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The Evaluation of Yield and Agronomic Traits of Flax Genotypes Under Latvian Conditions

Inga Stafecka
Institute of Agricultural Resources and Economics
Vilani, Latvia
email: inga.stafecka@arei.lv

Veneranda Stramkale
Institute of Agricultural Resources and Economics
Vilani, Latvia
veneranda.stramkale@arei.lv

Ieva Kroiča
Institute of Agricultural Resources and Economics
Vilani, Latvia

Aldis Starmkalis
Institute of Agricultural Resources and Economics
Vilani, Latvia

***Abstract*—This study aim was evaluated of flax genotypes regarding productivity, resistance to lodging and diseases as well as yield dependence relationships among phenotypic and quality traits. The 14 fibre flax genotypes were evaluated in field conditions on the background of natural infection from 2014 to 2018 for agronomically important traits and from 2015 to 2018 for occurrence diseases of flax. The data were recorded for the 15 following agronomic traits, such days to flowering, days to early yellow ripening stage, total plant height, technical height, stem yield, fibre content, 1000 seed weight, vessels per plant, harvest index, seed yield, oil content, resistance to lodging and fungal diseases during early yellow ripening stage. Genotypic and phenotypic correlations between yield and yield components were identified that total plant height, technical height and days to early yellow ripening stage played a major role on stem yield as well vessels per plant and harvest index on seed yield. The flax genotypes 'Vilani', 'L26-1', 'K9-1', 'T36-1', 'S37-1' exhibited significant highest stem yield ranging from 643.20 to 693.32 g m^{-2} and technical length ranging from 65.90 to 70.58 cm comparing to standard variety 'Vega 2'. The most perspective genotype of 'Vilani' with quit low susceptibility to anthracnose, pasmo and powdery mildew and resistance to lodging was identified.**

Key words—agronomic traits, correlations coefficient, diseases, fibre flax, yield

I. Introduction

Flax a multipurpose crop cultivated for fibre and seeds. Many investigators indicated that flax genotypes significantly differed in their growth habits and their response to cultural practices as well as production of fibre and oil, of them [1] – [4].

Similar like in the Latvia, in the Europe the aims of new flax varieties are: resistance to lodging reaching 9 points of the grade, middle early vegetation period, yield potential of stem reaching 7 – 8 t ha^{-1}, yielding potential of the seeds reaching 1.10 – 1.30 t ha^{-1} in the trials [5]. Yield is the most important and complex trait in crops that show correlations with other traits [6]. Being a polygenic trait it is greatly influenced by environmental fluctuations. To obtain superior varieties with high yielding potential, the plant breeder has to deal with characters, which are governed by polygenic systems and show continuous variation [7]. Other important agronomic traits such as flowering time, plant height, plant branching, and lodging resistance may also indirectly affect yield through various physiological mechanisms [6], [8], allowing crop phenology and plant architecture to be adapted to regional growing conditions, thus avoiding yield and quality losses [9]. Knowledge of association between yield and its attributes obtainable through estimation of genotypic and phenotypic correlation helps to formulate plant breeding strategies to develop suitable genotypes [10], [11]. The positive correlation between major yield components, breeding strategies would be very effective but on the reverse, selection becomes very difficult [12].

Flax yield and profitability can be greatly affected by diseases occurrences. Pasmo, anthracnose, powdery mildew are fungal diseases of flax and attacking all aboveground parts of the plant. These diseases can reduce the yield and quality of seed and fiber raw materials, with most losses resulting from premature ripening and loss of seed during harvest, although reductions in seed number per plant can occur with early infection [13] – [15].

In recent years, it has become more difficult to breed new fibre flax varieties with a better fibre quality, increased fibre yield, and the required resistance, due to repeated use of modern cultivars as crossing parents [5]. Therefore, the aim of this study was evaluated of flax genotypes regarding productivity, resistance to lodging and diseases as well as yield dependence relationships among phenotypic and quality traits.

II. Materials and methods

A. Field Trails

The research was conducted at the Institute of Agricultural Resources and Economics, Research Centre of Priekuli, research unit Vilani since 2014 to 2018 for agronomically important traits of flax and since 2015 to 2018 for occurrence of fungal diseases during early yel-

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low ripening stage. Experimental material for the study consisted of 13 fibre flax genotypes of the Latvian origin "(Table 1)" and 'Vega 2' (ST) as the standard variety of Lithuanian origin. Since 2017 the variety 'Vilani' (breeding line ('I18-1')) has been tested successfully for DUS and for VCU is still on the way.

TABLE 1
ESTIMATED FIBRE FLAX GENOTYPES

Nr.	Geno-type	Nr.	Genotype
1.	S29-1	**8.**	K9-1
2.	S29-2	**9.**	K9-2
3.	S37-1	**10.**	L26-1
4.	S37-2	**11.**	I7-1
5.	T36-1	**12.**	I7-2
6.	T36-2	**13.**	Vilani (I18-1)
7.	T36-3	**ST**	Vega 2

The experiment was set up in randomized block design in three replicates at 2 m^2 with a distance between rows 10 cm. Flax was grown in Humic Gleyic Podzols (*PZ-gl-hu*) soil [16]. The main agrochemical parameters of the arable soil layer were following: humus content – 6.5%, soil acidity (pH_{KCl}) – 6.4–7.0, available P_2O_5 – 130–145 mg kg^{-1} and available K_2O – 118–124 mg kg^{-1} soil. Complex fertilizer NPK 16:16:16 – 300 kg ha^{-1} was applied after first soil cultivation. 1700 flax seeds per 1 m^2 were sown by hand with sowing depth 1.5–2 cm at the field trial. Prior to sowing, germination tests were performed for all used genotypes. Seeds were sown during the first 10 days of May. For plants' further development a surface fertilizer - ammonium nitrate 30 kg ha^{-1} N in fir-tree like phase was applied. Insecticides (Fastac 50 0.4 L ha^{-1}, a.s. 50.0 g L^{-1} alpha-cypermethrin) were sprayed against flax flea beetles (*Aphthona euphorbiae)* as required by the instructions. The tractor-drawn sprayer "Pilmet 412" was used for insecticide application. Fungicides for flax diseases were not used at all. Plants were pulled manually at the stage of early yellow ripeness and then left on ground for air-drying for 5–8 days. The seed-vessels were removed by "Eddi" device. Seeds were cleaned with sample cleaner MLN (Pfeuffer GmbH, Germany). The yield of seeds was weighed and then re-calculated to weight by 100% purity and 12% humidity. Seed oil content was determined on grain quality analyzer "Infratec 1241" (FOSS, Denmark). The total and technical plant heights, fibre content were determined using randomly selected most typical 20 plants in each parcel area before the harvest. The yields of stem and seed were determined in each harvested parcel area. The resistance of plants to lodging, length of growth stages of flax were evaluated [17]. The harvest index (HI) was calculated in percentage as the ratio of seed yield to plant weight after plant maturity [10].

Thirty flax plants from each genotype at the 2 m^2 in the field trails were assessed during early yellow ripening stage under field conditions with natural infection background. The analyses of infected parts of the plants were done following the methodologies developed for phytopathological research [18]. The diseases were determined by morphological features were using disease descriptors [18], [19]. Percentage of the affected plants was estimated and disease severity was recorded for the whole plant for each disease following a five-point scale: 0 – healthy, 1 – weakly affected, 2 – moderately affected, 3 – heavily affected, 4 – very heavily affected or dead plants. Disease severity index "(1)" was calculated by applying formula [18]:

$$\mathrm{DSI} = \frac{\sum(\mathrm{ab}) \times 100}{\mathrm{A} \times \mathrm{S}}, \tag{1}$$

where DSI is disease severity index, %, a – number of infected plants, b – degree of infection used five-point scale, A – total number of plant samples (healthy and infected), S – the highest degree of infection.

B. Meteorological Conditions

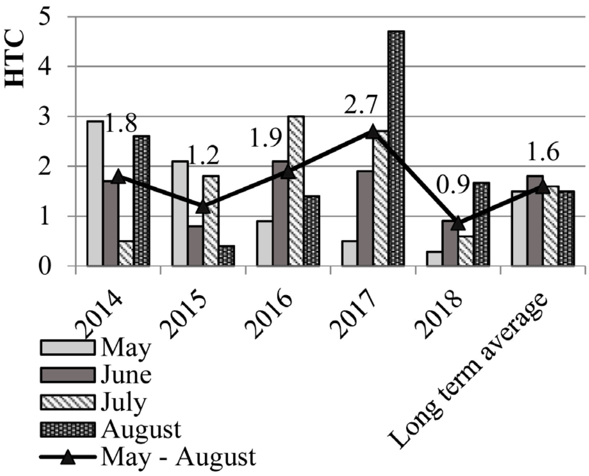

Fig. 1. Hydrothermal coefficients (HTC) during the growth period of flax from 2014 to 2018.

Agro-meteorological conditions were determined by ADCON installed meteorological stations connected to the computer program Dacom Plant Plus. The facility provides information directly to the nearby field trials. In this study hydrothermal coefficient (HTC) of each month was calculated during the growing season "(Fig. 1.)". The calculations were performed "(2)" by applying formula [20]:

$$\mathrm{HTC} = \Sigma x / \Sigma t \times 10, \tag{2}$$

where Σ x and Σ t – sum of precipitations and temperatures in the period, when the temperature has not been lower than 10°C.

Ranges of values of this index were classified according to Sielyaninov in the modification of [21] as: HTC ≤ 0.4 extremely dry; 0.4 < HTC ≤ 0.7 very dry; 0.7 < HTC ≤ 1.0 dry; 1.0 < HTC ≤ 1.3 relatively dry; 1.3 < HTC ≤ 1.6 optimal; 1.6 < HTC ≤ 2.0 relatively humid; 2.0 < HTC ≤ 2.5 humid; 2.5 < HTC ≤ 3.0 very humid; HTC > 3.0 extremely humid.

The hydrothermal conditions during the growing stages of flax differed "(Fig. 1.)". The relatively humid was recorded in 2014 and 2016 (1.8 and 1.9, respectively), relatively dry in 2015 (1.2) and dry in 2018 (0.9). The very humid was recorded in 2017, especially extremely higher humidity in August, where was about 317% higher than the long-term average.

C. Statistical Analysis

MS-Excel software was used for data statistical analysis and correlations. Significant differences among the measured characteristics of flax genotypes were compared by Fisher's protected least significant difference (LSD) tests ($p \leq 0.05$). Phenotypic and genotypic coefficients of correlation for yield and agronomic traits were identified [22; 23].

III. Results and discussion

All the agronomic traits measures determined for flax were significantly ($p \leq 0.05$) dependent on genotype "(Table 2)". The significant ($p \leq 0.05$) highest total plant height was observed of genotypes 'Vilani', 'K9-1', 'K9-2' and 'L26-1' with the range

from 82.42 to 85.35 cm, the technical plant height of genotypes 'T36-3', 'I7-2', 'T36-1', 'K9-2', 'T36-2', 'Vilani', 'K9-1' and '26-1' with the range from 64.26 to 70.58 cm and the fibre content of genotypes 'T36-3', 'T36-2', 'S37-2' and 'T36-1' with the range from 32.58 to 34.88% compared with the standard 'Vega 2'(ST). A study by [4], [24] has revealed that the plant technical height, fibre percentage and plant type (height, branch number, etc.) are the essential indexes for fibre flax breeding. In this study results was observed variable genetic resources where not all genotypes with highly technical height or stem yield had a great amount of fibre contents. Results have identified the diversity of flax genetic resources with perspective to find out genotypes useful for different purposes.

The significant ($p \leq 0.05$) highest stem yield was observed of genotypes 'S37-1', 'T36-1', 'K9-1', 'Vilani', 'L26-2' with the range from 643.12 to 693.32 g m^{-2} and the seed yield of genotypes 'S37-1', 'Vilani', 'S29-2', 'I7-1' with the range from 136.08 to 147.86 g m^{-2} compared with the standard 'Vega 2'(ST). The harvest index (HI) ranged from 15.49% to 20.87% between genotypes was identified insignificant different. According to [17] the flax descriptors list all genotypes were identified medium vegetation period where average day's number from seedling to flowering ranged from 57 to 61 days and to early yellow ripening stage from 98 to 104 days.

In this study, the genotypic and phenotypic correlation coefficient was similar in directions, while in magnitude, genotypic correlations were mostly higher than corresponding phenotypic correlations "(Table 3)".

TABLE 2
Agronomic traits of flax genotypes

Genotype	ToH, cm	TH, cm	StY, g m^{-2}	FC, %	SY, g m^{-2}	OC, %	HI, %	DF	VP
S29-1	74.80	59.82	538.12	29.58	123.76	42.65	19.19	60	99
S29-2	74.60	60.30	630.46	29.28	**145.20**	43.13	19.13	61	101
S37-1	75.72	60.92	555.32	**34.02**	**136.08**	43.00	20.58	60	102
S37-2	76.86	62.74	**643.12**	29.72	133.88	42.28	17.64	60	102
T36-1	79.46	**65.90**	**643.20**	**34.88**	107.04	**44.70**	15.49	58	99
T36-2	80.78	**67.88**	600.52	**33.68**	114.96	43.85	17.27	58	98
T36-3	77.62	**64.26**	552.96	**32.58**	135.50	**44.85**	20.57	57	99
K9-1	**83.36**	**69.00**	**649.06**	28.00	121.68	43.50	17.15	61	103
K9-2	**83.28**	**67.88**	610.72	26.04	127.22	43.33	18.92	61	103
L26-1	**85.12**	**70.58**	**693.32**	29.26	125.48	43.23	16.58	63	104
I7-1	78.04	63.06	598.32	26.60	**147.86**	41.50	20.87	58	100
I7-2	80.54	**65.86**	617.12	27.48	133.36	42.73	18.40	58	101
Vilani	**82.42**	**67.96**	**668.80**	29.02	**141.06**	42.43	18.68	58	98
Vega 2	72.98	58.32	556.80	26.38	115.28	42.68	18.18	59	101
$LSD_{0.05}$	*8.67*	*5.86*	*86.19*	*3.98*	*22.06*	*0.92*			

ToH- total plant height, TH - technical height, StY - stem yield, FC - fibre content, SY - seed yield, OC - oil content, HI - harvest index, DF - days to flowering, VP - days to early yellow ripening stage; LSD values significant at $p \leq 0.05$ are marked in bold comparing with 'Vega 2' (ST)

TABLE 3
GENOTYPIC AND PHENOTYPIC CORRELATION COEFFICIENTS AMONG THE 11 AGRONOMIC TRAITS OF FLAX GENOTYPES

ToH	TH	StY	FC	SY	HI	VpP	SW	OC	DF	VP	
ToH	-	**0.98****	**0.70****	**-0.10**	**-0.13**	**-0.55***	**0.09**	**0.7**	**0.19**	**0.29**	**0.22**
TH	0.93**	-	**0.70****	**0.03**	**-0.19**	**-0.59***	**-0.05**	**0.26**	**0.30**	**0.20**	**0.14**
StY	0.62*	0.57*	-	**-0.12**	**0.02**	**-0.63***	**0.13**	**-0.29**	**-0.03**	**0.39**	**0.29**
FC	-0.28	-0.17	-0.09	-	**-0.30**	**-0.14**	**-0.65***	**0.36**	**0.64***	**-0.30**	**-0.37**
SY	-0.23	-0.06	0.00	0.17	-	**0.76****	**0.75****	**-0.19**	**-0.53***	**0.02**	**0.05**
HI	-0.54*	-0.54*	-0.80**	0.11	0.56*	-	**0.49**	**0.04**	**-0.37**	**-0.22**	**-0.13**
VpP	0.40	0.19	0.22	-0.51	-0.12	-0.19	-	**-0.36**	**-0.72****	**0.29**	**0.35**
SW	-0.21	-0.10	-0.11	0.11	0.07	0.10	-0.20	-	**0.53***	**-0.76****	**-0.58***
OC	0.17	0.26	0.09	0.34	-0.23	-0.18	-0.40	0.23	-	**-0.17**	**-0.11**
DF	0.23	0.02	0.05	0.05	-0.53*	-0.38	0.28	-0.26	-0.01	-	**0.80****
VP	0.36	0.21	0.59*	0.18	-0.18	-0.64*	0.17	-0.27	0.06	0.63*	-

Genotypic correlation coefficient are marked in bold; ToH- total plant height, TH - technical height, StY - stem yield, FC - fibre content, SY - seed yield, HI - harvest index, VpP - vessels per plant, SW - 1000 seed weight, OC - oil content, DF - days to flowering, VP - days to early yellow ripening stage; * − correlation significant at $p \leq 0.05$; ** − at $p \leq 0.01$

The similar results [7], [10], [25] were obtained that genotypic correlation coefficients were higher than their respective phenotypic correlation coefficients for most of the characters. A study by [26], [27] has revealed that genotypic correlations are higher because of environment had a small role in the expression of the traits, which suggests an inherent association between these traits at the genetic level. In the present study, stem yield showed a positive significant genotypic and phenotypic relationships with total plant height (r_g=0.70**; r_{ph}=0.62*) technical height (r_g=0.70**; r_{ph}=0.57*) and phenotypic relationship with days to early yellow ripening stage (r_{ph}=0.59*). This fact suggests that flax accessions consist genotypes were showed the productivity of stem yield when are the highest plant heights and length of vegetation period. However, in this study stem yield and days to early yellow ripening stage have only phenotypic correlation where open the possibility find out for breeding of early highly productive genotypes. [28], [29] also drew similar conclusions under low correlation between these characters. The negative significant at genotypic and phenotypic level showed relationships harvest index with stem yield (r_g= -0.63*; r_{ph}=-0.80**), total plant height (r_g= -0.55*; r_{ph}= -0.54*), technical height (r_g= -0.59*; r_{ph}= -0.54*).

The positive significant genotypic and phenotypic relationship showed between seed yield and harvest index (r_g=0.76**; r_{ph}=0.56*) and at phenotypic level with vessels per plant (r_g=0.75**; r_{ph}=0.56*) as well significant negative at genotypic level with oil content (r_g=-0.53*). Similar results a findings about seed yield at phenotypic level and at both levels have been reported by [7], [30] – [34]. This analysis was indicated that for fibre flax the highest seed yield when the highest harvest index and vessels per plant.

The inter correlation between yield components characters may affect the plant breeding for component traits either in favourable or unfavourable direction. The positive significant genotypic and phenotypic relationship showed between technical height and total plant height (r_g=0.98**; r_{ph}=93**). The oil content showed a positive significant only at genotypic level relationships with fibre content (r_g=0.64*), 1000 seed weight (r_g=0.53*) and significant negative with vessels per plant (r_g=-0.72**). The 1000 seed weight showed a negative significant at genotypic level with days to flowering and days to early yellow ripening stage (r_g=-0.76**; r_g=-0.58*).

The flax yield formation of the majority of characters depends not on one factor, but on factors system and interaction between abiotic and biotic stresses. The new flax varieties should be resistant to lodging and diseases [35]. In this study the powdery mildew, anthracnose and pasmo severity index variable between the genotypes from 2015 to 2018. The powdery mildew severity index was identified the lowest range of genotypes ‘Vilani’, ‘T36-2’, ‘T36-1’ and highest ‘S29-2’ during four years period “(Fig. 2.)”. The flax genotypes were identified as more susceptible to powdery mildew in the dries years. The all genotypes were showed quite low susceptible to powdery mildew with DSI range from 2.50 to 7.92% and statistically not significant between genotypes.

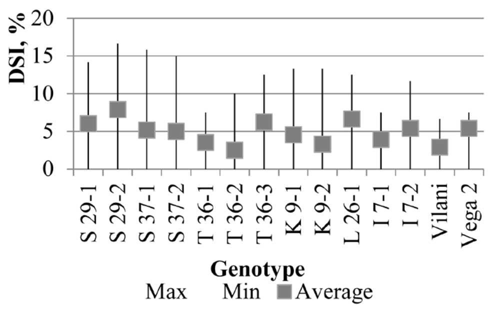

Fig. 2. Powdery mildew severity index during early yellow ripening stage of flax genotypes from 2015 to 2018 ($LSD_{0.05}$ = 8.61)

Anthracnose severity index of flax was identified the lowest range of genotypes ‘Vilani’, ‘Vega 2’, ‘T36-2’ and highest ‘I7-2’ during 4 year period “(Fig. 3.)”. The flax genotypes were showed more susceptible to anthracnose in the humidity years. All genotypes were observed quit low susceptible to anthracnose with average DSI range from 1.04 to 11.25% and statistically not significant between genotypes.

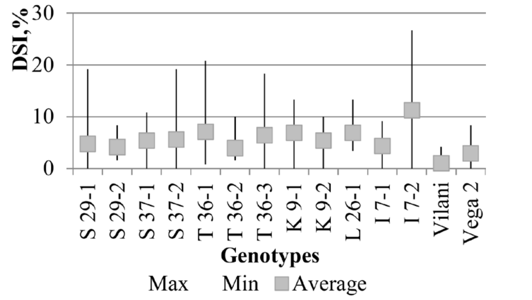

Fig. 3. Anthracnose severity index during early yellow ripening stage of flax genotypes from 2015 to 2018 ($LSD_{0.05}$ = 10.30)

Pasmo occurrence on the flax was identified more in the high humid conditions. The pasmo severity index lowest range of genotypes 'T36-1', 'T36-2', 'Vilani' and statistically significant ($p \leq 0.05$) highest genotypes 'S29-1', 'S29-2' was identified "(Fig. 4.)". The DSI average ranged from 1.46 to 13.13%.

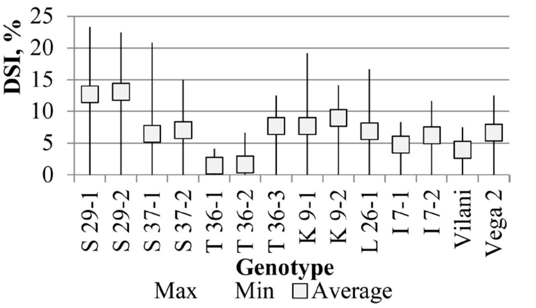

Fig. 4. Pasmo severity index during early yellow ripening stage of flax genotypes from 2015 to 2018 ($LSD_{0.05}$ = 9.60)

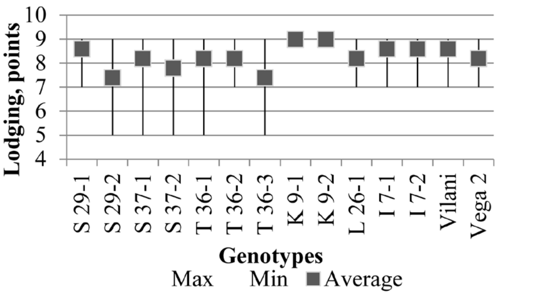

Fig. 5. Lodging during early yellow ripening stage of flax genotypes from 2014 to 2018

The resistance of flax to lodging between genotypes is variable from 2014 to 2018 "(Fig. 5.)". Highest resistance was identified of genotypes 'K9-1' and 'K9-2' as well lowest 'S29-2' and 'T36-3' and its reached up to 5 points in the certain years at the highest humidity conditions.

Summary was identified most perspective genotype of 'Vilani' with quit low susceptibility to anthracnose (1.04%), pasmo (3.96%) and powdery mildew (2.92%) and resistance (9) to lodging.

IV. Conclusions

The flax accessions 'Vilani', 'L26-1', 'K9-1', 'T36-1', 'S37-1' exhibited significant highest stem yield and technical height comparing to standard variety 'Vega 2' and are most valuable and perspective genotypes for flax breeding.

The information on the correlation of yield with related traits is the prerequisite to forming an effective plant breeding strategy aimed at its improvement. Genotypic and phenotypic correlations between yield and yield components were identified that total plant height, technical height and days to early yellow ripening stage played a major role on stem yield as well vessels per plant and harvest index on seed yield for fibre flax genotypes under Latvian condition.

Between all fax genotype were obtained most promising genotype 'Vilani' with complex highest resistance to fungal diseases and good lodging resistance.

V. Acknowledgements

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