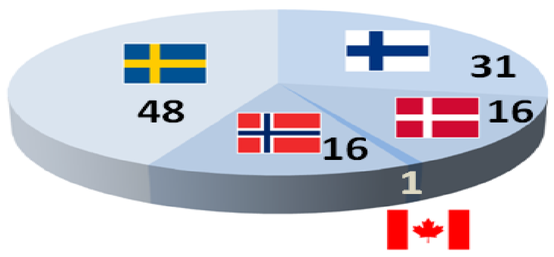
Duplicate accession identification in the VIR (Russia) and NordGen (Sweden) *Avena sativa* L. collections.

I. Perchuk[1*], A. Konarev[1], I. Loskutov[1], E. Blinova[1], L. Novikova[1], V. Horeva[1] and A. Kolodinska-Brantestam[2]
[1]Federal Research Centre – N.I. Vavilov Institute of Plant Genetic Resources (VIR), St. Petersburg, Russia
[2]Nordic Genetic Resource Center , (NordGen), Alnarp, Sweden
*e-mail: i.perchuk@ vir.nw.ru

Over time the collection (s) accumulated duplicate samples that require extra spending on its conservation and also leads to misrepresentation of the real level of the stored genetic diversity. In connection with the active cooperation of VIR and the NordGen it seems actual to search for possible duplicate cultivar accessions in their *Avena sativa* L collections.

Comparative study of Scandinavian and Canadian cultivar accessions was carried out both in the field and in the laboratory.



112 potential duplicate pairs (PDP)
were selected on the passport data base

1 (VIR) + 1 (norden) = **PDP**

cultivar accessions with the same name = PD-accessions

On the results of the Pushkin branch VIR field study PD-accessions were compared with each other by 26 morphological and breeding-valuable traits.

To evaluate the field differences of the earch pair PD- accessions ,the *D summ.* index was proposed . It accumulated the revealed differences both in qualitative and quantitative plant traits.

$$D_{summ.} = D_{quant.} + D_{qual.}$$

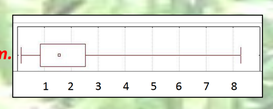
To assess differences by quantitative traits index $D_{quant.}$ was calculated according to the formula

$$D_{quant} = \sum_{i=1}^{m} \frac{|d_i|}{d_{max}}$$

d_i - the difference between the i-th trait values of the one pair PD-accessions
d_{max}- the i-th maximum difference value registered when comparing the PD accessions of all 112 pairs
m - quantitative trait number analyzed
To assess differences by qualitative traits index $D_{qual.}$ was calculated according to the formula

$$D_{qual.} = \sum_{i=1}^{n} p_i$$

p = 0 - the presence or the expression level trait was identical for both PD accessions
p = 1- traits are different
n - qualitative trait number analyzed



For all 112 pairs *D summ.* index value varied in the range of 0,1 ÷ 8,3.
***D summ.* variability structural analysis showed that its distribution is characterized by a pronounced right-sided asymmetry (the asymmetry coefficient was 1.83).**

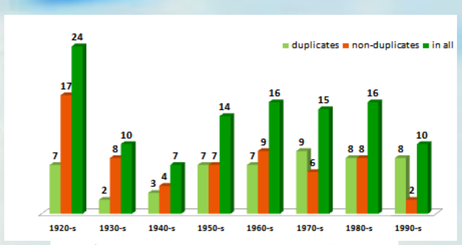
These data indicated that the tested oat sample was inhomogeneous and consisted of both duplicate and non-duplicate pair accessions. In accordance with *D summ.* Value, the PDPs were conventionally divided into three groups wherein duplicates could be identified with various degrees of probability.

Group 1 : the most likely duplicate pairs
***D summ.* 0.1- 1.5** — **56 pairs**

Group 2 : the duplicate and non-duplicate pairs
***D summ.* 1.6 – 3.9** — **46 pairs**

Group 3 : the least likely duplicate pairs
***D summ.* 3.9 – 8.3** — **10 pairs**

Electrophoresis of single seed avenins was used as a laboratory method. The accession composition was characterized in terms of the avenin biotypes frequency of occurrence with corresponding avenin banding patterns. Comparison of the PD- accession composition was performed by the Pearson $\chi 2$ criterion. Electrophoretic analysis proved that 46% of the 112 pairs may be regarded as duplicates, because their accessions had identical avenin biotypes composition.

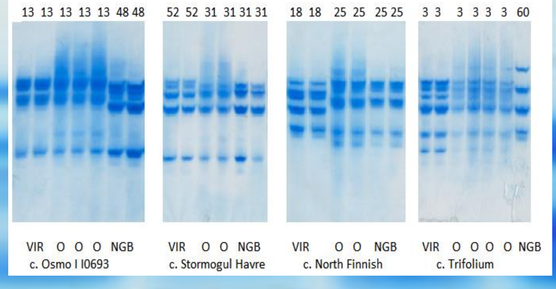


years of the original cultivar sample entering into the VIR collection

the number of VIR oat cultivars analyzed which are duplicate or non-duplicate with the corresponding cultivars of the NordGen collection.

Avenin biotype (avenin banding pattern) composition of some duplicate and non-dublicate accessions *Avena sativa* L (frequency of occurrence,%).

Cultivar name	Avenin biotype number, f %											
	7	12	13	18	25	26	28	42	52	79	86	96
Dublicate pairs												
Hvitling ,VIR			100									
Hvitling , NordGen			96		2				2			
Ribe ,VIR							100					
Ribe ,NordGen							100					
JO 0980 , VIR			67		4	2				23	2	2
JO 0980 , NordGen			72			2				26		
Non-dublicate pairs												
North Finnish ,VIR				100								
North Finnish NordGen					100							
Stil , VIR	35	16						49				
Stil NordGen								100				



3 , 13, 25…- electrophoretic banding patterns of some avenin biotypes

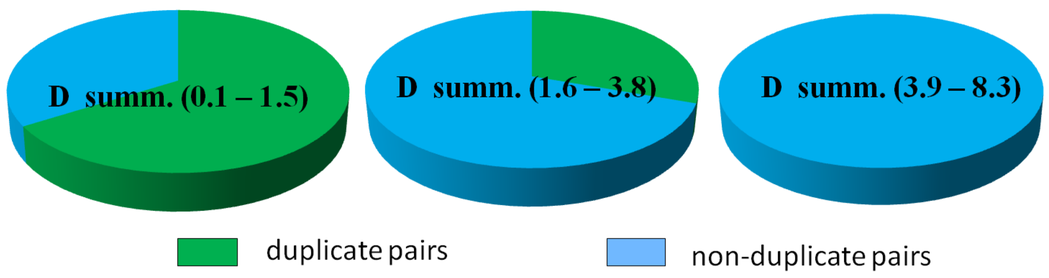
To decide which of the non-duplicate pair accessions is a true cultivar representative, it is possible to compare them with the original cultivar accession. The most reliable in this case is the use of standard laboratory methods, because original cultivar seeds may partially or completely lose germination especially upon prolonged storage. Clear electrophoretic spectra of seed storage proteins can be obtained even on the "century-old" seeds.
Some non-duplicate accessions (VIR, NGB) with avenin biotype composition differing dramatically were selected and compared with the corresponding original cultivar samples (O) preserved in the VIR collection from the 1920-s. According to the electrophoretic analysis the original cultivar representatives can be considered accessions of cvrs. Trifolium and Osmo II 0693 of the VIR collection and cvrs. North Finnish and Stormogult Havre of the NordGen's collection.

Comparison between field and laboratory trials showed:

The sets of duplicate and non-duplicate pairs identified by electrophoresis were significantly different in terms of D *summ*. index according MannWhitneyUTest. (p = 0.0001).

PD-accessions characterized by qualitatively different avenin biotype composition belonged only to groups 2 and 3. Compared with groups 1 and 2, composition differences between the accessions with same name were more expressed in group 3.

The lower was the group D *summ*. index, the more duplicate pairs were identified in the group by the protein markers.



Accession duplicatoin cannot be confirmed without comprehensive study of the material. The revealed conformity between the results of the field and laboratory tests shows that it is possible to use protein markers (avenin spectra) for identification of duplicate accessions in oat collections even before field trials. Field evaluation of crop accessions is interfaced with phenotypic variability of the majority of characters used in monitoring as well as with its duration. Molecular methods are more objective and reproducible in different laboratories, which is important for coordinating the work of different genebanks.