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First results on the phenotypic analysis of wild and cultivated species of *Pyrus* in Sicily

Abstract

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Phenotypic analysis of *Pyrus* in Sicily using a set of 19 characters on 71 accessions belonging to 7 species is here reported. Results show a high level of morphological variation in this genus. Cluster analysis of the morphological characters allows to identify two groups: the first closely related to wild pears and the latter related to *P. communis* s. l. and *P. sicavorum*. It is likely to think that many Ethno-Varieties, usually attributed to *P. communis*, on the contrary are attributable to wild Sicilian pears and belong to indigenous germplasm.

Key words: Morphological diversity, Phenotypic analysis, Agrobiodiversity, Mediterranean area.

Introduction

Pyrus is a taxon of tertiary origin, or it is even older (Rubtsov 1994). It was originated in the mountainous area of western China and it is supposed to evolve and spread eastward and westward (Challice & Westwood 1973; Hummer & Postman 2003). In spite of the wide geographic distribution, in *Pyrus*, as in other woody *Rosaceae* (Korban 1986) the species are intercrossable without major incompatibility barriers (Westwood & Bjornstad 1971). Also, the high morphological diversity and the lack of distinguishing characters among species have been reported (Westwood 1982; Voltas & al. 2007). Therefore, classification of pears is problematic and often confusing, giving different populations designated as different species by some authors (Aldasoro & al. 1996).

In the last years, four new species have been described from Sicily: *Pyrus vallis-demonis* Raimondo & Schicchi from the Nebrodi Mts, *P. sicavorum* Raimondo, Schicchi & P. Marino from the Sicani Mts, *P. castribonensis* Raimondo, Schicchi & Mazzola from the Madonie Mts and *P. ciancioi* P. Marino, G. Castellano, Raimondo & Spadaro from the Nebrodi Mts (NE Sicily) (Marino & al. 2012; Raimondo & Schicchi 2004; Raimondo & al. 2006a, 2006b).

Until now, no investigations on the morphological characterization of wild species of *Pyrus* in Sicily were performed. Therefore, it is necessary to assess the diversity of these

species in order to establish the linkage with the cultivated plants and to evaluate their origins (Schicchi & al. 2009).

Therefore, the main objective of the present study is to assess the phenotypic diversity within and among Sicilian populations of wild pears and to compare them with the cultivated varieties of *P. communis* s. l. domesticated in Sicily (Schicchi & al. 2008a, 2008b) on the one hand, and on the other hand, to clarify how the gene flow with several old cultivated forms could have affected the extraordinary diversity observed today in Sicily in wild *Pyrus* populations as already suggested by Raimondo & Schicchi (2009).

Materials and methods

All the characters were observed and measured on fresh material samples. Voucher specimens have been deposited in the *Herbarium Mediterraneum Panormitanum* (PAL). A set of 19 variables, including 3 binary, 11 qualitative and 5 quantitative measures (Tables 1 and 2), was collected on the basis of 31 observations. Analysis included 1 characters of the branch, 6 of the leaf and 12 of the fruit chosen on the basis of their traditional importance as key characters or their inclusion in the relevant taxonomic descriptions. Adult leaves, one-year-old shoots and ripe fruits were measured using a caliper. All of them were taken from all tree orientations, on central parts of the shoots, and only healthy and undamaged ones were selected.

The variations between accessions for each morphological character were analyzed using Cluster analysis and Euclidean algorithm as Similarity measure. The arithmetic mean of each

Table 1. List and type of characters used.

	Character	Type
1	Presence of spiny branches	Binary
2	Leaf shape	Qualitative
3	Leaf base	Qualitative
4	Leaf apex	Qualitative
5	Leaf margin	Qualitative
6	Petiole diameter	Quantitative
7	Petiole length	Quantitative
8	Fruit weight	Quantitative
9	Fruit shape	Qualitative
10	Peduncle diameter	Quantitative
11	Peduncle length	Quantitative
12	Cup deciduous	Binary
13	Fruit epicarp color	Qualitative
14	Fruit mesocarp lenticels	Binary
15	Fruit mesocarp color	Qualitative
16	Fruit mesocarp weaving	Qualitative
17	Fruit Taste	Qualitative
18	Flowering period	Qualitative
19	Ripening period	Qualitative

Table 2. Statistics of the quantitative characters, measures in mm.

Character / Statistic	6	7	8	10	11
Mean	1.17	40.90	41.13	2.16	32.87
Standard Error	0.31	9.66	18.29	0.81	11.48
Minimum	0,7	20	10	1	10
Q1	1	35	30	2	25
Median	1	40	40	2	30
Q3	1.5	50	52.5	2.75	40
Maximum	2	70	80	4	60

character was calculated. The similarity matrix was built up using standardized measures according to Everitt (1980), Pankurst (1991) and Domina & Mazzola (2003).

On the whole 71 accessions of *Pyrus* sp.pl. from native populations and from the living collection of Botanical Garden of Palermo (Schicchi & al. 2008) were analyzed (Table 3). Some of these accessions have been collected in the *Loci classici* of endemic taxa in the frame of the project to trace the places from where the plants endemic to Italy has been described and to characterize the toptotypical populations (Domina & al. 2012).

Results

UPGMA Cluster analysis of 1349 measures of 71 accessions of *Pyrus* including 6 wild species and 64 cultivars of *P. communis* s. l. was performed in this study. The phenotypic variability in all investigated genotypes are shown in Fig. 1. The dendrogram shows two main clusters: *a1* and *a2*. The first group of genotypes of pear under the cluster *a1* and represented by *P. spinosa*, *P. vallis-demonis*, *P. ciancioi*, *P. pyraster*, *P. castribonensis*, reveals close relationships with 14 traditional cultivars mainly distributed in the Madonie Mts and in the Northern Sicily. The second group *a2* include one wild species *P. sicanorum*: it shows affinity with 51 traditional cultivars traditionally ascribed to *P. communis* s.l.

Discussion

Results allow us to identify two groups of phenotypes: one closely related to those entities of wild *Pyrus* and the other including *P. communis* s.l. cultivars and *P. sicanorum*.

Regarding the cluster “a1” it can be argued that includes cultivars of native species derived from wild species historically present on the Island and closely related to indigenous genetic heritage.

The cluster *a2* include a large group of cultivars of *P. communis* s. l. in some way related to *P. sicanorum*. With regard to this cluster we can make two assumptions: a) *P. sicanorum* is a wild pear derived from the spread of the cultivated entities; b) cultivars of *P. com-*

Table 3. List of studied taxa and source of the material.

Species	Cultivar / Ethno-Var.	Source
<i>Pyrus ciancioi</i>		Floresta (Messina), <i>Locus classicus</i>
<i>Pyrus sicanorum</i>		Prizzi (Palermo), <i>Locus classicus</i>
<i>Pyrus vallis-demonis</i>		Caronia (Messina), <i>Locus classicus</i>
<i>Pyrus castribonensis</i>		Castelbuono (Palermo), <i>Locus classicus</i>
<i>Pyrus pyraister</i>		Botanical Garden of Palermo
<i>Pyrus spinosa</i>		Botanical Garden of Palermo
<i>Pyrus</i> cfr. <i>spinosa</i>		Conca Mt (Caltanissetta)
<i>Pyrus communis</i> s. l.	Azzolu dell'Etna Bagianello Biancu Bruttu beddu Butirra Cannatieddu Caracciulu Castagna Chiuppu Coscia Cucuzzaru Diavulu Ebreu Gaddruzzu Gallo, Garofalu, Gelatu, Genova, Gentili, Giambruni, Giglio, L'Abate, Lordu, Mastru Natali, Muddrisi, Napulitanu, Niuru, Nivuru, Palermu, Par dh San Juvanni, Paradisu, Paradisu tardiu, Partutu, Piriddu majulinu, Piriddu San Petru o Iazzolu, Pisciazzeru, Pottino, Pumu, Pumu di Palazzu, Putiri, Ramunnu, Reale, Realiddruni Reginu, Riiddru, Russignu, San Calò, San Giovanni, San Juvanni, Sant'Anna, Sanu malatu, Sittimminu, Spingula, Taccuni, Totò, Trunzu Tusa Ucciarduni Viridi fattu Viridi fattu grossu Virgulusu Virticchiolu Zuccarinu Zuccarinu dei Sicani	Botanical Garden of Palermo

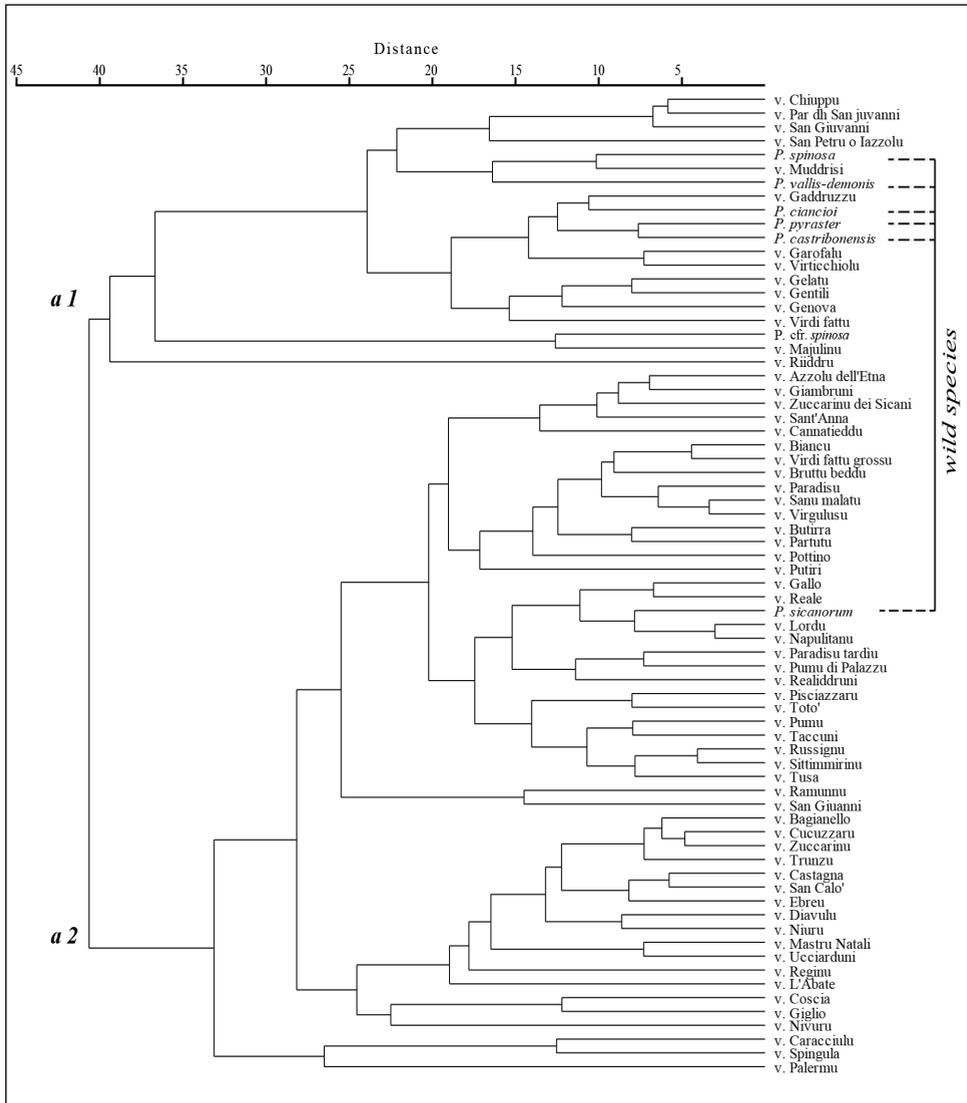


Fig. 1. Cluster analysis of the 71 accessions of *Pyrus* sp. pl. studied.

munis are correlated to *P. sicanorum* were also selected by the wild entity. The most plausible hypothesis is that *P. sicanorum*, quite widespread in the region, seems to be a taxon originated thanks to the spread of traditional cultivars.

Finally, we underline that many ethno-varieties usually attributed to *P. communis* are linked to Sicilian wild pears and belongs to the indigenous germplasm. These results are in agreement with Rivera & al. (1997) and give some new insights for the systematic arrangement of the cultivated pears.

Conclusions

These results open the field to new interpretations on the origins of the cultivated forms and, in our case, on the origin of many ethnovarieties in Sicily, island of considerable extent, inhabited for millennia. In particular, the diversity, rather than by a single taxon (*Pyrus communis* L.), would be to have polyphyletic origin. A second point, which enriches the meanings of this study, concerns the role played by cultivated forms in the diversification of wild plant populations. In this case, it is becoming increasingly evident the action of gene flow coming from the cultivated forms of *Pyrus* on the biodiversity of this genus in nature.

The results, therefore, justify the attention received in recent years by the wild progenitors of cultivated plants (eg, Heywood & Zohary 2007; Zohary & Hopf 2000). It is not, as can be seen, only biological heritage to be seen as a possible source of genes for genetic improvement of cultivated plants, but, in a broadest sense, as a reflection of traditional agricultural activities on the biodiversity evolution.

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