Response of some introduced genotypes of European rye crop (*Secale cereale* L.) to different seeding rates

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Abstract:

A field experiment was conducted at the Second Research Station of Agriculture College, Al-Muthanna University, in Al Bandar area (which is located 3 km southwest of the center Al-Muthanna Governorate at a longitude of 45.26 and a latitude of 31.31) during the 2022-2023 agricultural season. To study the effect of four seeding rates (80, 100, 120, 140) kg ha^{-1}, represented by the symbols S1, S2, S3, S4, on most growth traits of three genotypes (Krzuca v1, Daukowskie zlote v2, Horyzo v3) of the Rye crop. The experiment was carried out in a split-plot with (R.C.B.D) design with three replicates, with seeding rates occupying the main plots and genotypes occupying the subplots. The results of the experiment showed the following:

Daukowskie zlote genotype outperformed Krzuca genotypes in the height of the plant (131.64 cm) and the number of tillers (273.0 stalks m^{-2}), while Horyzo genotype outperformed Daukowskie zlote genotypes in the number of days from germination to 50% flowering (103.42 days), While Krzuca genotype was superior in biological yield. As for seeding rates, the 100 kg ha^{-1}level outperformed the 80 kg ha^{-1} level in the number of tillers (298.5 stalks m-^{2}), and the 120 kg ha^{-1} level outperformed the 100 kg ha^{-1} level in the number of days from 50% flowering to physiological maturity (60.78 days). At the interaction between the two factors, the combination (Horyzo × 120) outperformed the other combinations in the height of the plant (141.93 cm), and the combination (Horyzo × 100) outperformed the other combinations in the number of tillers (352.9 stalks m-^{2}) and biological yield.

Keywords: Rye; *Secale cereale* L.; split-plot design; days number from emergence to 50% flowering; plant height; tillers number.

Interaction :

Secale cereale L. is a cereal crop that belongs to the Poaceae family. It is the second most important crop for bread and other pastries [1]. Its products have a role in reducing human body weight because they are rich in dietary fiber [2]. Its grains contain a starch content ranging from 69% to 73% [3] and a protein content of 10.08% to 15.25%, of which the average (albumin, globulin) constitutes about 55% and is not able to form gluten when its flour is mixed with water. The content of (prolamin glutenin) in rye grains is about 45% of the total protein content. The storage proteins of the endosperm of rye grains are called "secalin" and have a fat content of 0.70% in addition to other minerals such as P, Mg, Ca, Fe, Zn, and Cu [4] [5] [6]. The global cultivated area was about 4,403,020 hectares, with a production of 11,274 million tons in 2018 [7] [8].

The introduction of high-yielding genotypes that are adapted to environmental conditions is the basis for expanding the crop's agricultural area and increasing its production, in addition to paying attention to other service factors [9], including planting at the optimum plant density, which is most important (preparing a good seedbed, soil fertility, the variety grown, the size of the grains, the germination rate, and the planting date) [10]. The amount of seed and the method of distributing plants in a unit area have a significant impact on the three yield components (spike number, number of grains per spike, and grain weight) in field crops [11]. Therefore, it is necessary to determine the optimum seed rate, as it plays an important role in increasing grain yield and increasing dry matter [12].

This study aims to:

- Evaluating the performance of the introduced genotypes for the rye crop under the environmental conditions of Muthanna Governorate and identifying the best ones in response to those conditions through growth characteristics.
- Determine the appropriate amount of seed as it is one of the crops grown for the first time in Iraq.
- Determine the best interaction between genotypes and seed quantity and determine the best growth for these combinations.

Materials and Methods

Location and design of the experiment

A field experiment was conducted in Muthanna governorate during A field experiment was conducted in Muthanna governorate during the 2022-2023 winter season at the Second Research Station of Agriculture College, Muthanna University in the Al Bandar area. The experiment was conducted using a split-plot design with a randomized complete block design (RCBD) with three replicates. The seeding rates were the main plots, while the genotypes were placed in the subplots. The factors were randomly distributed within each block, resulting in a total of 36 experimental units (3 × 4 × 3) and the area of the experimental unit was (4) m^2.

The type of soil in which the experiment was conducted was (Silty loam). Table (1) shows the most important chemical and physical properties of the field soil.

Table (1) some chemical and physical properties of soil

Chemical properties				Physical properties				
Texture	**Clay**	**Silt**	**Sand**	**K**	**P**	**N**	**EC**	**pH**
	%			mg\kg			ds\ m	
Silty loam	30	42.5	27.5	169.5	14.5	25.15	3.8	7.32

Experiment factors:

The first factor: Four seed quantities of rye crop seeds occupied the main panels of the experimental units, which are (80, 100, 120, and 140) kg ha^{-1} by the symbols S1, S2, S3, S4.

The second factor: Three genotypes introduced from the European rye crop occupied the secondary panels of (Krzuca, Daukowskie zlote, Horyzo) by the symbols V1, V2, V3 Experimental units

These genotypes were obtained through introduction from Poland, noting that they are approved varieties in that country [13] and as shown in Table (2).

Table (2) the date of adoption of the introduced genotypes in the country of origin

genotype name	Entry year	Year of official accreditation in the country of origin
Krzuca	2018	2013
Daukowskie zlote	2018	1968
Horyzo	2018|	2011

Field operations

Preparation and cultivation of the soil before planting was carried out, including cleaning and removing the remains of the previous crop, plowing the land allocated for the experiment using a reversible moldboard plow in a perpendicular manner, smoothing it with disk harrows, and then leveling it using a leveling machine. The field was divided into 36 experimental units according to the design used, and the area of the experimental unit was (4) m^2. A hand-operated machine was used to adjust the division of the experimental unit into 10 rows, with a distance of 20 cm between each row.

The seeds of the genetic compositions were planted on November 16, 2022, and were fertilized with urea fertilizer at a rate of 120 kg ha^{-1} (N 46%) in two installments, the first in the germination stage and the second in the tillering stage. The phosphate fertilizer was applied at a rate of 80 kg ha^{-1}(P21%) in the form of triple superphosphate in one installment before planting. The potassium fertilizer was applied in the form of potassium sulfate at a rate of 80 kg ha^{-1}(K42%) in one installment before planting, based on the recommendation for wheat crop [14]. Irrigation and weeding operations were carried out whenever necessary. The genetic compositions were harvested on May 10, 2023.

Studied attributes

The studied traits were:

- No. of days number from germination to 50% flowering (day)
- No. days number from 50% flowering to physiological maturity (day)
- Plant height (cm)
- Tillers number (tillers m^2)
- Biological yield (t ha^{-1})

Statistical analysis

The data were analyzed using the statistical program GenStat.12.1 according to a randomized complete block design with a statistically split-plate arrangement, and the means were compared using the least significant difference (L.S.D.) test at a significance level of 0.05 [15].

Results and Discussion

1- no. of days from germination to 50% flowering (day)

The results of Table (3) showed that there was a significant effect of the genotypes only on the number of days from germination to 50% flowering, while the seed rates and the interaction had no significant effect on this trait.

The results showed that there was a significant effect of the genotypes on the number of days from germination to 50% flowering, with the V3 genotypes recording the highest mean for this trait at 103.42 days, with no significant effect on the V1 genotypes with a mean of 102.67 days. Meanwhile, the V2 genotypes gave the shortest duration for the number of days from germination to 50% flowering at 100.92 days. Perhaps the reason for the superiority of the two genotypes mentioned above is due to the difference in the genotypes in their thermal requirements. The V3 and V1 genotypes were able to accumulate the heat units required for flowering for a longer period than the other compositions. This indicates the size of the genetic variation between the introduced genotypes. This result is in agreement with the findings of [16] and [17] in wheat, who confirmed the difference in varieties in the number of days from germination to 50% flowering.

Table (3) Effect of rye crop genotypes, seeding rates, and their interaction on days number from germination to 50% flowering (day)

Genotype (V)	Seeding rate (S)				Average genotypes
	S1	S2	S3	S4	
V1	100.33	100.67	104.67	102.00	102.67
V2	99.00	102.33	101.33	101.00	100.92
V3	101.67	103.00	104.33	104.67	103.42
Average seeding rates	100.33	103.00	103.44	102.56	
L.S.D $_{0.05}$	S		V	V×S	
	N.S		1.523	N.S	

2- *no. of days from 50% flowering to physiological maturity (day)*

The results of Table (4) showed that there was a significant effect of the seeding rates only on the number of days from 50% flowering to physiological maturity, while the genotypes and the interaction had no significant effect on this trait.

The seeding rates had a significant effect on this trait, with the S3 seed rate giving the highest mean for this trait at 60.78 days, with no significant difference from the S1 and S2 seed rates, which gave 58.00 and 59.11 days, respectively. Meanwhile, the S4 seed rate gave the lowest mean for this trait at 53.11 days. This result is in agreement with the findings of [18] in wheat and [19] in oats.

Table (4) Effect of rye crop genotypes, seeding rates, and their interaction on no. of days from 50% flowering to physiological maturity (day)

Genotype (V)	Seeding rates				Average genotypes
	S1	S2	S3	S4	
V1	58.33	58.00	60.33	53.00	57.42
V2	59.33	61.33	59.33	53.67	58.42
V3	56.33	58.00	62.67	52.67	57.42
Average seeding rates	58.00	59.11	60.78	53.11	
L.S.D 0.05	S		V	V×S	
	4.463		N.S	N.S	

3- Plant height (cm)

The results of Table (5) showed that there was a significant effect of the genotypes and the interaction on the trait of plant height, while there was no significant effect of the seed rates for this trait.

The genotypes had a significant effect on the trait of plant height, with the V2 genotypes giving the highest mean for this trait at 131.64 cm and not significantly different from the V3 genotypes, which gave a mean of 129.49 cm. Both of these compositions significantly outperformed the V1 genotypes, which recorded the lowest mean for this trait at 112.13 cm. The difference in the genotypes of rye in the trait of plant height may be attributed to the difference in the lengths of the internodes, especially the upper internode, which represents about half of the plant height. This result is in agreement with the findings of [20], [21] in rye and [22] in wheat, who pointed out that there is a difference between varieties in the trait of plant height.

The interaction was significant between the factors of the experiment, the genotypes and the seed rates in the trait of plant height. The treatment (V3 × S3) recorded the highest mean for this trait at 141.93 cm, while the treatment (V1 × S3) recorded the lowest mean for this trait at 103.37 cm. The reason for the superiority of this combination may be attributed to the fact that the V3 genotypes were superior in the factor of genotypes and are single, based on their genetic nature. In addition, level S3, although not significantly superior, was the highest of the remaining seed rates.

Table (5) Effect of rye crop genotypes, seeding rates, and their interaction on Plant height (cm)

Genotype (V)	Seeding rates				Average genotypes
	S1	S2	S3	S4	
V1	132.23	108.27	103.37	104.63	112.13
V2	123.63	132.10	134.77	136.07	131.64
V3	121.53	128.17	141.93	126.33	129.49
Average seeding rates	125.80	122.84	126.69	122.34	
L.S.D 0.05	S		V	V×S	
	N.S		3.450	7.679	

4- Tillers number (tillers m^2)

The results of Table (6) show that there was a significant effect of the genotypes, the seed rates, and the interaction between them on the trait of number of tillers.

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The results showed that there was a significant effect between the genotypes in the trait number of tillers, with the V2 genotypes significantly outperforming the V1, recording the highest mean for this trait at 273.0 tillers m-^{2}. The V3 genotypes were not significantly different from the V2 genotypes, which recorded a mean of 272.5 tillers m-^{2}. Both of these compositions significantly outperformed the V1 genotypes, which recorded the lowest mean for this trait at 247.3 tillers m-^{2}. The reason for this difference may be attributed to the genetic differences between the genotypes in the trait number of tillers due to the ability of the genotypes to tiller. This is in agreement with the findings of [17] in wheat and [23] in durum wheat, who pointed out that there was a significant difference between the genotypes or varieties in the number of tillers.

As for the seeding rates, they had a significant effect on the trait number of tillers, with the S2 seed rate giving the highest mean for this trait at 298.5 tillers m-^{2}. This mean was not significantly different from the S3 seed rate, which gave a mean of 290.8 tillers m-^{2}. Both of these seed rates significantly outperformed the S1 seed rate, which gave a mean of 238.3 tillers m-^{2}. The S4 seed rate gave the lowest mean for the number of tillers at 229.4 tillers m-^{2}. The increase in the number of tillers in the S2 seed rate may be attributed to the fact that it falls within the appropriate limits for tillering. This can be attributed to the fact that plants growing under these conditions are driven to increase the number of their tillers by the number of plants growing in conditions of higher plant density because they are in competition. The number of plants in a unit area is the determinant of the number of tillers in a plant. This result is in agreement with the findings of [24] in barley, who confirmed in his study that seed rates may differ significantly in the trait number of tiller.

As for the interaction between the levels of the study factors, it gave a significant effect between the genotypes and seed rates for the trait number of tillers. The treatment (V3 × S2) gave the highest mean for this trait at 352.9 tillers m-^{2}, while the treatment (V1 × S4) gave the lowest number of tillers with a mean of 172.5 tillers m-^{2}. The reason for the superiority of the above combination may be attributed to the superiority of the factors when they are separate, which led to the superiority of the interaction in this trait. The reason for the superiority was mentioned in the explanation of the individual factors.

Table (6) Effect of rye crop genotypes, seeding rates, and their interaction on Tillers number (tillers m^2)

Genotype (V)	Seeding rates				Average genotypes
	S1	S2	S3	S4	
V1	286.7	331.2	198.7	172.5	247.3
V2	230.4	211.2	348.8	301.7	273.0
V3	197.9	352.9	325.0	214.2	272.5
Average seeding rates	238.3	298.5	290.8	229.4	
L.S.D 0.05	S		V	V×S	
	12.21		8.68	17.34	

5- Biological yield (t ha^{-1})

The results of Table (7) showed that there was a significant effect of the genotypes and the interaction on the trait of biological yield, while the seed rates did not have a significant effect on this trait.

The results indicated that there was a significant effect of the genotypes on the trait of biological yield, with the V1 genotype significantly outperforming the others, recording the highest mean for this trait at 18.45 t ha^{-1}, with no significant difference from the V3 genotype, which gave a mean of 17.66 t ha^{-1}. Both of these compositions significantly outperformed the V2 genotype, which gave the lowest biological yield with a mean of 15.25 t ha^{-1}. The reason for the superiority of the V1 genetic composition may be attributed to its superiority in the number of days from germination to 50% flowering (Table 3), which led to the production and accumulation of photosynthetic products that differ from one composition to another depending on the degree of adaptation of the genotypes to the prevailing conditions. This is the result of the efficiency of its vegetative cover in intercepting the maximum possible amount of sunlight during its growth period, which caused an increase in net photosynthesis. This was also helped by the small number of its tillers per unit area (Table 6), which means less competition for light between the plants and more interception of light on the one hand, and less competition for the high yield of photosynthetic materials, which increased the weight of the plant on the other hand, and this was reflected in the biological yield. This is in agreement with what was indicated by [17] in wheat, who found a significant difference between the genotypes in the trait of biological yield.

The interaction between the genotypes and seed rates gave the combination (V3 × S2) the highest mean for this trait at 21.46 t ha^{-1}, with a significant difference from the combination (V2 × S3), which recorded the lowest mean of 13.56 t ha^{-1}. This disparity between the two combinations is attributed to the difference in the state of interaction between the genetic and environmental aspects from one composition to another.

Table (7) Effect of rye crop genotypes, seeding rates, and their interaction on biological yield (t ha^{-1})

Genotype (V)	Seeding rates				Average genotypes
	S1	S2	S3	S4	
V1	14.80	18.74	20.70	19.55	18.45
V2	15.07	18.05	13.56	14.30	15.25
V3	19.13	21.46	16.00	14.05	17.66
Average seeding rates	16.34	19.42	16.75	15.97	
L.S.D 0.05	S		V	V×S	
	N.S		1.234	3.066	

Conclusions

The genotype Daukowskie zlote was superior in the trait of plant height and number of tillers, while the genotype Horyzo was superior in the number of days from germination to 50% flowering, Krzuca genotype was superior in biological yield. As for the seed rates, the level of 100 kg t ha^{-1} was superior in the number of tillers, while the level of 120 kg t ha^{-1} was superior in the number of days from 50% flowering to physiological maturity. When the two factors interacted, the combination (Horyzo × 120) was superior in the trait of plant height, while the combination (Horyzo × 100) was superior in the number of tillers and biological yield.

Table (8) Analysis of variance for the studied traits represented by means of squares (M.S) for some growth traits

Sources of difference	Refined	Seed rates	mistakeA	Genotypes	Interference	mistakeB
Degrees of freedom	2	3	6	2	6	16
Days number from germination to 50% flowering	2	17.185	8.519	*19.750	2.602	3.097
Days number from 50% flowering to physiological maturity	2	*97.806	14.972	4.000	7.889	5.417
Plant height	2	41.53	29.89	**1374.25	**417.04	14.99
Tillers number	2	11282.8	112.1	**2595.4	**17820.7	100.7
Biological yield	2	22.066	5.284	**33.420	**20.809	2.035

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