various countries (Debelyi et al 1991; Kuptsov 2000).

Single pod descent F2 and F3 hybrid populations in *L. angustifolius* showed that resistant genotypes have two dominant non-allelic resistance genes to wilt. We call this gene Relation to *Fusarium oxisporum* (Rfo1,Rfo2). Susceptible genotypes have either two wild genes (++ ++) or one wild and one dominant resistant gene (++ Rfo2Rfo2 , or Rfo1Rfo1 ++). Crossing '++ Rfo2Rfo2' to 'Rfo1Rfo1 ++' segregates in 9:7 resistant to susceptible in F2, the same segregation was observed by crossing 'Rfo1Rfo1 Rfo2 Rfo2' to '++ ++' (Table 1, figs. 1,2).

It is recommended to use these resistant varieties as a source of resistance genes for breeding in areas with potential fusarium wilt problems.

a)

PP: Rfo1 Rfo2 + +
 = = X = =
 Rfo1 Rfo2 + +
 Resistant Susceptible

F1: Rfo1 Rfo2
 = =
 + +
 Resistant

b)

PP: Rfo1 + + Rfo2
 = = X = =
 Rfo1 + + Rfo2
 Susceptible Susceptible

F1: Rfo1 +
 = =
 + Rfo2
 Resistant



Gameter F1:

♀ \ ♂	+		Rfo1 +		+ Rfo2		Rfo1 Rfo2	
	+	+	+	+	+	+	+	+
+	+	+	+	+	+	+	+	+
+	=	=	=	=	=	=	=	=
+	+	+	Rfo1 +	+	+	Rfo2	Rfo1 Rfo2	
Rfo1 +	Rfo1 +							
Rfo1 +	=	=	=	=	=	=	=	=
Rfo1 +	+	+	Rfo1 +	+	+	Rfo2	Rfo1 Rfo2	
+ Rfo2	+	Rfo2	+	Rfo2	+	Rfo2	+	Rfo2
+ Rfo2	=	=	=	=	=	=	=	=
+ Rfo2	+	+	Rfo1 +	+	+	Rfo2	Rfo1 Rfo2	
Rfo1 Rfo2	Rfo1 Rfo2		Rfo1 Rfo2		Rfo1 Rfo2		Rfo1 Rfo2	
Rfo1 Rfo2	=	=	=	=	=	=	=	=
Rfo1 Rfo2	+	+	Rfo1 +	+	+	Rfo2	Rfo1 Rfo2	

F2: 9 resistant: 7 susceptible

Figure 1. Inheritance of Fusarium wilt resistance in *L. angustifolius* by two dominant non-allelic genes. a) resistant x susceptible cross. b) Susceptible line x to non-allelic susceptible cross. White indicates resistance and gray pattern indicate susceptibility.

PP: Rfo1 + Rfo1 Rfo2
 = = X = =
 Rfo1 + Rfo1 Rfo2
 Susceptible Resistant

 F1 Rfo1 +
 = =
 Rfo1 Rfo2
 Resistant

Gameter F1:

♀ \ ♂	<u>Rfo1</u> +	<u>Rfo1</u> +	<u>Rfo1</u> <u>Rfo2</u>	<u>Rfo1</u> <u>Rfo2</u>
<u>Rfo1</u> +	Rfo1 + = = Rfo1 +	Rfo1 + = = Rfo1 +	Rfo1 + = = Rfo1 Rfo2	Rfo1 + = = Rfo1 Rfo2
<u>Rfo1</u> +	Rfo1 + = = Rfo1 +	Rfo1 + = = Rfo1 +	Rfo1 + = = Rfo1 Rfo2	Rfo1 + = = Rfo1 Rfo2
<u>Rfo1</u> <u>Rfo2</u>	Rfo1 Rfo2 = = Rfo1 +	Rfo1 Rfo2 = = Rfo1 +	Rfo1 Rfo2 = = Rfo1 Rfo2	Rfo1 Rfo2 = = Rfo1 Rfo2
<u>Rfo1</u> <u>Rfo2</u>	Rfo1 Rfo2 = = Rfo1 +	Rfo1 Rfo2 = = Rfo1 +	Rfo1 Rfo2 = = Rfo1 Rfo2	Rfo1 Rfo2 = = Rfo1 Rfo2

Figure 2. Inheritance of Fusarium wilt resistance in *L. angustifolius* by two dominant non-allelic genes. a) Cross resistant line to susceptible with one dominant resistance gene. White indicate resistance and gray pattern indicate susceptibility

Table 1. : Segregation ratios in F₂ hybrids for Fusarium wilt resistance in *L. angustifolius*.

Cross	Number of studied plants								Expected ratio	X ²
	P ₁		P ₂		F ₂		F ₂ corrected			
	R	S	R	S	R	S	R	S		
LAG28/LAG24	32	3	165	10	65	3	69,9	-1,86	n.s.	-
LAW12/LAG24	0	67	165	10	54	21	57,2	17,8	3:1	0,07***
LAW12/LAW14	0	67	0	35	0	71	0	71,0	n.s.	-
LAW12/LAF6	0	67	0	74	41	36	41,0	36,0	9:7	0,28***
LAF6/LAG24	0	74	165	10	55	22	58,3	18,7	3:1	0,02***
LAG26/LAG24	0	38	165	10	56	21	59,3	17,7	3:1	0,17***
LAG36/LAG24	0	33	165	10	38	34	40,3	31,7	9:7	0,002***

(R indicate resistant, S - susceptible, n.s. – non segregation,)

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