



# Rationalization of a genebank cucumber collection with SSR markers

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## Introduction

The cucumber (*Cucumis sativus*) collection of the Centre for Genetic Resources, the Netherlands (CGN) consists of 937 accessions. The collection mainly includes old cultivars but also contains landraces and the crop wild relative *C. sativus* var. *hardwickii* (Table 1).

Passport data were updated in 2002, and used to rationalize the collection. Recently, the main part of the collection was screened for microsatellite (SSR) variation.

**Table 1.** Number of accessions of the CGN cucumber collection per population type

Breeders variety	Hybrid	Landrace	Research material	Wild	Undetermined	Total
377	1	128	17	5	409	937

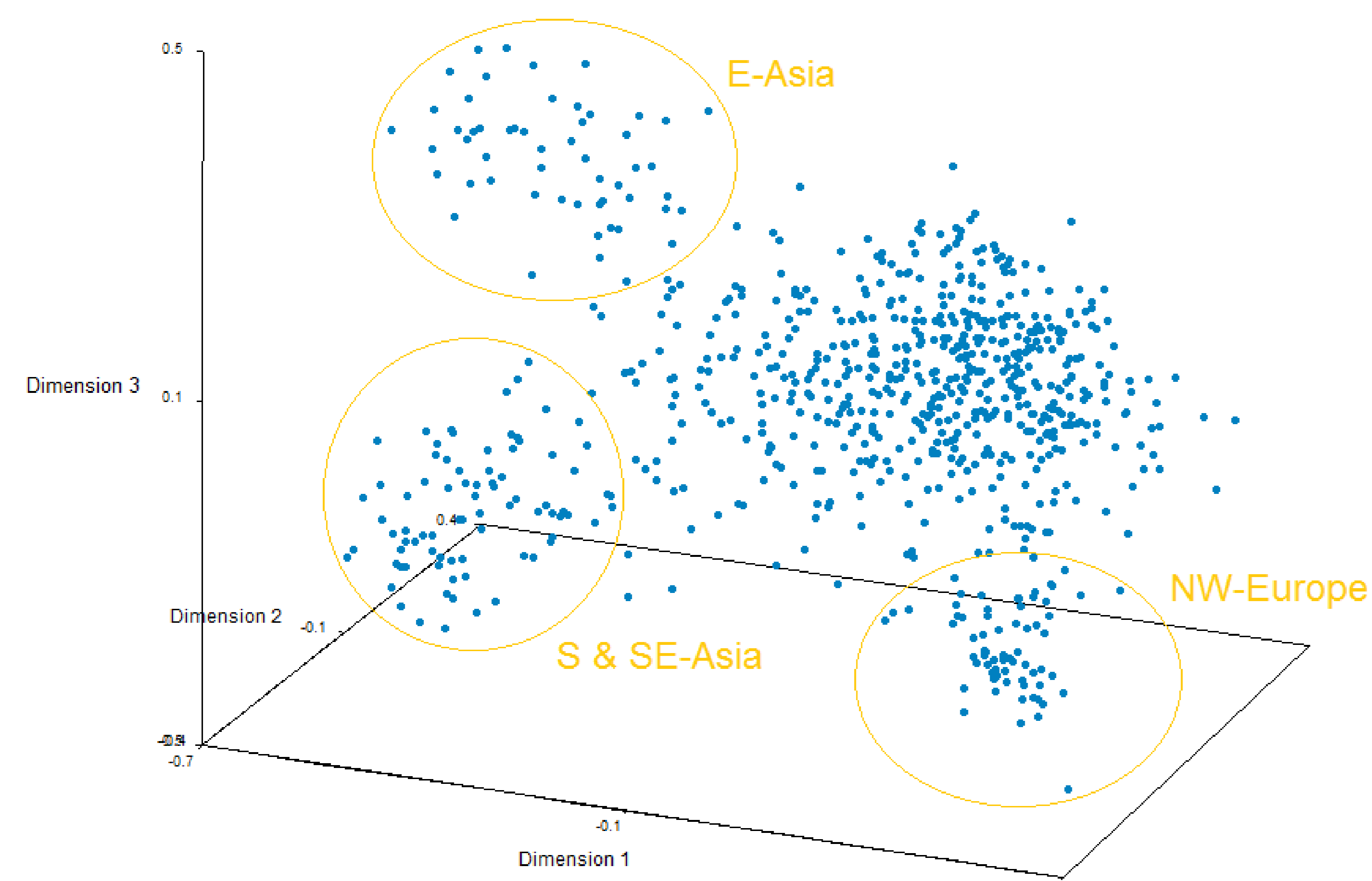
## Objectives

- Determination of collection structure
- Identification of potential redundancies
- Verification of passport data

## Methods

Bulked samples of five randomly chosen plants of each of 756 accessions were screened for variation at 23 polymorphic microsatellites. Genetic relationships among accessions were visualized by a Principal Coordinates (PCO) plot after calculation of Jaccard similarity coefficients (Figure 1).

## Genetic structure of the collection



**Figure 1.** Three-dimensional PCO plot

## Results

- A total number of 198 SSR alleles observed
- Five distinct clusters of accessions identified
  - Accession of *C. sativus* var. *hardwickii*
  - Predominantly landraces from South – Southeast Asia (India, Indonesia, Nepal, Thailand and Vietnam)
  - Accessions predominantly originating from East Asia (China and Japan)
  - Accessions predominantly originating from Northwest Europe
  - Rest group of accessions originating predominantly from Europe, North America and Central/West Asia
- No clear separation observed between members of the “Cucumber” and “Gherkin” group
- Twenty-six duplicate groups identified, comprising a total of 63 accessions
- Discrepancies observed between passport and molecular data for several accession comparisons (Figure 2)



**Figure 2.** Example of accessions with different variety names and identical SSR profile

## Conclusions

- CGN’s collection consists of several genetically distinct groups originating from different geographic regions
- The classification of accessions into a “Cucumber” and “Gherkin” group will no longer be followed
- The identified potential duplicates need to be verified in a follow-up morphological evaluation
- The SSR data are helpful for verifying and improving passport data.

## Acknowledgements

The SSR data used in this study were generated in the framework of a more comprehensive project initiated by the Institute of Vegetables and Flowers of the Chinese Academy of Agricultural Sciences in Beijing. Reference: ‘Genetic diversity and population structure of cucumber (*Cucumis sativus* L.)’ by Lv *et al.* (PLoS ONE, in press).