

Landraces and Wild Species of the *Secale* Genus in the Georgia (Caucasus Ecoregion)

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Abstract

Genus of *Secale* contains one cultivar rye and five wild species in the territory of Georgia, Caucasus ecoregion. Historically, cultivar rye (*Secale cereale*) was distributed in the territories of Georgia from lowlands to high mountain areas at high altitudes of 2300 m. *S. cereale* had 14 varieties in many areas of Georgia and 5 varieties are distributed only on territories of Caucasus ecoregion. Some varieties had erosion and degradation and their seed material are distributed to genbanks. Two semi-wild ryes (*S. segetale* and *S. vavilovii*) growing as weedy rye in the fields with wheat and barley from lowlands at elevations higher than 1400 m and are related to semi-arid climates in eastern and south territories of Georgia. Two wild species (*S. anatolicum* and *S. montanum* subsp. *kuprijanovii*) are located on high forest zone and on subalpine meadows at higher elevations of 2300 m to lesser and Western Greater Caucasus Mountains. Another wild species (*S. sylvestre*) grows on lowlands at 200 m from Black Sea dunes in Georgia. Morphometric analysis revealed similarity between cultivated rye and these wild species. This hypothesis was proposed that cultivar rye forms can arise as a result of interspecific hybridization processes between studied wild species.

Keywords: Rye cultivar; CWRs; *Secale* genus; Taxonomy; Weedy rye

Abbreviations: CWRs: Crop Wild Relatives; SE: Standard Error; PCA: Principal Components Analyses; DFA: Discriminant Function Analysis; CDF: Canonical Discriminant Function; GMOs: Genetically Modified Organisms

Introduction

Rye – the genus *Secale* L. (Poaceae) includes the cultivated crops (*S. cereale*) and other five wild species which are distributed in the Georgia, Caucasus ecoregion. Rye is a member of the wheat tribe (*Triticeae*) and it is closely related to barley (*Hordeum*) and wheat (*Triticum*). Rye was used for making alcohol and as forage. Georgian population use rye for bread with wheat in the lowlands and for beer with barley in the high mountain areas [1,2]. The crop wild relatives (CWRs) are taxa related to species of direct socio-economic importance, which includes the progenitors of crops. According to modern concept of wild relatives, under CWRs we should understand all species related to cultivated crops of rye. Although, classical definition of CWRs is restricted only to species related to cultivated crops including such important field crops as wheat (*Triticum aestivum*), barley (*Hordeum vulgare*), rye (*Secale cereale*), oats (*Avena sativa*), sorghum (*Sorghum halepense*), proso (*Panicum spp.*), foxtail millet (*Setaria spp.*), grain legumes such as *Phaseolus*, *Vicia*, *Vigna*, *Lens*, *Lathyrus*, *Cicer* and some vegetables and fruit crops. Almost all landraces are associated to CWRs distributed on the territory of Georgia. Total of 31 plant families, 96 genera and

559 species were identified as wild relatives of ancient crops in Georgia [3].

Georgia is located in the South Caucasus with a territory of 69,700 square kilometers, and the country's population remains at least 3.73 million. It is a mountainous country made up of two separate mountain systems: the Greater Caucasus Mountain Range, lying northwest to east-southeast between the Black Sea and Caspian Sea; and the Lesser Caucasus Mountains, which run parallel to the greater range, at a distance averaging about 100 km south. Two thirds of the country is mountainous, with an average elevation of 1200 m. The highest peaks are Mount Shkhara (5068 m) in the Western Greater Caucasus and Mount Didi Abuli (3301 m) in the Lesser Caucasus [4]. The high mountain areas were suitable for cereal domestication because they are seasonal in climate, with a wide range of temperature and rainfall due to differences of altitude and aspect.

Archaeological data clearly show that the Caucasus, and particularly Georgia, was settled from prehistoric times, and agriculture was developed there during the Early Neolithic period [5]. Vavilov NI [6] in his work determines 8 centers of

crop origin and diversity. Among them is the 4th center which includes South Caucasus, Asia Minor, Iran and Turkmenistan. The main crops domesticated in this center are wheat, rye, oats, seed and forage legumes, fruits, etc., some 83 species. The importance of CWRs in their ability to exchange genes with the crops was first emphasized by Vavilov NI [6]. It is evident that natural crosses between crops and their wild relatives have occurred since the beginnings of agriculture. It is evident that natural crosses between crops and their wild relatives have occurred since the beginnings of agriculture. The fundamental work on domestication and origin of wheat and barley in this region was done by famous Georgian botanist Menabde V [7]. Most varieties of rye are growing from the lowlands to high mountain areas and they are local landraces and cultivars [8]. Wild species of genus *Secale* are located in different habitats and some reaches to the high mountain alpine zone and some wild species of this *Secale* genus are originated as crop wild relatives of rye cultivars [1].

Human has used CWRs germplasm to improve production and food quality of cultivars originated previously due to domestication of crop ancestor species. CWRs have already made substantial contributions to improving food production through the useful genes that they contribute to new crop varieties. We have found some wild species of the *Secale* genus in the territory of Georgia and determine their morphological size. The cultivated rye (*S. cereale*) called as 'Chvavi' and remains in high mountain areas of Svaneti. One wild species (*S. segetale*) called 'Svila' is widespread as weedy rye in wheat and barley fields and it is harvested together with them. The bread of wheat with 'Svila' is considered to be very nutritious and has good taste. An endemic species of rye is *S. vavilovii*. It is also called 'Caucasian rye'. This species was found in wheat field in Georgia [7]. One species (*S. sylvestre*) is distributed in Black Sea coast habitats and two

species (*S. anatolicum* "Mountain Rye" and *S. montanum* subsp. *kuprijanovii*) are oriented in high forest zones and subalpine meadows. They have provided resistance to pests and diseases in a wide range of crops. The genes that come from CWRs and other wild plants make a direct contribution to increased human well being through improving agricultural production and maintaining sustainable agroecosystems. Therefore, the effective conservation and sustainable use of CWRs and all wild plants are essential elements for increasing food security, eliminating poverty and maintaining a healthy environment.

Materials and Methods

Plant material

A total 120 individuals of 5 wild species and one cultivated rye (*S. cereale* L.) were sampled in natural habitats and agrarian fields (Table 1). There are 5 wild CWRs and naturalized species of rye in Georgia:

1. *Secale anatolicum* Boiss. (SAN)
2. *S. montanum* subsp. *kuprijanovii* Grossh. (SMK)
3. *S. segetale* (Zhuk.) Roshev. (SSE)
4. *S. sylvestre* Host (SSY)
5. *S. vavilovii* Grossh. (SVA)

All these species has different names for Latin as synonyms and subspecies. They according to other classification systems and these species are synonyms. However, these names are remained in Caucasian and Georgian Flora [9]. Distribution sites with coordinates and elevation data have been determined for all species. Chromosome numbers are known for all publications (Table 1).

Table 1: Cultivars and wild species of *Secale* genus distribution in Georgia: location with coordinates with degrees and minutes, elevation with above sea level in meters, gene pool (GP) and number of chromosomes (N = 6).

Species	Location	Coordinates	Elevation (m)	Chromosome Numbers	Primary Gene Pool
<i>S. anatolicum</i>	Samtskhe-Javakheti region	N 41°20'/41°28' E 43°10'/43°20'	1300-2300	2n=14	GP2
<i>S. cereale</i>	Georgia	N 41°02'/43°34' E 40°00'/46°43'	300-2300	2n=7; 14; 28	GP1A
<i>S. montanum</i> subsp. <i>kuprijanovii</i>	Abkhazeti, Svaneti, Racha	N 42°70'/43°50' E 40°46'/43°42'	900-2300	2n=14	GP2
<i>S. segetale</i>	Kakheti, Kartli, Meskhети	N 41°10'/41°60' E 42°55'/46°23'	300-1400	2n=14	GP1B
<i>S. sylvestre</i>	Black Sea coast	N 41°37'/43°24' E 40°05'/41°31'	10-200	2n=14	GP3
<i>S. vavilovii</i>	Kakheti, KvemoKakheti	N 41°15'/42°03' E 45°00'/46°05'	250-1300	2n=14	GP1B

Methodology

Cultivated rye (*S. cereale*) involves the comparison of 'total' natural CWR rye diversity as already actively conserved either *in situ* or *ex situ*. This is the basis for gap analysis, which can be divided into four consecutive steps [10]. Assessment of the effectiveness of current conservation coverage in relation to natural *in situ* diversity identifies the element of diversity that is under conserved, i.e. the 'gaps' in the existing conservation strategy and helps refocus the strategy to conserve the maximum diversity and fill these gaps. The revised priorities are likely to require complementary *in situ* and *ex situ* conservation actions to ensure the comprehensive conservation of the target taxon's gene pool. According to this concept three Gene Pools are distinguished as follows: Primary Gene Pool (GP-1) within which GP-1A are the cultivated forms and GP-1B are the wild or weedy forms of the crop; Secondary Gene Pool (GP-2), which includes less closely related species from which gene transfer to the crop is possible but difficult using conventional breeding techniques; Thus, combined use of the gene pool and taxa group concept proposed above provide the best pragmatic means available to determine whether a species is a CWR and how closely related a CWR is to its crop. Gene pool was related to CWRs study of *Secale* genus species (Table 1).

Statistical analyses

Mean and standard error (SE) were calculated for each quantitative descriptor datasets of stalks, leaf, spikes, etc. Means were compared using a one-way ANOVA post hoc range tests. Turkey's honestly significant difference test was used to assume equal variances, with $P < 0.05$. Individual F-values were computed for continuous variables of each quantitative leaf descriptor to determining the overall between-group differentiation. The test of independence (Chi-square) was used to investigate whether distributions of categorical variables differed from one another. For each classification, the differentiation between group mean vectors was assessed by the Wilks' Lambda multivariate statistic, which can be approximated by an F-test statistic for comparing between-group and within-group variability. Frequency and percentages of distribution of morphological traits were determined for qualitative descriptors.

The principal components analyses (PCA) were based on the covariance matrix of the coefficients and not on the correlation matrix, because coefficients with small variance and covariance values of harmonics of Fourier coefficients are generally not important for explaining the observed morphological variations of stalks, leaf, spikes, etc. shape, revealing a pattern of variation that is consistent with the distribution rate of wild species and cultivated rye. Stepwise discriminant function analysis (DFA) was used to determine which quantitative stalks, leaf, spikes, etc. shape traits are more useful for discriminating among the studied taxa. The significance level corresponding to the F-value for entering or removal on a specific trait at each step was set at

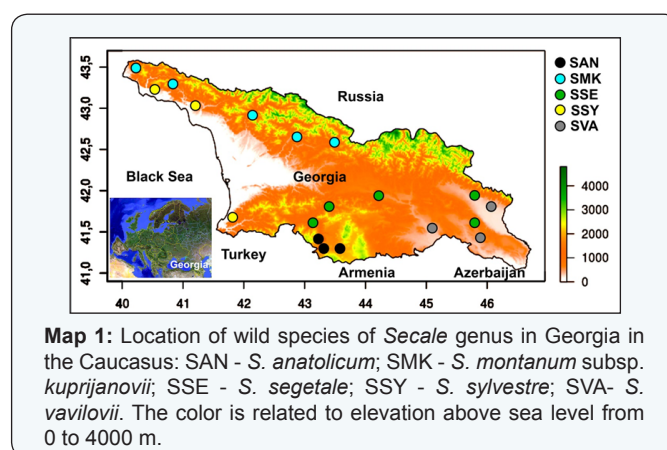
$P < 0.05$ and $P < 0.1$. For the selected traits, Mahalanobis distances have been used. All traits that remained in the model when the selection process stopped were considered to discriminate significantly between species. Canonical discriminant function analyses (CDF) and predicted group membership classification were performed. In the classification, wild species were used both as two groups and in other calculation as separate cultivars.

Hierarchical cluster analyses were done by Statistica 6.0 software; this method uses an analysis of variance approach to evaluate the distances between clusters. This attempts to minimize the Sum of Squares of any two (hypothetical) clusters that can be formed at each step. The distance measure interval is Euclidean distance, computing distances between objects in a multidimensional space. The analysis was performed using the software packages SPSS v.16.0 for Windows and Statistica 6.0.

Results

Elevation of *Secale* genus species

Two wild species (*S. anatolicum* and *S. montanum* subsp. *kuprijanovii*) are distributed on mountain slopes. *S. anatolicum* is located to Lesser Caucasus Mountains and *S. montanum* subsp. *kuprijanovii* is in Western Greater Caucasus Mountains. These species are located on high forest zones and on subalpine meadows at elevations of 2300 m in different coordinates (Map 1; Table 1). *S. montanum* subsp. *kuprijanovii* is accepted as endemic species of the Caucasus in Georgia and Russia but it is noted for western Black Sea coasts and Asia Minor. Two semi-wild ryes (*S. segetale* and *S. vavilovii*) are mixed as weedy ryes with wheat and barley in the fields both in lowlands at elevations higher than 1400 m a.s.l. and are related to semi-arid climates in eastern and south territories of Georgia. Cultivated rye (*S. cereale*) grows at elevations of high mountain areas at 2300 m (Table 1). One wild species *S. sylvestre* grows on friable sandy soils and Black Sea dunes in Georgia (Map 1). It is found in sandy steppes in Eastern Europe.



Map 1: Location of wild species of *Secale* genus in Georgia in the Caucasus: SAN - *S. anatolicum*; SMK - *S. montanum* subsp. *kuprijanovii*; SSE - *S. segetale*; SSY - *S. sylvestre*; SVA - *S. vavilovii*. The color is related to elevation above sea level from 0 to 4000 m.

Primary gene pool

Cultivated rye (*S. cereale*) is crop breeding and evaluation with GPA1 (Table 1) and it is not distributed in natural habitats

and grows only in the fields. Historically, it was growing in many areas of Georgia and 14 varieties are determined in 1930s years. Five varieties are distributed only on territories of Caucasus ecoregion: var. *fuscum* – brown-spiked; var. *nigrescens*– black-spiked; var. *armeniacum* – red, pubescent; var. *persicum* – brown, var. *pubescent*; var. *laxum* –open spiked. As far as wild-growing, *S. cereale* is concerned to two wild species - *S. montanum* subsp. *kuprijanovii* (GP1B) and *S. segetale* (GP1B). Other two species (*S. anatolicum*; *S. vavilovii*) are belonging to the same section as crops (GP2). *S. sylvestre* has different morphological data and has no concern to Georgian cultivated rye varieties (GP3). Chromosome numbers are similar for all wild species ($2n=14$) and varieties of cultivated rye (*S. cereale*) are with many polyploidization and mutations ($2n=7; 14; 28$).

Morphological characters

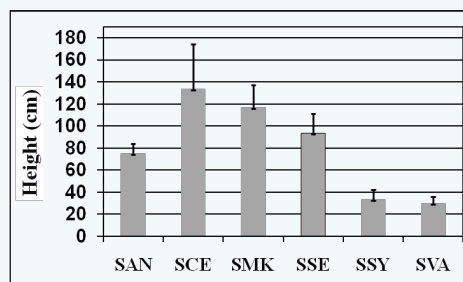


Figure 1: Mean and standard error (SE) of culms height (cm) of 6 species of *Secale* genus: SAN - *S. anatolicum*; SCE- *S. cereale*; SMK - *S. montanum* subsp. *kuprijanovii*; SSE - *S. segetale*; SSV - *S. sylvestre*; SVA- *S. vavilovii*. (N=120).

Table 2: Mean and standard error (SE) of elevations and morphological data, the results of one-way analysis (ANOVA) of variance. F-test and significance values are presented. Wilk's lambda and Chi-Square obtained by multivariable DFA on the base of the studied 5 wild species of *Secale* genus species and one cultivars (*S. cereale*) with elevations, culms height and diameters, leaf width, spike height, glume and lemma size in centimeters. (N=120).

Species	Elevation (m)	Culms height(cm)	Culms diameter (cm)	Leaf blade: width (cm)	Spike height(cm)	Glume (cm)	Lemma(cm)
<i>S. anatolicum</i>	1866,67±296,27	758.55	2.5±0.29	0.27±0.03	7±0.58	0.9±0.06	1.07±0.58
<i>S. cereale</i>	1333,33±578,31	133.3±40.55	4.67±0.88	0.97±0.15	9,67±2.89	2.67±0.33	1.5±0.01
<i>S. montanum</i> subsp. <i>kuprijanovii</i>	1966,67±145,30	116.67±20.28	5.67±0.33	1.4±0.31	11.33±0.67	1.13±0.07	1.37±0.12
<i>S. segetale</i>	683,33±381,15	93.33±17.64	4.67±0.88	0.63±0.07	10.3±2.89	1.1±0.21	1.5±0.04
<i>S. sylvestre</i>	103,33±54,87	34.23±8.82	1.67±0.32	0.23±0.03	5.87±2.31	1.93±0.23	1.08±0.01
<i>S. vavilovii</i>	665,67±328,30	30.2±5.77	0.5±0.03	0.7±0.06	6.2±1.15	0.93±0.07	1.23±0.15
One-way analysis of variance (ANOVA)							
Sum of Squares	8244000.0	27206.944	63.278	2.913	81.611	20.818	0.691
df	5	5	5	5	5	5	5
Mean Square	1648800.0	12885.833	12.656	0.583	16.322	4.164	0.138
F	4.715	10.096	14.018	9.364	1.354	0.884	6.379
Wilks' Lambda	0,034	0,000	0,002	0,245	0.654	0,511	0.001
Chi-Square	2.0	3.667	3.778	5.0	4.0	4.0	12.333
Significance	0.013	0.008	0.000	0.001	0.308	0.521	0.004

Morphological data shows differences between these wild species of rye (Figure 1 & Table 2). *S. montanum* subsp. *kuprijanovii* has most high culms (80-150 cm) and *S. anatolicum* is lower (60-90 cm). These species are growing in high mountains. Semi-wild rye (*S. segetale*) and cultivar rye (*S. cereale*) needs to 180-200 cm for stalks culms. Other species (*S. sylvestre* and *S. vavilovii*) are lower and have the less height of culms of 20-40 (50) cm. Stalks diameter (5-6 mm) is high in 3 species (*S. cereale*, *S. montanum* subsp. *kuprijanovii* and *S. segetale*). Differences of site are on leaves and spikes (Table 2). Spike high reaches to 15 cm in the same 3 species (*S. cereale*, *S. montanum* subsp. *kuprijanovii* and *S. segetale*). One-way ANOVA procedure rendered low significance levels ($P < 0.0001$) for all quantitative descriptors showing high level of between-group differentiation (Table 2). Glumes and

lemma acuminate with similar size and significance levels are high ($P < 0.308$; $P < 0.521$).

The classification system "cultivars" was used in DFA to differentiate between separate cultivar names and related wild species of rye and was based on morphological characters (Table 3). *S. cereale* showed very low percentage was between different wild species -*S. montanum* subsp. *kuprijanovii* and *S. segetale*. The DFA scatter plot shows distribution of the plots of 6 species types against the first two canonical discriminant functions axes (Figure 2). The three groups of *S. cereale* are located in the right and it has of middle part the plot, respectively. *S. montanum* subsp. *kuprijanovii* groups are shown on upper part. *S. Sylvestre* is located on lower part of the plot with lower high of elevation

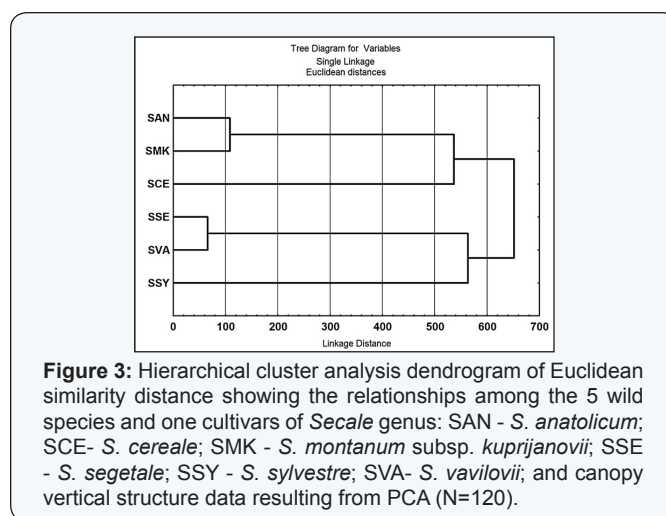
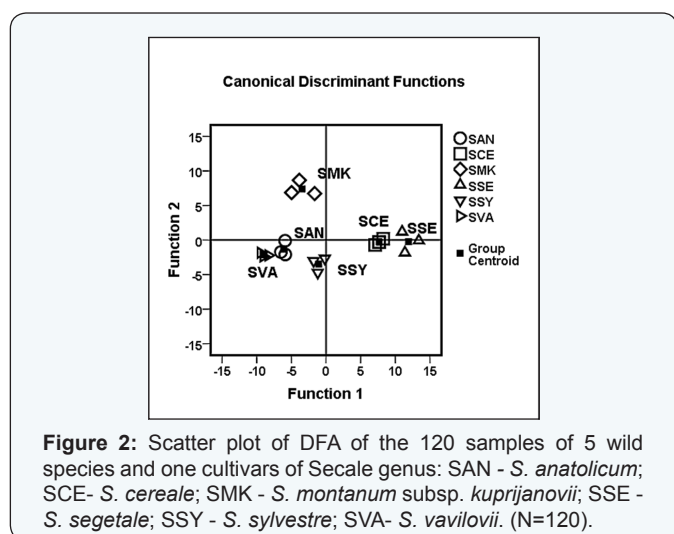
and culms height. This data shows very similar contact between the rye species (Figure 2).

Hierarchical cluster analysis dendrogram of Euclidean similarity distance showing similarity of several wild and cultivated rye species (Figure 3). The relationships among the 6 species of morphological data are reflected in the dendrogram of a hierarchical cluster analysis using Euclidean distance. The 6

species in the dendrogram are clustered into four main groups. *S. anatolicum* and *S. montanum* subsp. *Kuprijanovii* are contains from two clusters and they are growing in high mountains and have similar morphological data. *S. segetale* and *S. vavilovii* are contacted in cluster and they are growing on lowlands and semi-arid zones. *S. cereale* and *S. sylvestre* have contacts not to right with other species.

Table 3: Results of the DFA. Grouping variables of 5 wild species of genus *Secale* and one cultivar's (SCA) on descriptors of the leaf, culms and spike morphometric data and third grouping variables are based on PCs obtained by 3 from 6 morphological traits. (N=120).

Data after Grouping Variable							
Functions	Eigen value	% of Variance	Cumulative %	Canonical Correlation	Δ Wilks' lambda	Chi-square	Significance (P)
1	82.813	75.7	75.7	0.994	0.000	113.173	0.000
2	18.357	16.8	92.4	0.974	0.002	66.673	0.000
3	6.248	5.7	98.1	0.928	0.034	35.561	0.002
4	1.086	1.0	99.1	0.722	0.245	14.763	0.064
5	0.956	0.9	100.0	0.699	0.511	7.043	0071
Classification Data after Grouping Variable							
Group	SAN	SCE	SMK	SSE	SSY	SVA	Total
SAN	20	0	0	0	0	0	20
SCE	0	18	1	1	0	0	20
SMK	0	1	19	0	0	0	20
SSE	0	1	0	19	0	0	20
SSY	0	0	0	0	20	0	20
SVA	0	0	0	0	0	20	20
Classification percentage data after grouping variable							
Group	SAN	SCE	SMK	SSE	SSY	SVA	Total
SAN	100	0	0	0	0	0	100
SCE	0	90	5	5	0	0	100
SMK	0	5	95	0	0	0	100
SSE	0	5	0	95	0	0	100
SSY	0	0	0	0	100	0	100
SVA	0	0	0	0	0	100	100



Discussion

Georgia owns very old agricultural traditions that have preserved to our time. Mountain landraces of rye (*S. cereale*) and barley (*Hordeum vulgare* L.var. *nudum* Hook, *H. vulgare* var. *pallidum* Ser.) reach their highest elevations of 2300 m a.s.l. in v. Ushguli [2,11]. This village was very competitive with wheat and barley in high-mountainous regions. Nowadays, fields of ryes are found in v. Chunchkha in ground of peasant South Georgia, Meskheta. The naturalization of rye and its occurrence in the wheat fields as weed is normal in both Meskheta and Javakheti regions [12]. Often, rye seeds are mixed with wheat and appear on wheat fields. In mountains, it occupied abandoned wheat fields as weed. It is supposed that weedy form might be another species of rye (*S. segetale*) which is usually mixed with cultivated rye. The environmental conditions in the region are very good for distribution and cultivation of rye.

Genus *Secale* including several cultivated and wild species and *S. cereale* occurs wild as a weed among winter wheat in the Caucasus ecoregion and southern part of the Central Asia. This wild rye has recently been described by bensen as a distinct species, but in our opinion, it does not differ morphologically from cultivated rye and is directly involved in the origin of the latter. Vavilov NI [6] was the first to elucidate the problem of provenance of cultivated rye. According to his theory, the ancient cultivation of winter wheat carried rye with it as a weed. As wheat cultivation spread northward into more severe climatic conditions, rye, as a weed, began to displace the cultivated plant and thus marked the initiation of a new crop. As far as wild-growing *S. cereale* is concerned, it is closely related to a group of species referred to as *S. montanum* subsp. *kuprijanovii*, *S. anatolicum* and *S. vavilovii* an annual species with a brittle spike. According to Vavilov NI [6], rye was domesticated in the Near East region as a secondary weedy crop (*S. cereale* subsp. *segetale*) and only thereafter spread to European countries and was used as a distinct crop. Hybridization between cultivated wheat and rye has resulted in the triticale which has resistance to several diseases. The present-day weedy ryes with brittle and semi-brittle rachis are products of hybridization of the cultivated non-brittle *S. segetale* with wild rye *S. vavilovii*.

Several taxa have previously been recognized within genus *Secale*, but most of them are difficult or even impossible to distinguish morphologically. We recognize all 5 wild species as having contacts with cultivated taxa and the wild or weedy taxa that have more or less fragile rachis. The presence and distribution of the most important highly repetitive DNA sequences of rye in cultivated and wild species of the genus *Secale* were investigated using fluorescence in situ hybridization. Accurate identification of individual chromosomes in the most commonly recognized species or subspecies of the genus *Secale* (*S. anatolicum*, *S. cereale*, *S. montanum* subsp. *kuprijanovii*, *S. segetale*, *S. sylvestre*, and *S. vavilovii*). Transcaucasia specimens of *S. sylvestre* differ

from the type in low, strongly geniculate culms and long spikes, with relatively long awns. Additional accumulation of herbarium material will make it possible to test the homogeneity of *S. sylvestre* over its entire distribution area.

The origin of cultivated rye has been studied, taking into consideration evidence from various fields. Based on morphological resemblances and cytogenetic affinities, cultivated rye is included in *S. cereale*. Cultivated rye was selected from weedy ryes for non-brittle rachis and bigger caryopsis both unconsciously and consciously by man. It spread from this area as a weed in wheat and barley fields towards the north, east and west and imposed itself as a secondary crop under conditions unfavorable for wheat and barley. Triticale is a hybrid cereal derived from crossing wheat with rye. The objective in crossing the two cereals was to combine the desirable characteristics of wheat such as grain quality, productivity and disease resistance with the vigour and hardness of rye. Rye thus became a crop in its own right in several places independently, in addition to it being known by the people living in the Caucasus and Transcaucasia from very early agricultural times.

The natural populations of many species of CWRs are increasingly at risk. The primary causes of diversity loss of wild plant species are habitat loss, degradation and fragmentation. Many cereal CWRs, including wild wheat and millet species, occur in arid or semi-arid lands and are severely affected by over-grazing and desertification. Climate change is having significant impacts of species distributions and survival in a concrete habitat. One of the most important threats to the diversity of CWRs is genetic erosion and pollution. The threat of genetic pollution or introgression, either from genetically modified organisms (GMOs) or from conventionally bred crops, to wild species has become an increasing risk to the *in situ* genetic conservation of crop wild relatives.

The first sign of cereal domestication is the evidence that ears of cultivated *Secale* crops became less brittle in difference with their wild relatives characterized by easy shattering of spikes into spikelets upon maturity, which is essential for seed dispersal and survival in the wild, whereas forms with non-brittle ears survive only under cultivation. It is generally assumed that most Triticeae crops have been domesticated from their wild relatives by selection of non-shattering individuals which sporadically appear in wild populations as rare mutants. A hypothesis was proposed that rye and wheat forms with varying ear fragility may have arisen as a result of interspecific hybridization processes between different wild species.

Conclusion

Another problem is that many species of important *Secale* genus occur in centers of plant diversity and crop diversity located mainly in developing countries, which often lack resources to invest in the necessary conservation activities. South

Caucasus and Georgia in particular is the center of origin and diversity of many of the world's important crop plants. Although, additional resources are urgently needed in such areas of high diversity to identify priority species for conservation, determine the necessary conservation activities, monitor the status of key species, improve the use of these valuable resources.

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