



OWC 2020 Paper Submission - Science Forum

Topic 1 - Ecological approaches to systems' health

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WHITE LUPIN (*LUPINUS ALBUS*) ANTHRACNOSE RESISTANCE PRE-BREEDING PROJECT IN SWITZERLAND

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Abstract: White lupin (*Lupinus albus*) could contribute to the recent increase of organic grain legume production in Switzerland. However, its production is impaired by anthracnose (*Colletotrichum lupini*), against which FiBL is running a resistance pre-breeding project. In 2019, 196 new genetic resources and 60 F4 breeding lines were compared on-farm to the progeny of 288 accessions selected from 2015 to 2018. Relative disease scores compared to reference cultivar Amiga (mean score 6.9 on a scale from 1 (no symptoms) to 9 (plants completely dead)) were calculated and ranged from -2.25 to +2. Mean relative scores of selected genotypes and breeding lines were -0.7 and -0.5, respectively, compared to -0.33 in the new accessions. The frequency of more resistant genotypes was about twice as high in the selected accessions and breeding lines than in the new accessions. These are valuable data for breeding as well as for development and validation of genetic markers for resistance screening.

Introduction: Bio Suisse, the Swiss organic farmers' association, will restrict concentrated feed in ruminants' diet to 5% from 2020 onwards. By then, 90% of ruminant feed must be from Swiss Organic farming, rising to 100% by 2022. This enhances Swiss organic grain legume production (Aebi 2019). Lupins could complement soybean, pea and faba bean, especially white lupin (*Lupinus albus*), having higher yield potential, seed protein content, and weed competition than blue lupin (*Lupinus angustifolius*). However, due to its susceptibility to anthracnose, caused by *Colletotrichum lupini*, it is hardly grown in Switzerland at present. FiBL has run a white lupin pre-breeding project since 2014 in order to find resistant germplasm (Arncken et al. 2018). Totally 288 white lupin accessions from five genebanks were assessed and selected under natural disease pressure from 2015 to 2018. In 2019, 196 new accessions and 60 breeding lines were compared to the existing gene pool of selected accessions.

Material and methods: Three test groups of white lupin (*Lupinus albus*) genotypes were sown in single unreplicated rows of 1 m length between spreader rows of cultivar Amiga, known to be susceptible to anthracnose, caused by the fungal agent *Colletotrichum lupini*. The test groups were: **a)** new genebank accessions obtained from the Spanish and from the Australian genebanks (n = 196), **b)** selected genotypes from genebank accessions obtained from 2015 to 2018 from the German, Ethiopian, Polish, and Russian Genebanks and from INRA material obtained via CREA, as well as from some

breeding lines from Erik von Baer (Semillas Baer, Chile) and Edwin Nuijten (LBI, NL) (n = 160), and **c**) selected F4 breeding lines from crossings performed in 2015 (n=60). The newly admitted German cultivar Frieda for which a better anthracnose resistance is claimed was also included in groups **a**) (n = 7) and **b**) (n = 9). The number of seeds sown in each row was 5-16 (av. 11) for the new genebank accessions (a), 7-16 (av. 16) for the selections (b), and 4-16 (av. 14.9) for the breeding lines (c). If enough seed was available, 16 seeds were sown. The trial was sown on March 28th, 2019, on a field of the biodynamically managed farm bioböhler, in the direct vicinity of the Rhine river in Rümikon, Canton Aargau, Switzerland. The soil was normally drained, moderately deep brown soil (Cambisol) to slightly humous loam with a pH of 6.7. The preceding crop was winter wheat, followed by a mixture of forest perennial rye, berseem clover (*Trifolium alexandrinum*) and Persian clover (*Trifolium resupinatum*) as a catch crop. Mechanical weed control was performed on May 7th, 2019. Pods were hand harvested from August 13th to August 16th, 2019. Symptoms of anthracnose disease, caused by the fungal agent *Colletotrichum lupini*, were regularly assessed by scoring on a scale from 1 (no symptoms) to 9 (plants completely dead) from mid May until end of July. Group **a**) was scored on May 17th and 27th, June 4th, July 2nd, July 16th, and July 30th. Group **b**) was scored on May 16th, June 4th, June 26th, July 9th, July 23rd, and August 5th. Group **c**) was scored on May 7th, July 9th and July 23rd. In order to refer to spatial differences in disease incidence, the Amiga spreader rows were also assessed. Calculating the difference between the genotype score and the mean score of the two neighbouring Amiga rows resulted in the relative scores given here. Negative relative scores indicate more resistance towards anthracnose than Amiga. Correlations between scorings at different dates were calculated. The latest July scoring was analysed more thoroughly since it is the basis for selection.

Results: At the field trial site in Rümikon, all plants showed severe symptoms of anthracnose. Scores in late July ranged from 5.5 to 9, with an average score of the reference cultivar Amiga of 6.9. No complete resistance against the disease was observed. The best genotype had a late July score that was only 2.25 grades better than Amiga (relative score = - 2.25). The most susceptible genotype was 2 grades worse than Amiga (relative score = +2). The mean relative score of the new German cultivar Frieda in late July was -0.625. The two scorings done in July had a correlation coefficient of r = 0.75 for group **a**), r = 0.67 for group **b**), and r = 0.4 for group **c**). Mean relative scores of the latest July scorings are given for each group in Table 1, together with more information on the distributions of the relative scores. Only 7 % of the new genebank accessions (group **a**) were more than one score better than the reference cultivar Amiga, whereas this was the case for nearly 19 % of the genotypes that had already undergone one or more years of field selection (group **b**). In the F4 lines, 21.7 % were more than one score better than Amiga.

Group	a	b	c
Group description	New genebank accessions	Selected accessions (2015-2018)	Selected F4 lines of own crosses
N	196	160	60
Normal distribution?	no ($P_{HA} < 0.0001$)	no ($P_{HA} < 0.034$)	Yes ($P_{HA} = 0.69$)
Determination coefficient of the two latest July scorings	r = 0.75	r = 0.67	r = 0.4
Latest July			

scoring:			
Mean absolute score	6.61	5.81	6.14
Mean relative score	-0.3	-0.7	-0.5
SD of relative score	0.66	0.52	0.53
Frequency of relative score <-1	32 (=16.3 %)	58 (=36.3%)	18 (=30.0 %)
Frequency of relative score <-1.25	14 (=7.0%)	30 (=18.8%)	13 (=21.7%)

Tab.1: Anthracnose scoring results of three groups of white lupin genotypes from the 2019 field trial in Rümikon, Switzerland.

Discussion: The data suggest no qualitative but only quantitative resistance. Cv. Frieda is a new standard for resistance screening. Genebanks only provide a limited number of seeds, so we started with unreplicated scorings. Correlations between repeated scorings suggested focusing on late season data. Improved mean relative scores of groups **b)** and **c)** compared to the randomly assembled group **a)** suggest a success of previous years' field selection. Moreover, higher frequencies of more resistant genotypes in groups **b)** and **c)** compared to group **a)** show an accumulation of interesting germplasm for breeding. Lupin breeding programmes in Australia, Poland, Germany, Italy, and France are currently developing tools for marker assisted selection for anthracnose resistance (Abraham et al. 2019). Phenotypic data generated under high natural disease pressure are valuable for both development and validation of such tools. Moreover, they can be used directly for breeding of resistant genotypes.

References:

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Image:

Image 1: pods of white lupin showing heavy anthracnose symptoms (Photograph: C. Arncken, FiBL)

Image 2: healthy pods of maturing white lupin (Photograph: C. Arncken, FiBL)



Image 2:



Disclosure of Interest: None Declared

Keywords: anthracnose, Colletotrichum, genetic resources, on-farm, resistance breeding, white lupin