**Box 1
Criteria to be followed by the Working Group
for the selection of MAAs for Cucurbits**

A. Criteria for selection of unique accessions

- ➢ Split the analysis into different crops
- ➢ Assign a small group of experts for each crop
- ➢ Improve the quality of ECCUDB with EURISCO and holders' data
- ➢ Do not include hybrids. Include landraces, wild cucurbits, old varieties and breeding material
- ➢ Identify accessions received from other collections (check DONORCODE and DONORNUMB):
  - Do not include accessions that are still available in the collection of origin
  - If accessions were donated from genebanks outside the ECPGR area (e.g. USDA, Japan, etc.): select as MAA
- ➢ Study the field ACCENAME:
  - Accessions with unique ACCENAME: select as MAA
  - Accessions with the same ACCENAME:
    - If they are from different origins: select as MAA
    - If they (two or more) are from the same place (country, locality): potential duplicates (in case of wild material select all the accessions)
      - ◆ With characterization data:
        - o Select all the accessions if they look different
        - o If not, follow the sequence of "Without characterization data"
      - ◆ Without characterization data
        - o Accessions collected with an interval of more than 10 years: select all the accessions
        - o Accessions collected with an interval of less than 10 years:
          - → Select the accession having undergone the fewest regeneration cycles or select one at random until new information is obtained
  - Accessions without ACCENAME:
    - Include if they have a unique origin
    - Do not include if no additional information is available

B. Additional crop-specific criteria

As cucurbits are allogamous plants, the number of seeds of the collected sample and the number of plants used for regenerating the accession (one regeneration or more) should be considered when these data are available. The order of priority of these criteria is the following:

- ➢ The number of plants used in the regeneration trials
- ➢ The number of regeneration cycles
- ➢ The number of seeds of the original sample