



Selection criteria for identification the Most Appropriate Accessions

Igor Loskutov

i.loskutov@vir.nw.ru

N.I. Vavilov Institute of Plant Industry
Russia

<http://www.vir.nw.ru>



Most Appropriate Accession (MAA)

is an **accession** of an **original** seed lot or seed sample that is **genetically** as close as possible to the **original** population
it shall be true to **name**,
held in the **country of origin** or introduced material of importance for **breeding and research** and used in Europe,
accompanied by **passport data**,
and **characterized** morphologically or
with markers.



Volume of collections

The European *Avena* Database contains about 34,000 entries from more than 20 genebanks.

The main problem is to identify Most Appropriate Accession and duplicates accessions

National level –
within collection in framework national genebanks

International level –
between collections in framework EADB



Tools for identification MAA and duplicats

FAO/IPGRI MULTI-CROP PASSPORT DESCRIPTORS

Comprehensiveness of **passport information**



Primary selection criteria

Genetically unique

**(i.e. genetically distinct accessions;
assessment based on available data and/or
on the recorded history of the accession)**

Agronomically

and/or historically / culturally important



Types of accessions are included in collection of GR

- I. Wild populations
(most of collected acc. are unique)**
- II. Landraces (local)
(most of collected acc. are unique)**
- III. Obsolete improved varieties
(all collected before 1950s are unique)**
- IV. Advanced improved varieties
(to divide to unique acc. and duplicates)**
- V. Breeding/research materials
(most of collected acc. are unique)**



First step.

To select accessions that have been **collected or bred in the country** where they are **being conserved**.

To identified on national level within collection

I. Wild populations

II. Landraces (local)

III. Obsolete improved varieties

IV. Advanced improved varieties

V. Breeding/research materials/Genetic stocks



Second step.

To select unique accessions that have been **collected or bred in European countries.**

To identify on international level between collections

I. Wild populations

II. Landraces (local)

III. Obsolete improved varieties

IV. Advanced improved varieties

V. Breeding/research materials/Genetic stocks



Third step.

To select accessions that have been **collected or bred in non-European countries.**

To identify on international level between collections

I. Wild populations

II. Landraces (local)

III. Obsolete improved varieties

IV. Advanced improved varieties

V. Breeding/research materials/Genetic stocks



List the most important fields of descriptors

1. Taxonomical group

- 5. Genus (GENUS) I-V
- 6. Species (SPECIES) I-V
- 7. Species authority (SPAUTHOR) I-V
- 8. Subtaxa (SUBTAXA) I-IV
- 9. Subtaxa authority (SUBTAUTHOR) I-IV

2. Geographical group

- 13. Country of origin (ORIGCTY) I-V
- 14. Location of collecting site (COLLSITE) I-II
- 22. Collecting/acquisition source (COLLSRC) I-V
- 23. Donor (country) institute code (DONORCODE) I-V



3. Name and Numeric group

- 2. Accession number (ACCENUMB) I, V
- 3. Collecting number (COLLNUMB) I, II
- 11. Accession name (ACCENAME) III, IV
- 12. Acquisition date [YYYYMMDD] (ACQDATE) I-V
- 18. Collecting date of sample [YYYYMMDD] (COLLDATE) I, II
- 24. Donor accession number (DONORNUMB) I-V
- 25. Other identification (numbers) associated with the accession (OTHERNUMB) I-V

4. Genetic group

- 21. Ancestral data (ANCEST) III-IV and some genetic information V



**Field and labs
characterization and evaluation data**

Molecule-biology evaluation data



N.I. Vavilov Research Institute of
Plant Industry



Thank you for
your attention