Workshop:
Collezioni Vegetali Specializzate
XI Giornate Scientifiche SOI
14 – 16 settembre 2016
Gruppo di lavoro
Collezioni Vegetali Specializzate

La caratterizzazione delle accessioni vegetali: potenzialità e limiti degli strumenti utilizzati

Valentina Scariot
Dip. Disafa – Università di Torino
valentina.scariot@unito.it

Biodiversity in Italian gardens

In Italy there is no region that does not boast some famous garden.
From those of the fourteenth and fifteenth century up to those built today with modern standards, Italy has a long and glorious garden history that retraces all architectures, styles and tastes.
The variety of the Italian climate is reflected not only in the architecture but also in their botanical-floristic composition.

- Gardens from dazzling green meadows of the Po Valley, Lombardy, Veneto, and Piedmont are dominated by species with minor climate requirements such as azalea, rhododendron, camellia, maple, magnolia, etc., and dark green conifers which mirror in hill and alpine lakes.

Isola Madre, an island of Lake Maggiore renowned for its botanical collections.

- The floras of the tropical and subtropical countries have largely contributed to enrich gardens of Liguria with succulents (agave, aloe, cactus, opuntia, etc.), palms, cycads, and araucaria.

Tropical and subtropical floras in Liguria.

- Gardens of central Italy (Lazio and Tuscany) are dominated by cypress, pinaster, olive tree, vine, oak, and buxus.

Formal garden in central Italy

- Finally those of insular and south central regions are rich in plants with exuberant vegetation, such as ficus, opuntia, palms, and citrus.

The garden of Donnafugata Castle in Sicily.

Botanical collections

- The interest of scholars, professionals, and plant lovers towards the botany and the favourable climate of our regions have led to the creation of real botanical gardens and collections of ornamental plants such as roses, camellias, azaleas, rhododendrons, and cactaceae.
- The richness of these collections have given or may give a contribution to the development of floriculture.
- Here some noteworthy examples are reported.

Roses

- In the overview of botanical collections, definitely deserves to be mentioned:
- the “Carla Fineschi Botanical Rose Garden” located at Cavriglia (Tuscany). The rose garden came to life in 1967 thanks to Prof. Gianfranco Fineschi, a teacher at the faculty of medicine at the Cattolica University of Rome and has become bigger as years have passed. It collects over 6000 species and hybrids from all over the world, representing a unique private collection.

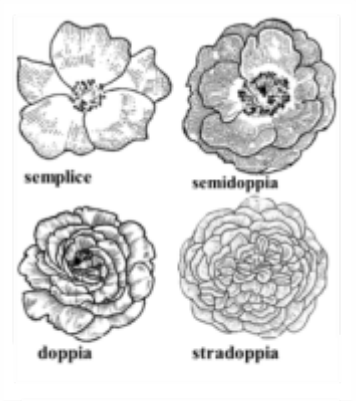
- Other notable rose gardens are present in Piedmont (“La sorpresa”). Lombardy (Villa Reale in Monza), Liguria (Nervi) and Lazio (Rome).

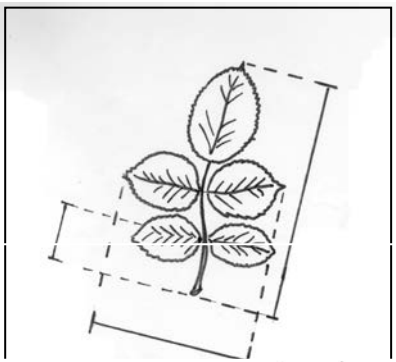
Collections of garden roses are widespread throughout the country.

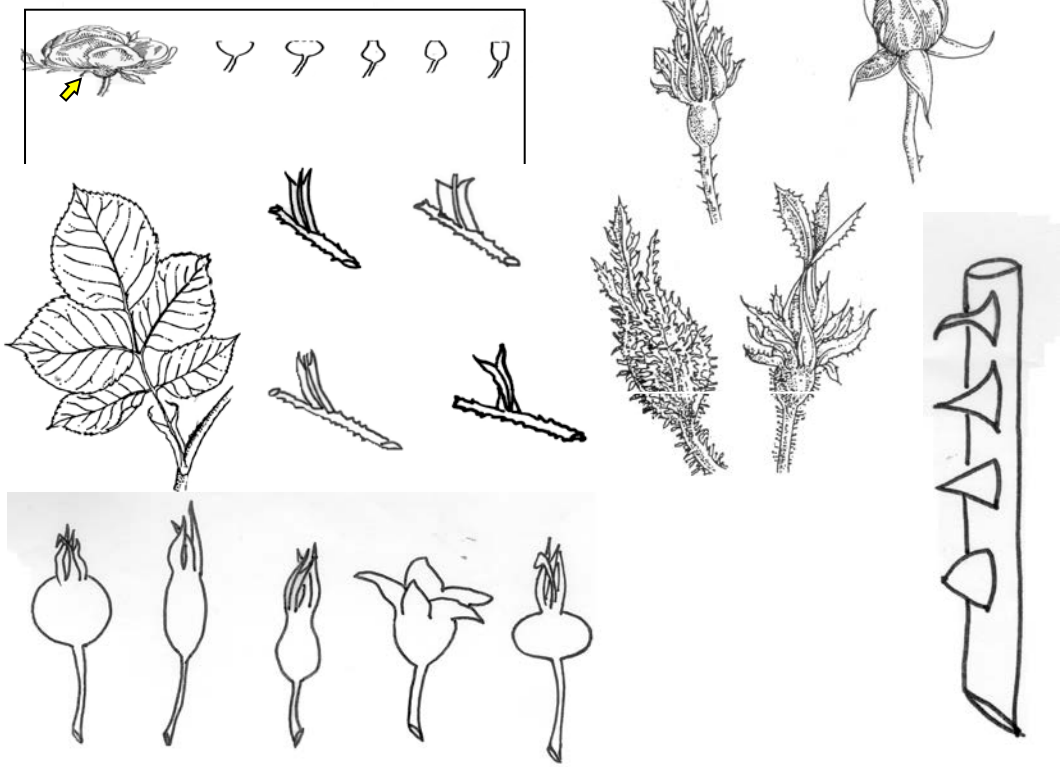
Case study:

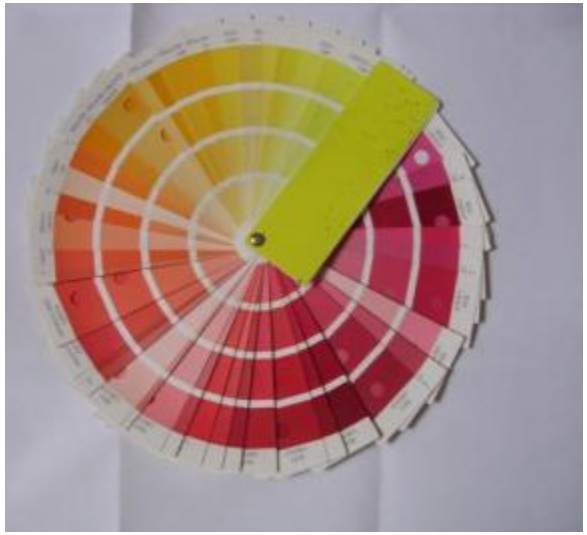
Roses

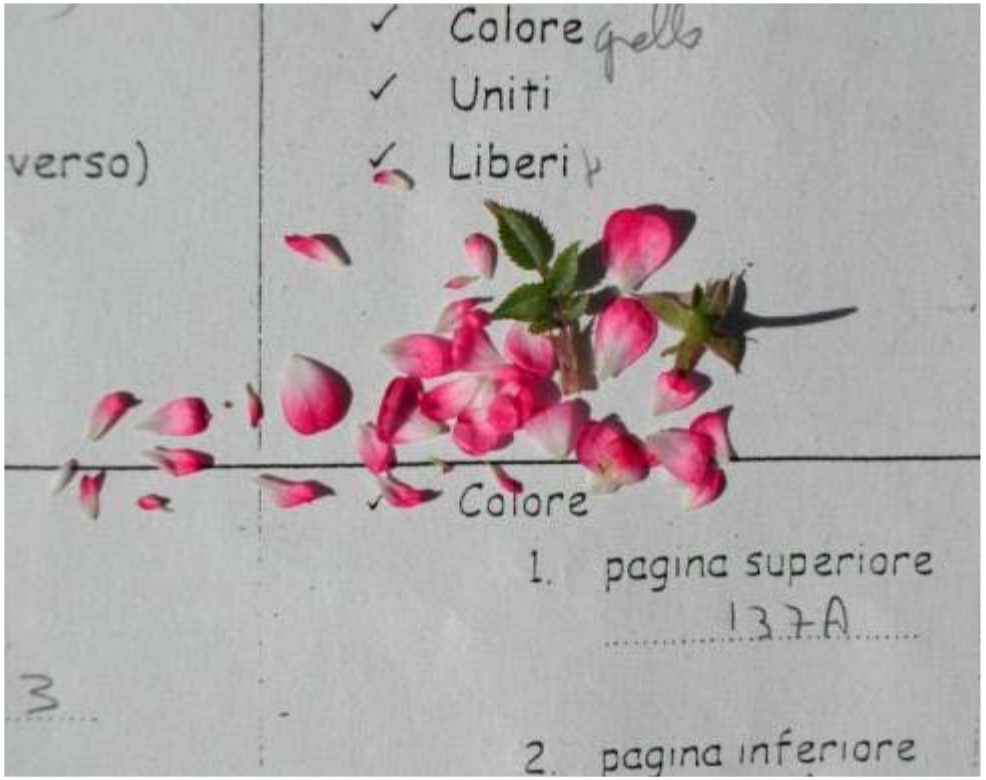
Carla Fineschi Botanical Rose Garden










✓ Colore giallo
✓ Uniti
verso)
✓ Liberi
✓ Colore
1. pagina superiore
137A
3
2. pagina inferiore

Theatrum rosarum a cura di E. Accati e E. Costa, ed. Allemandi

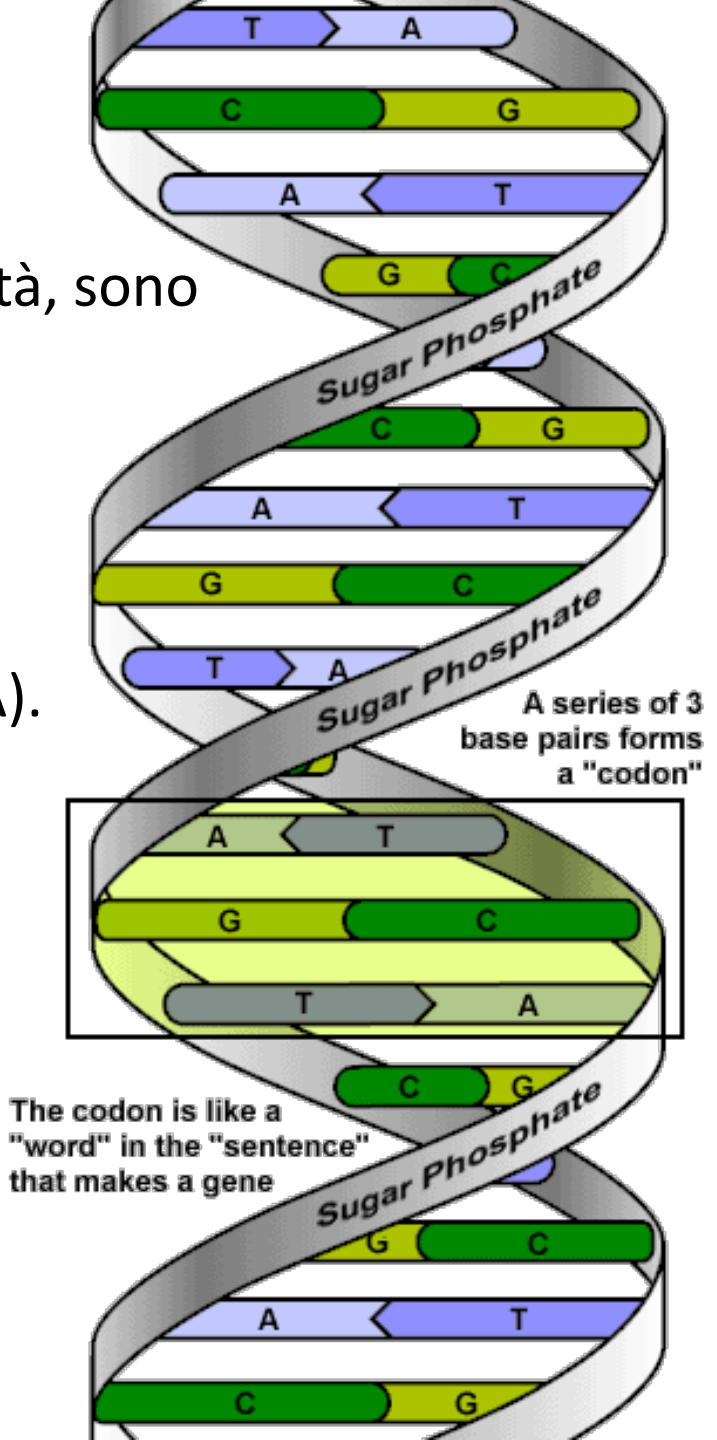
Analisi del DNA

Tradizionalmente, per valutare la biodiversità, sono stati impiegati i dati morfologici.

In anni recenti, al fine di disporre di migliori marcatori di diversità, sono state sviluppate diverse tecniche molecolari (analisi del DNA).

Molti vantaggi, relativi soprattutto alla loro indipendenza da:

- ✓Ambiente
- ✓Età della pianta
- ✓Tipo di tessuto analizzato



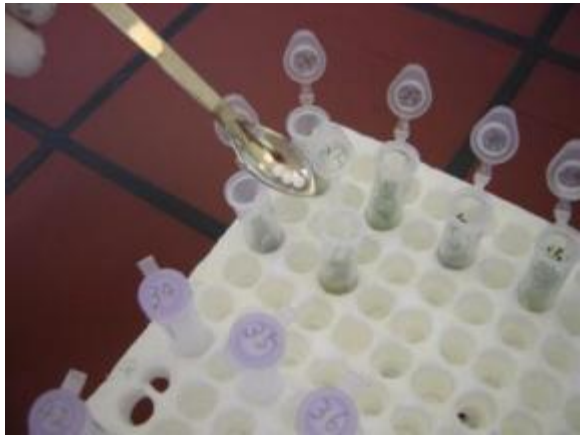
J. Amer. Soc. Hort. Sci. 131(1):66–73. 2006.

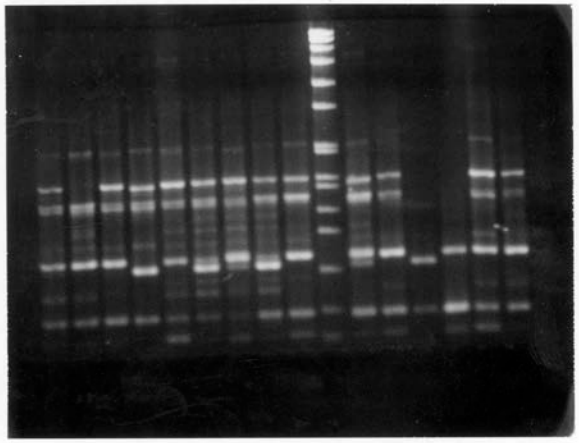
Characterization and Genetic Relationships of Wild Species and Old Garden Roses Based on Microsatellite Analysis

Valentina Scariot[1], Aziz Akkak[2], and Roberto Botta[2]
Università degli Studi di Torino, Via Leonardo da Vinci 44, 10095 Grugliasco (TO), Italy

Additional index words. *Rosa*, DNA, SSR, STMS, molecular markers, allelic phenotype, classification

Abstract. **Six polymorphic sequence-tagged microsatellite sites (STMSs) were used to characterize 65 accessions of old garden roses [OGRs (*Rosa* L. spp.)] from seven botanical sections and 13 horticultural groups. Aims of the study were to define the genetic profiles of accessions and to provide information useful for the classification and pedigree reconstruction of OGRs. In roses, a precise botanical classification is difficult due to repeated hybridization carried out in breeding; OGRs are classified in horticultural groups on the basis of their original parentage or of their morphological traits. A total of 82 alleles were detected at six loci. The number of alleles per locus ranged from six to 21, with an average of 13.7 alleles per locus. A dendrogram was constructed by cluster analysis, displaying the relative genetic similarities between species' accessions, hybrids, and cultivars. Cluster analysis grouped the genotypes into seven major clusters that were substantially consistent with their classification into botanical sections and horticultural groups. Several hypotheses of apportionment of accessions to horticultural groups were evaluated on the basis of the relative position in the dendrogram of the analyzed individuals. Results demonstrated that DNA analyses can contribute to drawing the botanic classification of rose accessions, improving the genetic knowledge on the background of modern rose, and providing the basis for breeding programs.**





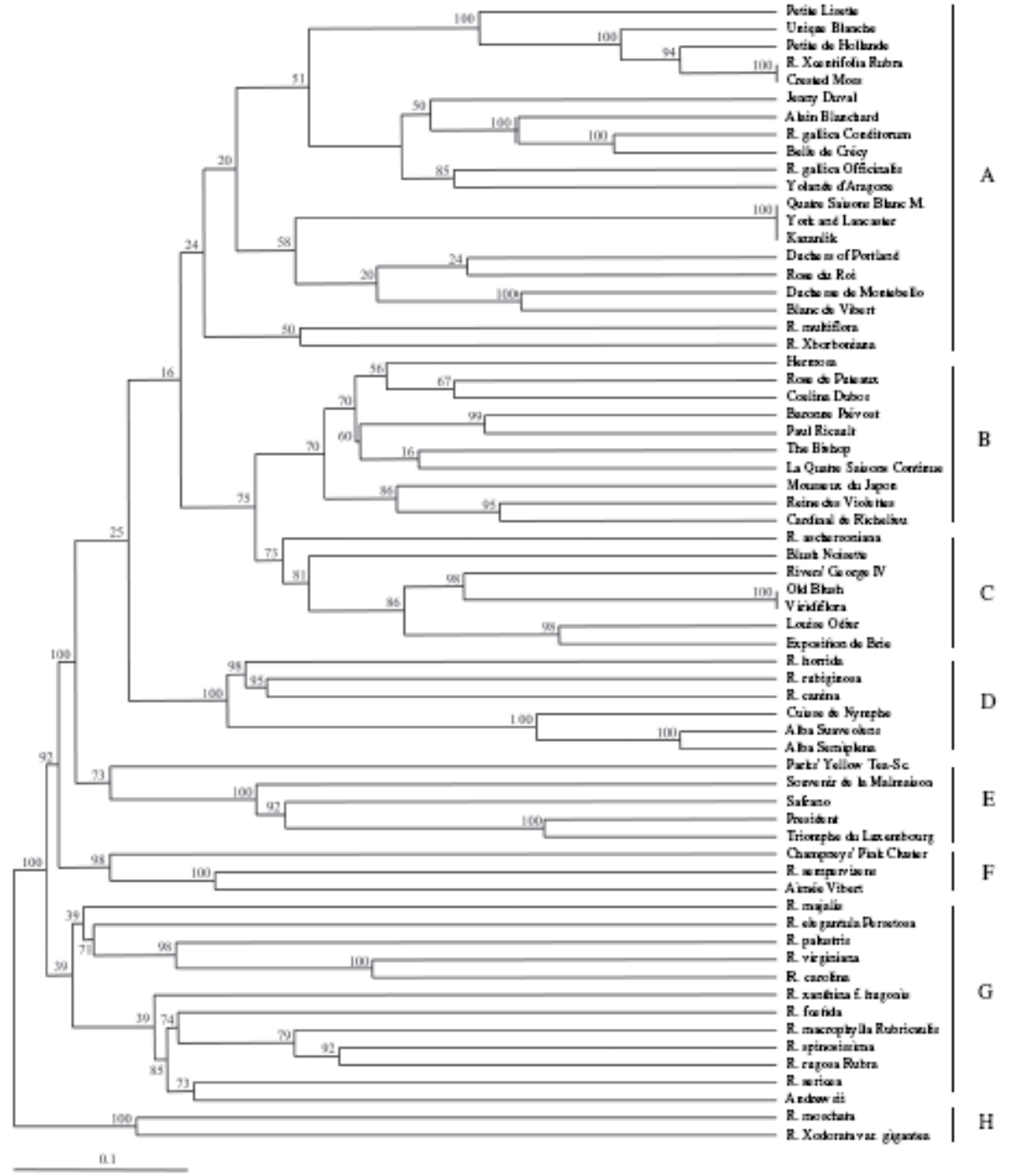


Fig. 1. Dendrogram depicting the genetic relationships among 65 *Rosa* accessions (Jaccard similarity coefficient; UPGMA clustering) with indication of bootstrap values of 100 datasets.

CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources 2007 2, No. 052

Review

Understanding genetic relationships of wild and cultivated roses and the use of species in breeding

Katrien De Cock[1], Valentina Scariot[2], Leen Leus[1], Jan De Riek[1,*] and Johan Van Huylenbroeck[1]

Address: [1] Plant Unit – Applied Genetics and Breeding, Institute for Agricultural and Fisheries Research (ILVO), Caritasstraat 21, 9090, Melle, Belgium. [2] Department of Agronomy, Forest and Land Management, University of Turin, via Leonardo da Vinci 44, 10095 Grugliasco (TO), Italy.

***Correspondence:** Jan De Riek. Email: jan.deriek@ilvo.vlaanderen.be

Received: 26 February 2007
Accepted: 9 July 2007

doi: 10.1079/PAVSNNR2007052

The electronic version of this article is the definitive one. It is located here: http://www.cababstractsplus.org/cabreviews

Abstract

The existence of numerous wild species, the variability within species and the wide geographical distribution in combination with the weak barriers to interspecific and intersectional hybridization, make genetic relationships within the genus *Rosa* difficult to unravel. The use of molecular techniques has revealed some new insights in taxonomy and phylogenetic relationships. The understanding of these relationships among species and cultivars is a prerequisite for the effective utilization of the available genetic variability to tackle the new demands from growers and consumers. Many wild species have interesting traits. The rose breeders' challenge is to introgress the desirable beneficial genes from wild species to tetraploid cultivars in order to accelerate the production of superior rose germplasm.

Keywords: Biodiversity, Genetics, Interspecific hybridization, Phylogeny, Ploidy, *Rosa*, Taxonomy

Acidophilic plants

- The basin of the Lake Maggiore (Piedmont and Lombardy) is very interesting for the consistence of the collections of acidophilic species such as camellias, azaleas, and rhododendrons.
- These plants arrived in the nineteenth century, thanks to adventurous plant hunters, from the Far East, through northern Europe, Britain and Belgium. Over the years they have gradually acclimated to the environment and established a close link with the territory.

Azalea collections in Lake Maggiore district are present both in nurseries and parks.

A rich collection of autumn and winter flowering camellias has been established by the University of Torino in the park of Villa Maioni (Verbania).

Case study:

Azaleas

Euphytica (2007) 158:47–66
DOI 10.1007/s10681-007-9425-3

A contribution to the classification of evergreen azalea cultivars located in the Lake Maggiore area (Italy) by means of AFLP markers

Valentina Scariot · Takashi Handa · Jan De Riek

Received: 9 June 2006 / Accepted: 21 March 2007 / Published online: 19 June 2007

Abstract The amplified fragment length polymorphism (AFLP) technique was employed to assess the genetic conformity within a gene pool of evergreen azaleas. Ninety-three genotypes grown in historical gardens and nurseries of the Lake Maggiore area (Northern Italy), locally classified in the groups Indica, Japonica and Amoena, 44 reference cultivars of the four more or less universally recognized groups Belgian, Hirado, Kurume and Satsuki, and 40 species and species accessions that most concurred in the origin of the reference groups were included. Aims of the study were to define the genetic profiles of the Italian accessions and to provide useful information for their classification and pedigree reconstruction. Ordination analyses were used to evaluate if the AFLP technique can be applied to establish phylogenetic relationships and to investigate the DNA-based relatedness within the Italian gene pool and between the latter and the reference one. The results regarding the Italian accessions were compared with morphological data by means of Mantel's test. Assignment tests both on the level of the groups and on individual plant level for the reference and Italian genotypes were applied to further evaluate the relatedness of the groups or individual accessions. Results demonstrated that the AFLP technique together with morphological characterization can contribute to depict the phylogeny of the evergreen azalea. Comparing the reference and Italian genotypes, conclusions about the classification of the evergreen azalea cultivars located in the Lake Maggiore area were drawn.

Keywords Assignment tests · DNA · Morphological characters · Phylogeny · *Rhododendron* spp. · *Tsutsusi*

Plant Breeding 126, 207—212 (2007)

Comparative study of the discriminating capacity and effectiveness of AFLP, STMS and EST markers in assessing genetic relationships among evergreen azaleas

V. Scariot[1], E. De Keyser[2], T. Handa[3] and J. De Riek[2]

[1]Department of Agronomy, Forest and Land management, Università degli Studi di Torino, Via Leonardo da Vinci 44, I-10095 Grugliasco, Torino, Italy, E-mail: valentina.scariot@unito.it; [2]ILVO-Plant Sciences Unit, Caritasstraat 21, B-9090 Melle, Belgium; [3]Graduate school of Life and Environmental Sciences, University of Tsukuba, Tennodai 1-1-1, Tsukuba, Ibaraki 305-8572, Japan

With 1 figure and 5 tables

Received June 21, 2006/Accepted August 31, 2006
Communicated by G. Forkmann

Abstract

The application of amplified fragment length polymorphism (AFLP), sequence tagged microsatellite site (STMS) and expressed sequence tag (EST) markers to study the genetic relationships in an evergreen azalea gene pool was investigated. STMS and EST markers revealed a higher genetic distance detection capacity than AFLPs, which, nevertheless, were the most efficient marker system due to their highest polymorphism detection capacity. Similarity matrices showed weak, yet significant, correlations when Mantel's test was applied. To assess the usefulness of the overall information provided by these marker data for establishing phylogenetic relationships and horticultural classification, cluster analysis was performed. The joint AFLP, STMS and EST data were demonstrated to be remarkably effective for group discrimination and phylogenetic studies. The use of these polymerase chain reaction marker systems is discussed in terms of the choice of appropriate marker techniques for different aspects of evergreen azalea germplasm evaluation.

(AFLP) technique has already proved to be successful in assessing the genetic variation of a breeder's collection (De Riek et al. 1999) and for identifying 33 Chinese species (Dendauw et al. 2002). Sequence tagged microsatellite site (STMS) markers have been developed in *Rhododendron simsii* hybrids by Dendauw et al. (2001). Molecular markers from the transcribed region of the genome have also great potential for applications in plant genotyping. Among them, expressed sequence tag (EST) markers have already shown a good degree of polymorphism in various plants (e.g. ryegrass and related species of Poaceae, Lem and Lallemand 2003), but have not previously been developed in *Rhododendron*.

This paper reports on the comparison of AFLP, STMS and EST markers in order to determine their relative efficiencies in a study of genetic diversity among 84 evergreen azalea species and cultivars. Ten microsatellite loci, 10 ESTs and three AFLP primer combinations with six selective bases were chosen.

Chapter 30

Azalea Phylogeny Reconstructed by Means of Molecular Techniques

Ellen De Keyser, Valentina Scariot, Nobuo Kobayashi, Takashi Handa, and Jan De Riek

Abstract

Plants belonging to the *Rhododendron* subgenera *Pentanthera* (deciduous) and *Tsutsusi* and *Azaleastrum* (evergreen) are called azaleas. Concerning their natural phylogenetic positions, the *Pentanthera* subgenus is closer to evergreen rhododendrons (subgenera *Rhododendron* and *Hymenanthes*) than to the *Tsutsusi* subgenus. Both azalea types are important ornamentals with a long breeding tradition. Different hybrid groups are often named after the supposed principal ancestor species. Molecular techniques for phylogenetic and kinship research have been evaluated to a great extent. First, some studies using comparative gene sequencing are presented; this approach was then widened to the use of molecular markers to reveal more detailed genetic relationships. Finally, the use of candidate genes as functional markers for the assessment of genetic diversity is presented. This opens new research lines to the genetic mapping of plant traits and azalea genomics.

Key words: Azalea, Phylogeny, Molecular markers, Genetic diversity

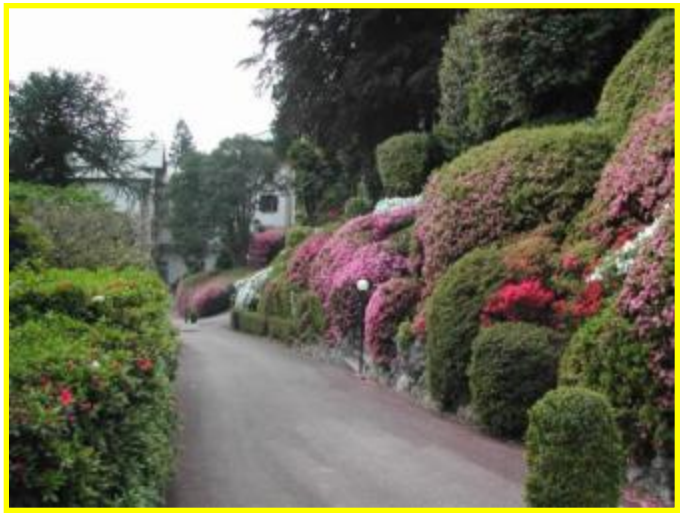
1. Introduction

The genus *Rhododendron* of the heather family (*Ericaceae*) is well known for the beauty and diversity of floral and vegetative form of its more than 1,000 species. Because of the many species within this genus, during history taxonomists have made several classifications mainly based on morphological data (i.e. flowers, leaves, hairs, etc.). The genus is divided into eight subgenera, the four most important subgenera being *Tsutsusi* (evergreen azaleas except *Brachycalyx* section), *Pentanthera* (deciduous azaleas), *Rhododendron* (lepidote rhododendrons) and *Hymenanthes* (elepidote rhododendrons) (1). *Hymenanthes* species are evergreen

Morphological Characteristics and AFLP Markers for Classifying an Italian Genepool of Evergreen Azaleas

- 93 Italian accessions
  - 48 Indica
  - 41 Japonica
  - 4 Amoena
- 40 species and varietas
- 44 cultivars
  - 19 Belgian
  - 6 Hirado
  - 14 Kurume
  - 5 Satsuki

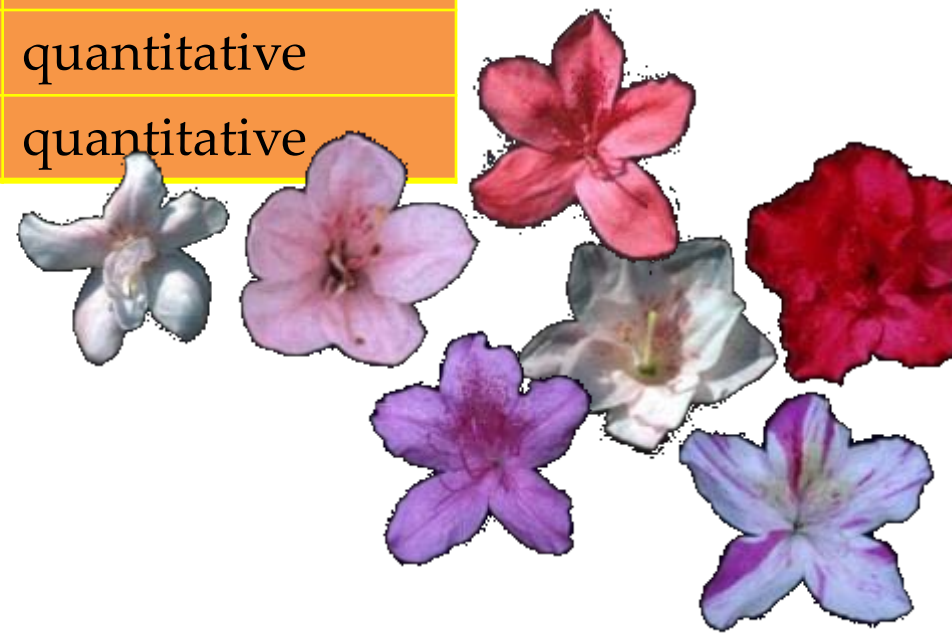
reference



10 morphological traits

3 AFLP primer combinations

	Characteristic	Type
Flower	diameter	quantitative
	depth	quantitative
	form	multistate
	hose in hose	binary
	colour	multistate
	flavonoids	binary
	stamens	multistate
Leaf	length	quantitative
	width	quantitative
	petiole length	quantitative



DNA isolation, AFLP reactions and PAGE

- DNA was extracted from approximately 0.30 g tissue using the Qiagen Dneasy® Plant Mini kit or a 2% CTAB buffer.

- Selective amplification was carried out using 3 fluorescent labelled *Eco*RI-*Mse*I primer combinations with 6 selective bases:

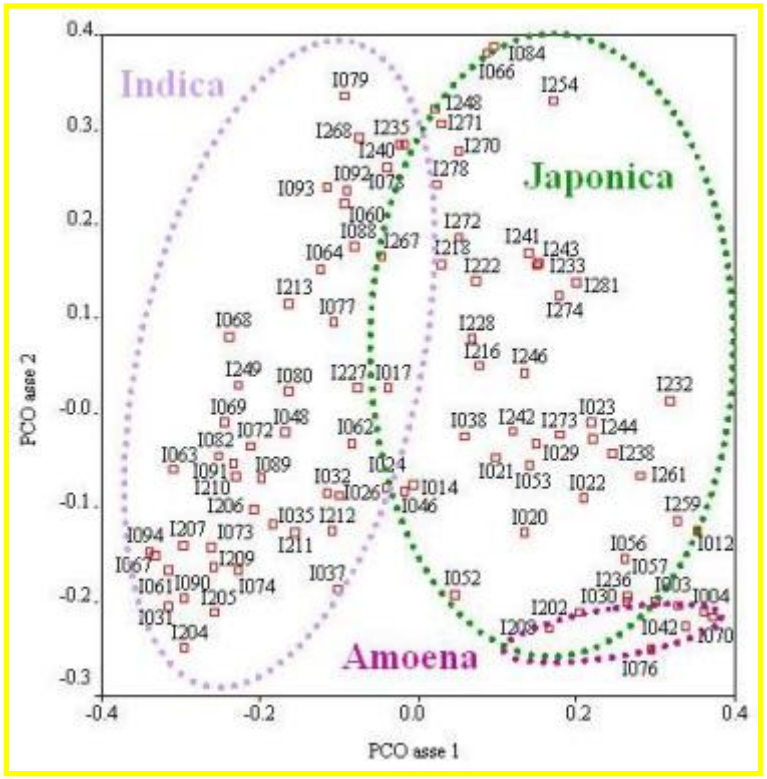
  *Eco*RI-ACT/*Mse*I-CTA (PC1)
  *Eco*RI-ACT/*Mse*I-CAT (PC2)
  *Eco*RI-AAG/*Mse*I-CTA (PC3)

- Fluorescent DNA fragments were separated on a 4.25% denaturating polyacrylamide gel using an ABI-PRISM 377 DNA sequencer with GeneScan software.

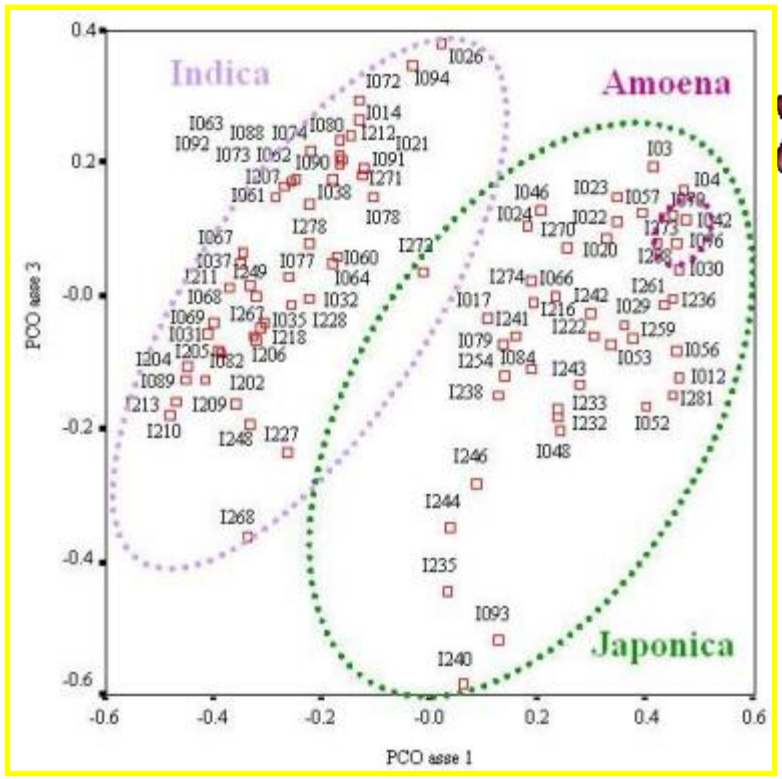
Relatedness within the Italian gene pool

Principal Co-ordinate Analysis

AFLPs



Morphological traits



- Axis 1 separates the Indica accessions from the Japonica and Amoena group, however, there seems to be a kind of continuum between two poles.
- The low level of correlation (Mantel test) suggests these two kinds of data can give complementary information.

Relatedness within the Italian gene pool

Cluster Analysis

Indica

Maria Ratti

Rosmini Antonio

Commendatore S. Bianchi

Carla Ferrero

Japonica

Verbania

Mario Carmine

Rosa intenso Cavadini

Intra

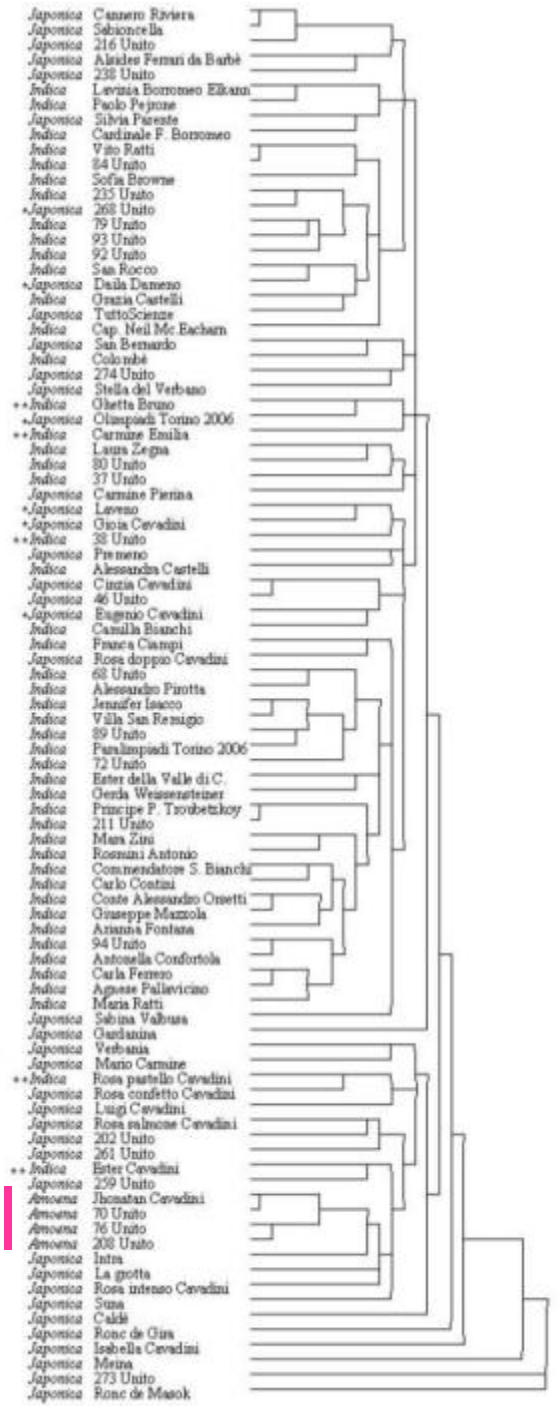
Amoena

Jhonatan Cavadini

76 Unito

86 Unito

208 Unito



Case study:

Camellias

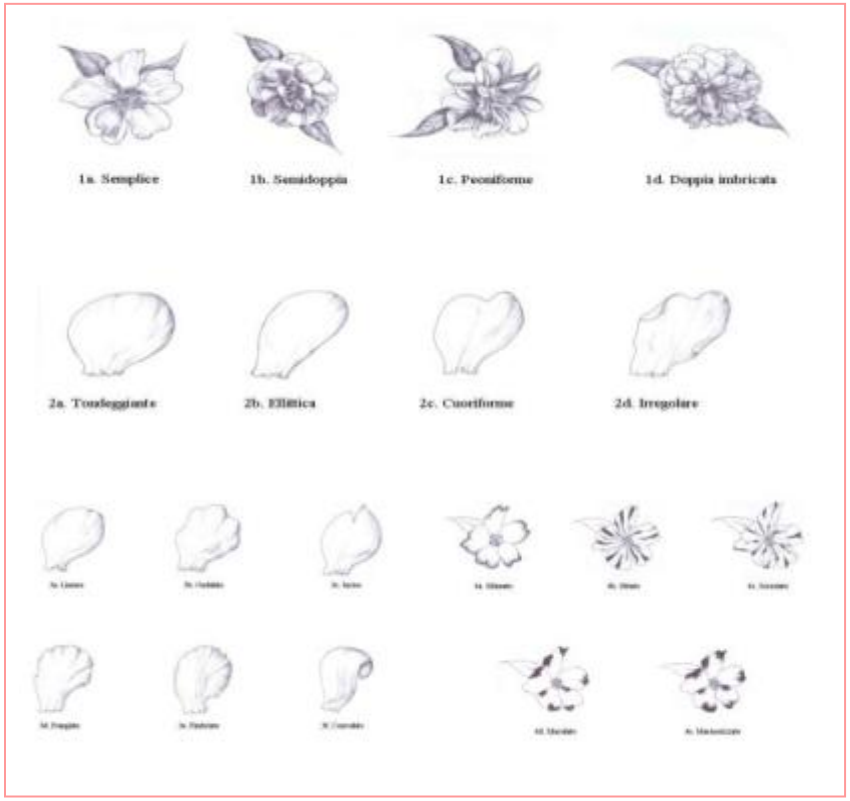
Morphological characterization

C. sasanqua 'Narumigata'

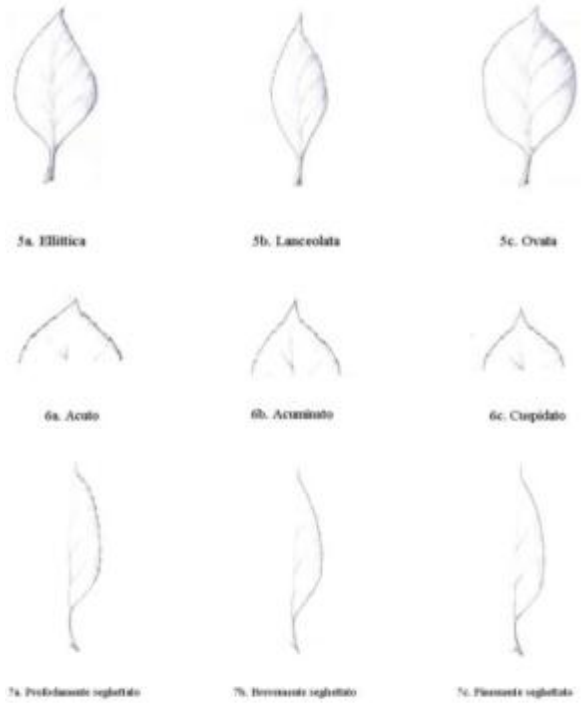
C. x vernalis 'Hiryû'

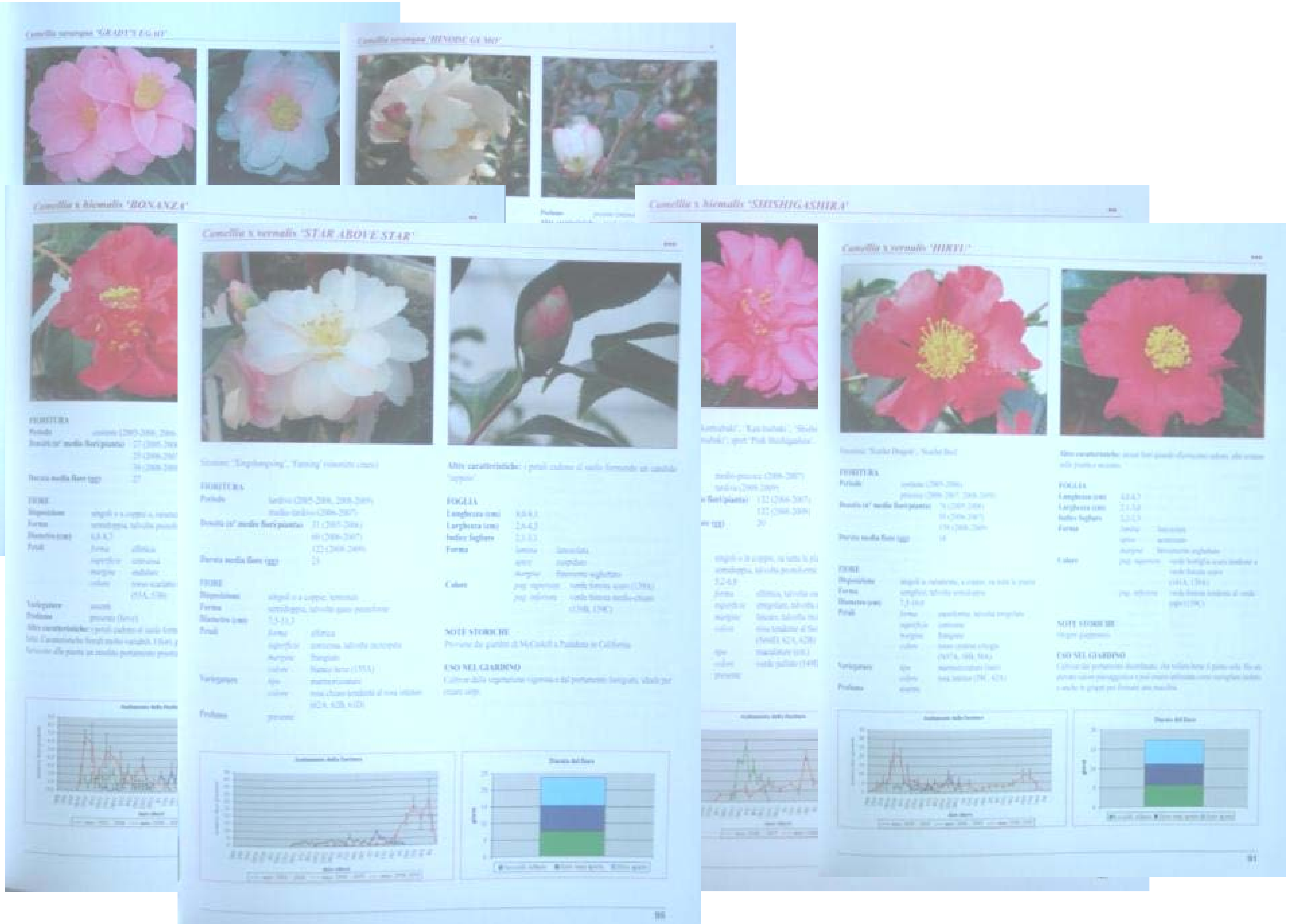
Fiore

Petalo

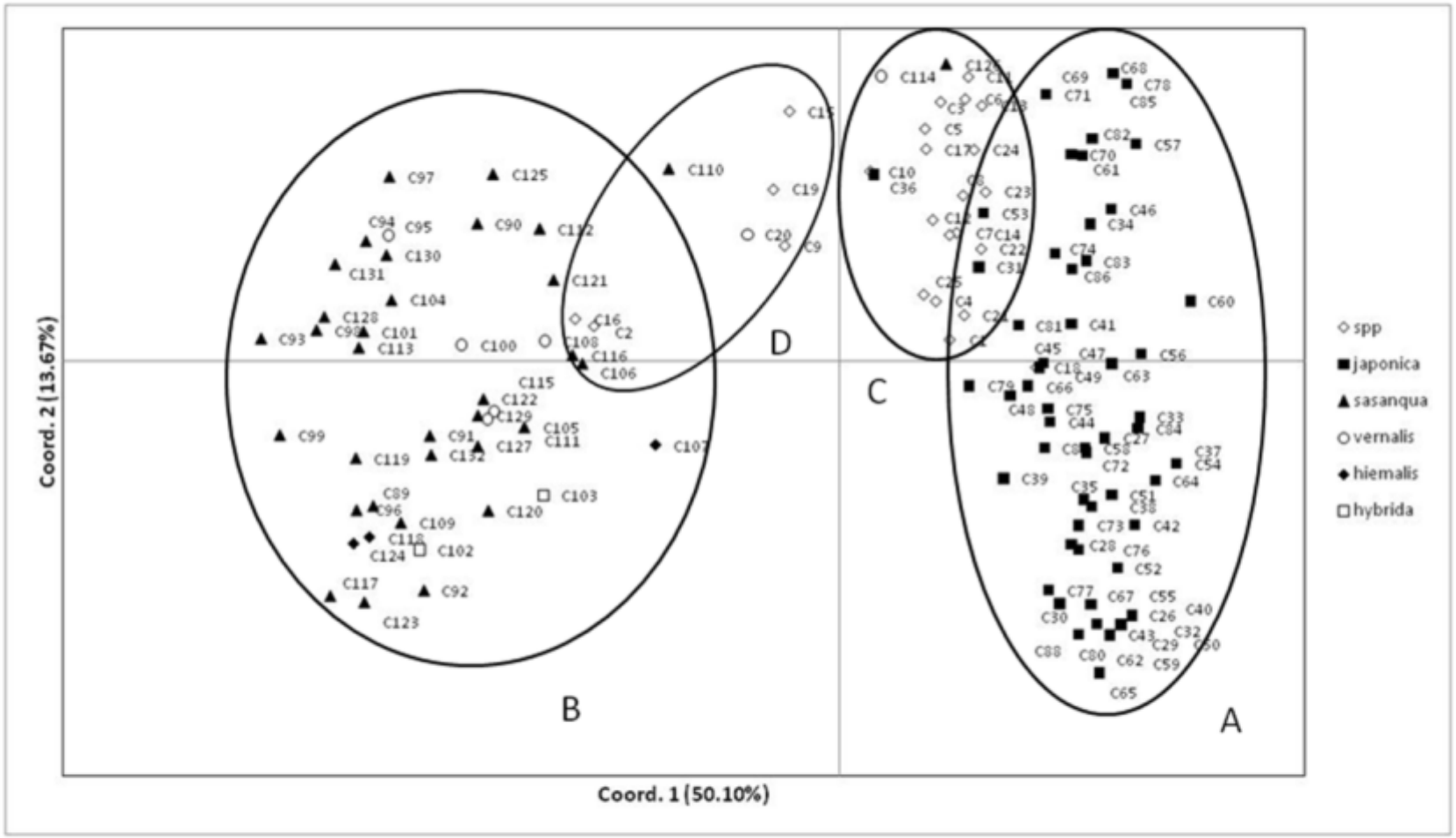


Foglia




Camellia x hiemalis 'BONANZA'
Camellia x vernalis 'STAR ABOVE STAR'
Camellia x hiemalis 'SHISHIGASHIRA'
Camellia x vernalis 'HIRYU'

Molecular characterization



Acidophilic plants

- A unique collection of rhododendron is located in the Special Natural Reserve of the Burcina Park "F. Piacenza" (Piedmont). The Rhododendron valley was realized between 1892 and 1925 by Felice Piacenza. This valley covers an area of about two hectares and holds one thousand plants of evergreen rhododendron.

- A large variety of maples is also present in gardens and nurseries of the area.

The Rhododendron valley in the Special Natural Reserve of the Burcina Park "F. Piacenza" (Pollone).

Maples with different shapes and colours characterize the production of Biella.

Case study:

Rhododendrons

Special Natural Reserve of the Burcina Park "F. Piacenza" (Piedmont). The Rhododendron valley

Scientia Horticulturae 125 (2010) 469–476

Contents lists available at ScienceDirect

Scientia Horticulturae

journal homepage: www.elsevier.com/locate/scihorti

Are rhododendron hybrids distinguishable on the basis of morphology and microsatellite polymorphism?

Matteo Caser[a,*], Aziz Akkak[b,1], Valentina Scariot[a]

[a] Department of Agronomy, Forest and Land Management, University of Turin, via L. da Vinci 44, 10095 Grugliasco, TO, Italy
[b] Department of Arboriculture and Pomology, University of Turin, via L. da Vinci 44, 10095 Grugliasco, TO, Italy

ARTICLE INFO

Article history:
Received 23 December 2009
Received in revised form 20 April 2010
Accepted 22 April 2010

Keywords:
Biodiversity
Rhododendron spp.
Microsatellites
Principal coordinate analysis
Principal component analysis
Cluster analysis
Morphological traits

ABSTRACT

Sequence Tagged Microsatellite Sites (STMSs) and morphological trait markers were used to evaluate 33 rhododendron germplasm for genetic diversity assessment and discrimination power. The average genetic diversity estimates were 0.724 (morphological traits) and 0.174 (STMSs) marker datasets. The Shannon index was higher for morphological traits (1.797) than STMS (0.302). The correlation coefficients obtained by the Mantel matrix correspondence test, which was used to compare the cophenetic matrices for the two markers, showed that estimated values of relationships given for morphological and STMS were not significantly related ($p > 0.05$). The dataset from STMS, supported by the total probability of identity (1.13×10^{-5}) and total paternity exclusion probability (0.9999), allowed all accessions to be uniquely identified. In summary, STMS marker proved to be an efficient tool in assessing the genetic variability among old broad leaf rhododendron genotypes. The pattern of variation appeared to be consistent, and it can be used for germplasm conservation and management for restoration of historical genetic resources.

Characterization of a Genepool of Old Broad Leafed *Rhododendron* Hybrids by Means of STMS Markers

M. Caser[a] and V. Scariot
Department of Agronomy
Forest and Land Management – University of Turin
via L. da Vinci 44
10095 Grugliasco (TO)
Italy

Keywords: biodiversity, molecular markers, principal coordinate analysis, genetic diversity, microsatellites, morphological traits

Abstract

During the 19th century many broad-leafed woody evergreen *Rhododendron* cultivars (subgenus *Rhododendron*) were introduced in Italy as ornamental garden plants. The most comprehensive collection is located in the Special Natural Reserve of Burcina Park "F. Piacenza" (Biella-Piedmont), that represents a rich reservoir of germplasm for its favourable climatic and pedologic conditions. The aim of the present work was to deepen the knowledge about these cultivars that represent an important genetic patrimony, since a number of them are deceased world wide. In order to investigate the genetic diversity of 10 rhododendron hybrids and 4 supposed related species (*R. arboreum*, *R. catawbiensis*, *R. ponticum* and *R. caucasicum*), 17 variables referring to flower and leaf morphology and four polymorphic sequence-tagged microsatellites sites (STMSs) were evaluated. Similarities among accessions were assessed performing a Principal Coordinate Analysis (PcoA) based on Gower coefficient. In the scatter plot the hybrids clustered in groups that were consistent with their supposed pedigrees and further bibliographic information. Based on these results, some hypotheses about the origins of the cultivars with unknown parentage included in the analysis could be drawn. In conclusion, the evaluated morphological and molecular markers appeared to be a useful tool for solving identification and classification problems of the old broad leaf rhododendrons hybrids and for clarifying their origins.

INTRODUCTION

The genus *Rhododendron* L. belongs to the *Ericaceae* family and comprises over 800 distinguishable species (Chamberlain et al., 1996). Most of them are present in Yunnan, Szechuan and Japan (Leach, 1961), in South-East Asia from Thailand and Vietnam to Malaysia and Indonesia and in coastal areas and Rocky Mountains of North America. In Europe, *R. hirsutum* L., *R. ferrugineum* L., *R. palustre sbp. palustre* L., *R. myrtifolium* K., *R. lapponicum* L. and *R. ponticum* L. are indigenous.

At the end of the 18th century, several plant hunters introduced many species and thousands of new hybrids from Asia to Europe, particularly in Great Britain. In Italy, accessions of subgenus *Rhododendron* started to appear later, during the first years of the 19th century in botanic and private gardens. At present, among the surviving collections, the Burcina Park (Piedmont-Italy) constitutes an important source of germplasm with over 120 old cultivars of notable merit, mainly derived from Belgian and French nurseries, such as Van Houtte and Croux & Fils and Barbier, as reported in the still available delivery notes. Anyway, the few information about this germplasm and labelling mistakes occurred over time have lead to the present difficulty in identifying these rhododendron hybrids. In addition, the parentage of most cultivars is unknown and their phylogenetic relationships are not clear (Remotti and Accati, 2001).

[a] matteo.caser@unito.it

Proc. I[st] IS on Hort in Europe
Ed.: G.R. Dixon
Acta Hort. 817, ISHS 2009

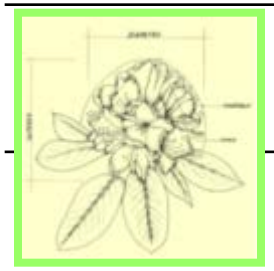
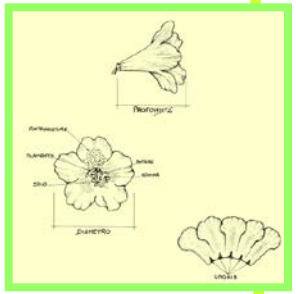
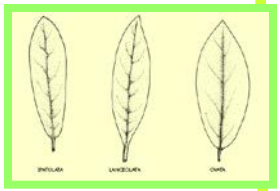
33 genotypes (Parco Burcina, Villa Taranto e Missouri Botanical Garden U.S.A.)

- ***R. ponticum***
- ***R. catawbiense***
- ***R. arboreum***
- ***R. caucasicum***
- ***R. fortunei***
- ***R. edgeworthii***
- ***R. griffithianum***
- ***R. maximum***

'Cunningham's White' (*R. caucasicum* x *R. po*

17 caratteri morfologici

(Remotti and Accati, 2001)

	Variable	Type
	Plant habit	Multistate
	Blooming time	Multistate
	Bloom density	Multistate
truss	Shape	Multistate
	Diameter	Quantitative
	Height	Quantitative
flower	Number	Quantitative
	Diameter	Quantitative
	Deep	Quantitative
	Brink	Multistate
	Petioles lenght	Quantitative
leaf	Shape	Multistate
	Surface	Multistate
	Lenght	Quantitative
	Width	Quantitative
	Adaxial tomentous colour	Quantitative
	Abaxial tomentous colour	Quantitative

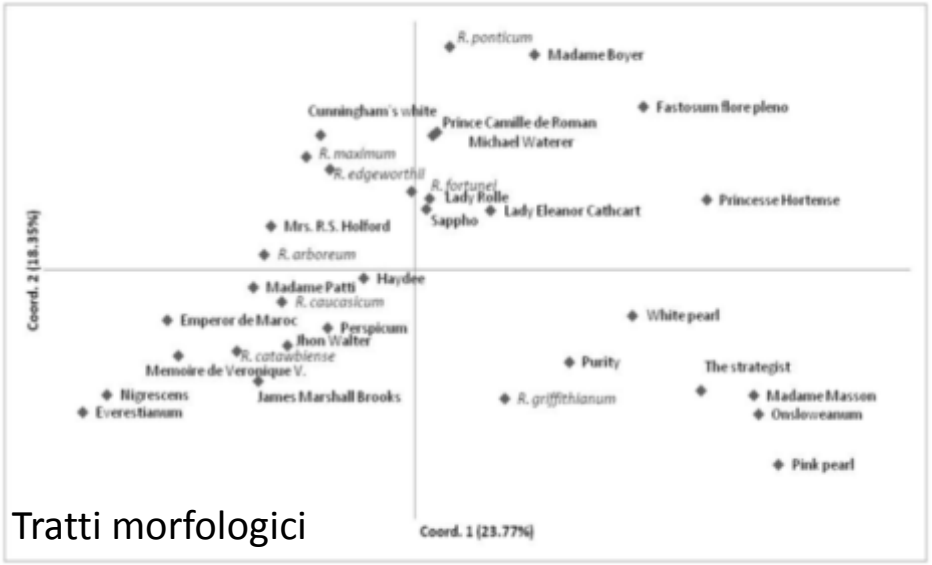
Trait	Mean	Minimum	Maximum	Standard Error
Number of flowers per truss	15.55	3	23	0.73
Flower diameter (mm)	64.03	40	106	2.49
Flower deep (mm)	37.27	24	64	1.44
Leaf lenght (mm)	132.30	75	200	4.51
Leaf width (mm)	46.91	31	70	1.7

Marker system	Shannon Index (I)	Diversity (range)
Morphological	1.797	0.724 (0.415-0.955)

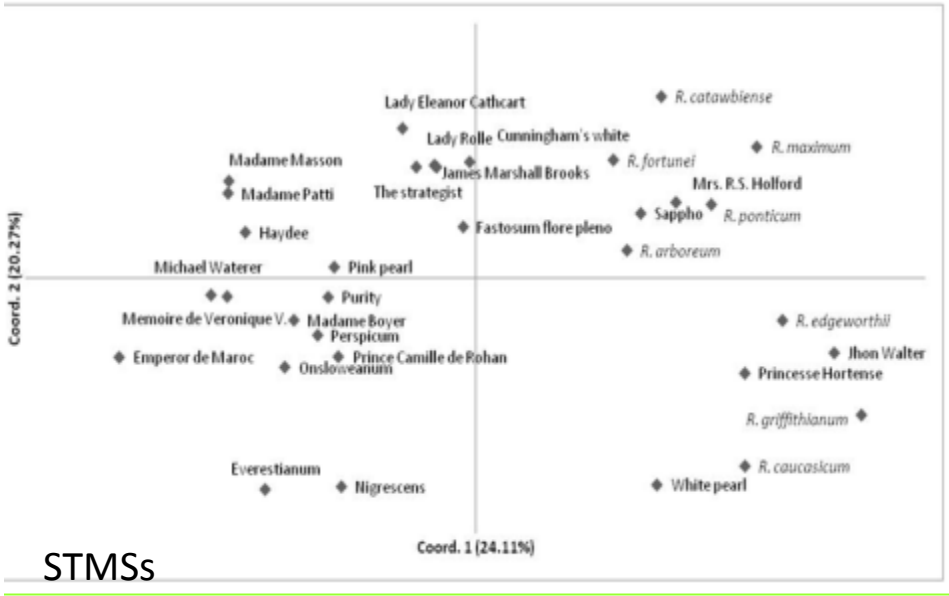
…è stata osservata un'ampia diversità, indicatrice di elevata variabilità tra i genotipi studiati…

Caratterizzazione molecolare

- Estrazione del DNA (Thomas et al. 1993)
- 4 STMS (Dunemann et al. 1998)
- Tutti i primer sono stati marcati con Fluorochrome (6-FAM or HEX)



Tratti morfologici



STMSs

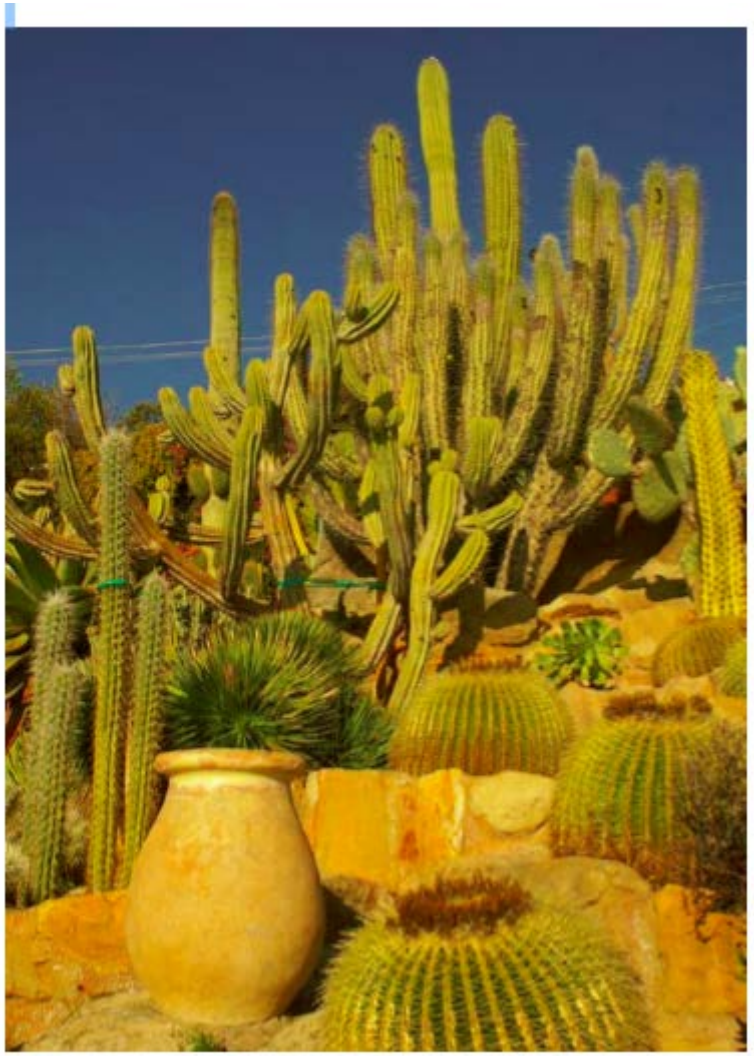
gli STMS hanno permesso un'elevata probabilità di identificazione varietale in Rhododendron…

In particolare sono state rilevate correlazioni tra 'Madame Boyer', 'Lady Rolle', e 'Sappho' con *R. ponticum*; tra 'Perspicuum' e *R. caucasicum*; tra 'Madame Patti' e *R. maximum*,e tra 'Memoire de Dominique Vervaene' e *R. catawbiense*, suggerendo possibili parentele…

Ed. Regione Piemonte

Cactaceae

- One of the most complete and important exotic parks in Italy is the “Exotic Garden Pallanca”. This private collection is the result of the passionate and patient work Pallanca family for four generations: from 1989 became institution open to the public.
- It houses specimens of cacti from all over the world, who over the years have gradually acclimated to the environment of Liguria, acquiring some exceptional size, and rare plants and curious.



The Exotic Garden Pallanca (Bordighera).

Case study:

Palms

BIOLOGIA PLANTARUM 53 (1): 164-166, 2009

BRIEF COMMUNICATION

Development and evaluation of microsatellite markers in *Phoenix dactylifera* L. and their transferability to other *Phoenix* species

A. AKKAK[1]*, V. SCARIOT[2], D. TORELLO MARINONI[3], P. BOCCACCI[3], C. BELTRAMO[3] and R. BOTTA[3]

Dipartimento Scienze Agro-Ambientali, Chimica e Difesa Vegetale, Università degli Studi di Foggia, Via Napoli 25, I-71100 Foggia, Italy[1]
Dipartimento di Agronomia, Selvicoltura e Gestione del Territorio[2]*, and Dipartimento di Colture Arboree*[3]*, Università di Torino, Via Leonardo da Vinci 44, I-10095 Grugliasco, Italy*

Abstract

Forty one simple sequence repeats were isolated from two microsatellite enriched libraries of date palm (*Phoenix dactylifera* L.). After screening, 17 selected microsatellite loci were characterized and evaluated on a set of 31 cultivars and clones from Algerian and Californian germplasm. All primer pairs produced an amplification product of the expected size and detected high polymorphism among the analysed samples. These nuclear simple sequence repeat (SSR) markers are expected to be a very effective tool for evaluating genetic diversity in date palm germplasm. Across-taxa amplification showed the usefulness of most SSR markers in 14 other species across the genus *Phoenix*.

Additional key words: across-taxa transferability, date palm, simple sequence repeats.

Floriculture

- Floriculture is made of a very broad and diverse group of herbaceous and woody plants grown in open field and greenhouse to produce cut flowers and ornamental foliage, houseplants and flowering potted plants.
- In Italy the cultivation of cut flowers on an industrial scale began in Liguria around 1856. The species grown in those years were essentially carnation, violet and rose.
- Gradually the number of species has increased so much that they are now sold over 60 species of cut flowers and foliage.
- While the production of foliage remains the prerogative of Liguria, the cut flower production is shifting more and more towards the south Italy, with the Campania region as a leader.

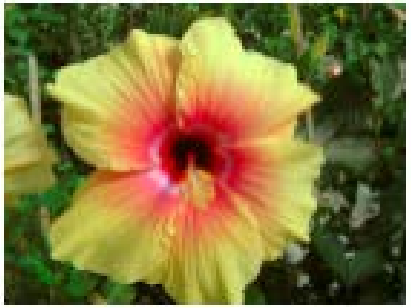
- Collections are mainly preserved by historic private breeding companies.

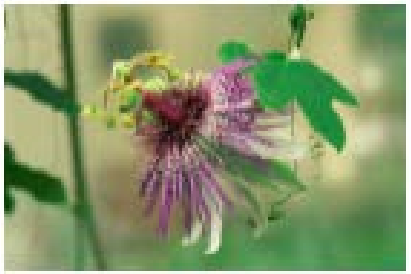
The Liguria region continues to play a predominant role with valuable germplasm of roses, carnations, ranunculus, alstroemeria, aromatic plants and cactaceae.

In parallel, some research institutes of the territory keep rich collections of daisy, hellebore, sage, rosemary, hibiscus, helichrysum, and passionflower.

Hellebore and daisy collections at the Regional Institute for Floriculture (Sanremo).

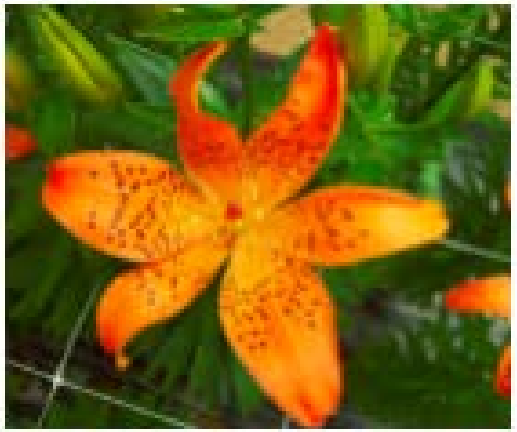
- In Northern Italy, a high degree of specialization has been reached also for poinsettias, geraniums, chrysanthemums, cyclamens and hydrangeas.

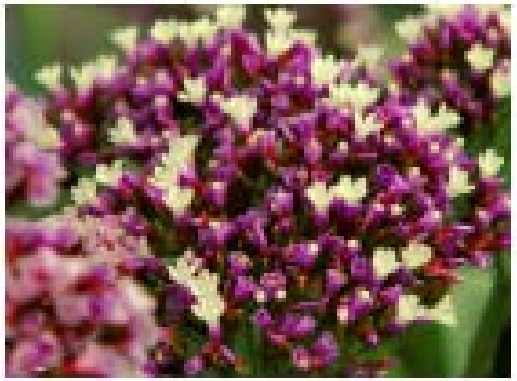




Sage, rosemary, hibiscus, and passionflower, collections at the CRA FSO (Sanremo).

- Moving further south, in Tuscany, we find rich collections of lilies, hydrangea and limonium.

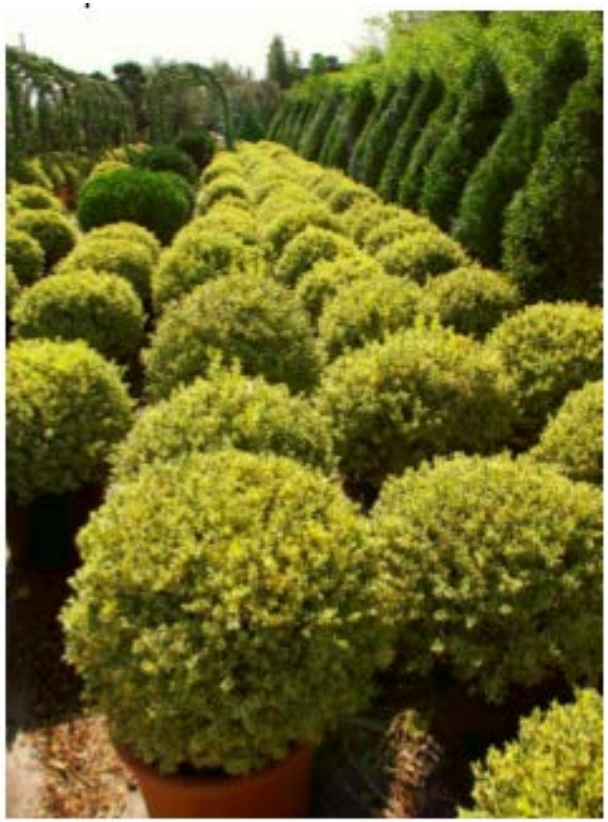




Lilium, hydrangea and limonium collections at the CRA VIV (Pescia)

Ornamental nurseries

- In the field of ornamental nurseries, the region that plays a prominent role is Tuscany.
- Here leading companies mainly located in the Pistoia area have rich collections of Mediterranean plants, citrus, evergreens, fruit trees, climbers, and topiary plants.
- “Hesperidarium” is a unique, international garden with over 200 varieties of ornamental citrus plants from all over the world. A real botanical garden where visitors can admire citrus plants from the 15th century but also rare exotic varieties as well as more recent ones originating from the southern hemisphere.



Production of diverse Mediterranean plants in Tuscany.

Local flora

The Italian spontaneous flora, rich in genera and species, with multiple shapes and blooms, offers interesting possibilities for innovation in the field of floriculture.

From the Alps to Sicily, Italy is characterized by very different environments and climates.

Spontaneous *Cistus salviifolius* in Sicily. A rich collection of *Cistus* spp. was established by the University of Catania.

The remarkable biodiversity found in different habitats of the peninsula is undoubtedly a botanical patrimony for breeding programs. As an example, in the framework of a project (Revflor) funded the Italian Ministry of Agriculture, several universities and research institutes collected and evaluated ornamental potentialities of Arbutus unedo, Campanula, Centranthus, Cistus, Eryngium, Euphorbia, Hydrangea, Limonium, Myrtus, Pancratium maritimum, Peucedanum, Salvia, and Verbascum.

International Journal of Plant Biology 2010; volume 1:e5

Consequences of geographical habitats on population structure and genetic diversity in *Campanula spp.*

Matteo Caser,[1] Valentina Scariot,[1] Paul Arens[2]

[1]Department of Agronomy, Forest and Land Management, University of Turin, Grugliasco (TO), Italy;

[2]Plant Research International (PRI), Wageningen, The Netherlands

diversity in populations is function of gene flow, mutation, inbreeding, population size, and social organization, and has been modelled by biological, ecological, and historical factors related to geo-climatic events.[2-4] Over the last few decades, the study and safeguarding of genetic variation in nature for plastic responses has progressed significantly.[5,6]

Campanula L. species might be considered genetic resources able to persist under a wide range of ecological conditions.[7] In fact, their habitat can vary considerably, from seashore to very high altitude, with colonies found in all major environments from forests to grasslands, and even in rocks.

In the West Italian Alps, five species deserve highlighting above others: 1) *C. barbata* L. (2n = 34;[8]), a hairy short-lived perennial or biennial plant, growing in dry grassland on the siliceous soils of the alpine regions of central and boreal Europe; 2) *C. latifolia* Brantwood (2n = 34;[11]), a perennial plant originating from Northern Europe, growing in acidic soils and forests in the Italian Alps and Northern Apennines; 3) *C. rapunculoides* L. (2n = 68; 2n = 102; [12,13]), a perennial plant, growing on stony and wooded areas of Europe, except for the arctic regions and islands; 4) *C. spicata* L. (2n = 34;[8]), a perennial plant, growing on stones and cliffs and widespread in the Italian Alps and Northern Apennines; and 5) *C. trachelium* L. (2n = 34;[14]), a perennial species native to Europe, from England, throughout the Mediterranean basin, to Northern Africa.[15]

Molecular studies may prove useful in improving spatial genetic variation knowledge and for delineating evolutionary genetic processes.[16-18] Neutral markers such as ampli-

Correspondence: Marco Caser, Department of Agronomy, Forest and Land Management, University of Turin, via L. da Vinci 44, 10095 Grugliasco (TO), Italy.
E-mail: matteo.caser@unito.it

Key words: NBS profiling, myb profiling, campanula, genetic typing.

Acknowledgments: we thank all the staff of the Unito-Floriculture unit for helping collect samples and Hanneke van der Schoot and all the staff of the Plant Breeding Department (Plant Research International-University of Wageningen) for assistance in NBS and myb profiling.

Authors' contributions: MC, main contributor to conception and design, acquisition, analysis, and interpretation of data. VS, critical revision. PA, substantial contributions to conception of the data and final approval of the version to be published. The Authors report no conflicts of interest.

Received for publication: 8 September 2009
Revision received: 18 December 2009
Accepted for publication: 28 December 2009

International Journal of Plant Biology 2010; 1:e5
doi:10.4081/ijpb.2010.e5

by having a structurally conserved DNA binding domain – the MYB DNA binding domain

Fig. 1 *C. barbata* nei pressi della diga del (Moncenisio, TO; 2010 m s.l.m.)

Fig. 2 *C. latifolia* nei pressi della Certosa di Pesio (Valle Pesio, CN; 1400 m s.l.m.)

Fig. 3 *C. rapunculoides* a Troncea (Val Troncea, TO; 1818 m s.l.m.)

Fig. 4 *C. spicata* a Riva Valdobbia (Val Sesia, NO; 1150 m s.l.m.)

Fig. 5 *C. trachelium* a Creola (Val Sesia, NO; 448 m s.l.m.)

GRAZIE