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# Molecular survey of the genetic diversity from commercial *Pelargonium x hortorum* cultivars compared to botanical accessions

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The genus *Pelargonium* contains more than 250 species, mainly found in southern Africa. Some specimens were imported to Europe during the 17<sup>th</sup> and 18<sup>th</sup> centuries. From the collected accessions several cultivated groups have been created by hybridisation resulting in more than 4000 varieties. The "so-called" geraniums (*P. x hortorum* Bailey) are the most economically important. Nowadays commercial cultivars look like quite similar in shape and colour. This similarity may be due to a narrow genetic basis according to the limited number of specimens at the origin of the European germplasm. In order to test this hypothesis, we compared the amount of variability available in a set of 16 tetraploid and 4 diploid commercial cultivars belonging to three breeding companies with the amount of variability evidenced in 16 botanical accessions. These accessions were mainly chosen in the Ciconium section from which modern *P. x hortorum* cultivars are considered to originate.

## Material and methods

Plant material (table 1) was obtained from different collectors and breeders. All accessions were from Ciconium section except two: B018 (*Dibrachya*) and B020 (*Peristera*). DNA extractions were performed on young leaves or buds using CTAB protocol. Molecular characterisation was realized using 10 microsatellites primer pairs developed during a previous work (EU Project FAIR3 CT96-1796, Becher *et al* 2000). PCR products were separated on 5% denaturing acrylamide gel and silver stained (fig. 1).

Bands were scored for presence or absence. Principal component analysis (PCA) was done using the SAS Princomp procedure (SAS 1997) on 59 markers and 25 individuals due to missing data. Individuals with missing data were taken into account on the graph as supplementary observations. UPGMA phenogram was drawn from the SAS calculated Jaccard's dissimilarity coefficients matrix using Neighbor and Drawgram programmes from Phylip 3.57c (Felsenstein 1995).

Code	Species
B002	zonale
B003	zonale
B005	zonale
B009	acetosum
B010	scandens
B012	scandens
B013	salmoneum
B014	inquinans
B015	x kewense
B017	x bastard
B018	peltatum
B020	saxifragoides
B065	frutetosum
B066	zonale
	x inquinans
B074	frutetosum
B084	tongaense
VA111	x hortorum
VA173	x hortorum
VA184	x hortorum
VA202	x hortorum
VB198	x hortorum
VB199	x hortorum
VB200	x hortorum
VB201	x hortorum
VC012	x hortorum
VC175	x hortorum
VC177	x hortorum
VC178	x hortorum
VC186	x hortorum
VC187	x hortorum
VC194	x hortorum
VC195	x hortorum
VD019	x hortorum
VD029	x hortorum
VD031	x hortorum
VD047	x hortorum

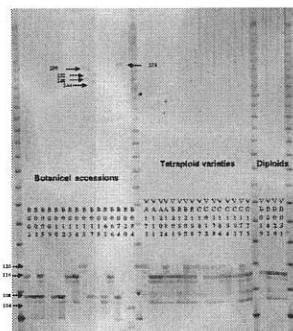


Fig. 1 Electrophoresis of Phi26 primer pair's PCR products

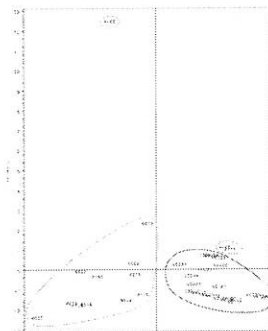


Fig. 2 Principal component analysis based on 59 markers and 25 individuals.

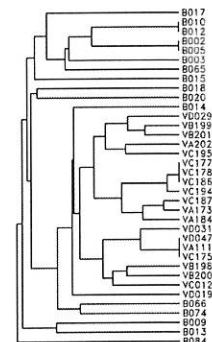


Fig. 3 UPGMA phenogram (Jaccard's dissimilarity coefficients)

## Results and Discussion

The allelic diversity is quite higher in the botanical group. 81 fragments were scored, resulting in 70 different ones. Among them, 30 are present only in botanical accessions and 5 only in cultivars. The two first axes of the PCA (fig. 2) explain 31% of the variation. In both representations of the variability (fig. 2 and 3), botanical accessions are spread over the graphs while cultivars are clearly clustered together. Moreover, botanical accessions are clearly separated from varieties, except two: a specimen of *P. inquinans* (B014) and another *P. zonale* x *P. inquinans* hybrid (B066). This supports the important contribution of *P. inquinans* specimens to the modern germplasm of *P. x hortorum* as shown by James (1995).

The limited number of markers did not allow us to distinguish two pairs of botanical accessions, as well as some cultivars. The two pairs of botanical accessions present very narrow phenotype. Molecular results will help us in the decision of conserving just one of two accessions in each pair. Cultivated varieties could be phenotypically distinguished during the protection test. This demonstrates that breeding on ornamental traits isolated some private alleles in each cultivar. Nevertheless, the global molecular similarity reveals a common genetic basis for the cultivated group.

## Conclusion

This study shows that breeding of modern cultivars has taken a limited part of the available genetic variability. Genetic variability may be recovered from botanical specimens, which represent a source of potentially interesting genes such as disease resistance ones. These botanical specimens should primarily be chosen in closely related species to *P. x hortorum*, such as *P. inquinans*, in order to perform successful crosses.

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