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The Definition of the European Almond Core Collection

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Abstract

The European project 068 AGRI GEN RES 870/2004 has as an aim the definition of the European almond core collection. The methodology for creation of any core collection has to define how best to select entries using complex and incomplete accession data, as well as how and when to revise these decisions over time. The acquisition of data has been based on specific varietal descriptors, including morphological, physiological, phytopathological, genetic and chemical traits, following the descriptors defined by IBPGR/Bioversity, UPOV and the ECP/GR *Prunus* Working Group. Newly defined traits, not included in these descriptors, have also been considered because they are very important in defining the range of variability of the species. These traits include chilling and heat requirements for blooming, the molecular markers for genotype identification and the different chemical components of the kernel, as possible parameters for defining almond quality. As a result, a strategy to define the almond core collection was identified by highlighting the main steps to achieve in the next future.

INTRODUCTION

The European project "Safeguard of hazelnut and almond genetic resources: from traditional uses to novel agro industrial opportunities" (SAFENUT, 068 AGRI GEN RES 870/2004) has, among other objectives, the aim of defining the European almond core collection. A core collection of any species consists of a limited set of accessions chosen to represent the genetic variation of the crop with minimum repetition (Brown, 1989). The methodology for creation of any core collection has to define how best to select entries using complex and incomplete accession data, as well as how and when to revise these decisions over time, with the purpose to capture the common and rare alleles within a fraction (5-10%) of the original collection (Brown, 1989). Thus, the following steps must be taking into account (van Hintum, 1999):

1.- Definition of the material that should be represented.

2.- Division of the domain into groups. Every group of accessions is divided into as genetically distinct subgroups as possible.

3.- Choice of the number of entries in the core and allocation of entries over the groups based on their relative importance and expected diversity.

4.- Selection of the entries from each group that will be included in the core so that the diversity of groups is represented as well as possible.

5.- A preliminary, larger core collection may be created, being characterized further to reduce the number of entries.

In this way, not only geographic and phenotypic characteristics may be used in defining the accessions of the core collection, but also genetic data. Furthermore, a large collection may develop targeted subsamples focused on specific traits or localities of interest. Thus, for the period of this project, wild species will be excluded and only cultivars considered, deciding to establish a large base core collection from which to proceed in further steps.

MATERIALS AND METHODS

The CITA almond collection (Espiau et al., 2002) was taken at the base for the core collection definition because it contains accessions from all over the world and is the GREMPA reference collection. Data from collections of the other participants were also included for the complex analysis.

The methodology for creation of any core collection has to define how best to select entries using complex and incomplete accession data, as well as how and when to revise these decisions over time. The traits for accession characterization were reviewed in order to obtain a wide spectrum of almond variability. The acquisition of data has been based on specific varietal descriptors, including morphological, physiological, phytopathological, genetic and chemical traits, following the descriptors defined by IBPGR/Bioversity (Gülcan, 1985), UPOV and the ECP/GR *Prunus* Working Group. Newly defined traits, not included in these descriptors, have also been considered because they are very important in defining the range of variability of the species. These traits include chilling and heat requirements for blooming (Alonso et al., 2005), the molecular markers for genotype identification (Fernández i Martí et al., 2009) and the different chemical components of the kernel (Kodad, 2006), as possible parameters for defining almond quality (Socias i Company et al., 2008).

Thus, in the CITA collection, representing a very wide range of almond genotypes, molecular analysis have been undertaken for genotype characterization, as well as for chemical analysis. Samples of fruits of some other partners have also been received in order to complete the chemical analysis with a wide range of local cultivars, such as those from Slovenia. The French samples have been analyzed with fruits from the CITA collection

RESULTS AND DISCUSSION

As a first approach to define the almond core collection, a dendogram of a high number of the CITA genotypes has been constructed utilizing only molecular markers (Fig. 1). This dendogram is showing the wide diversity observed among the almond genotypes, showing in addition a close geographical grouping of cultivars (Fernández i Martí et al., 2009).

The biochemical composition of the kernels may also allow to construct a similar dendogram as it has been done with other genotypes (Kodad, 2006). The morphological

and physiological observations will also be added in order to obtain a more reliable dendogram. The final dendogram, combining all the results, will be applied in selecting the genotypes to be included in the almond core collection in order to cover the larger variability with the minimum number of accessions.

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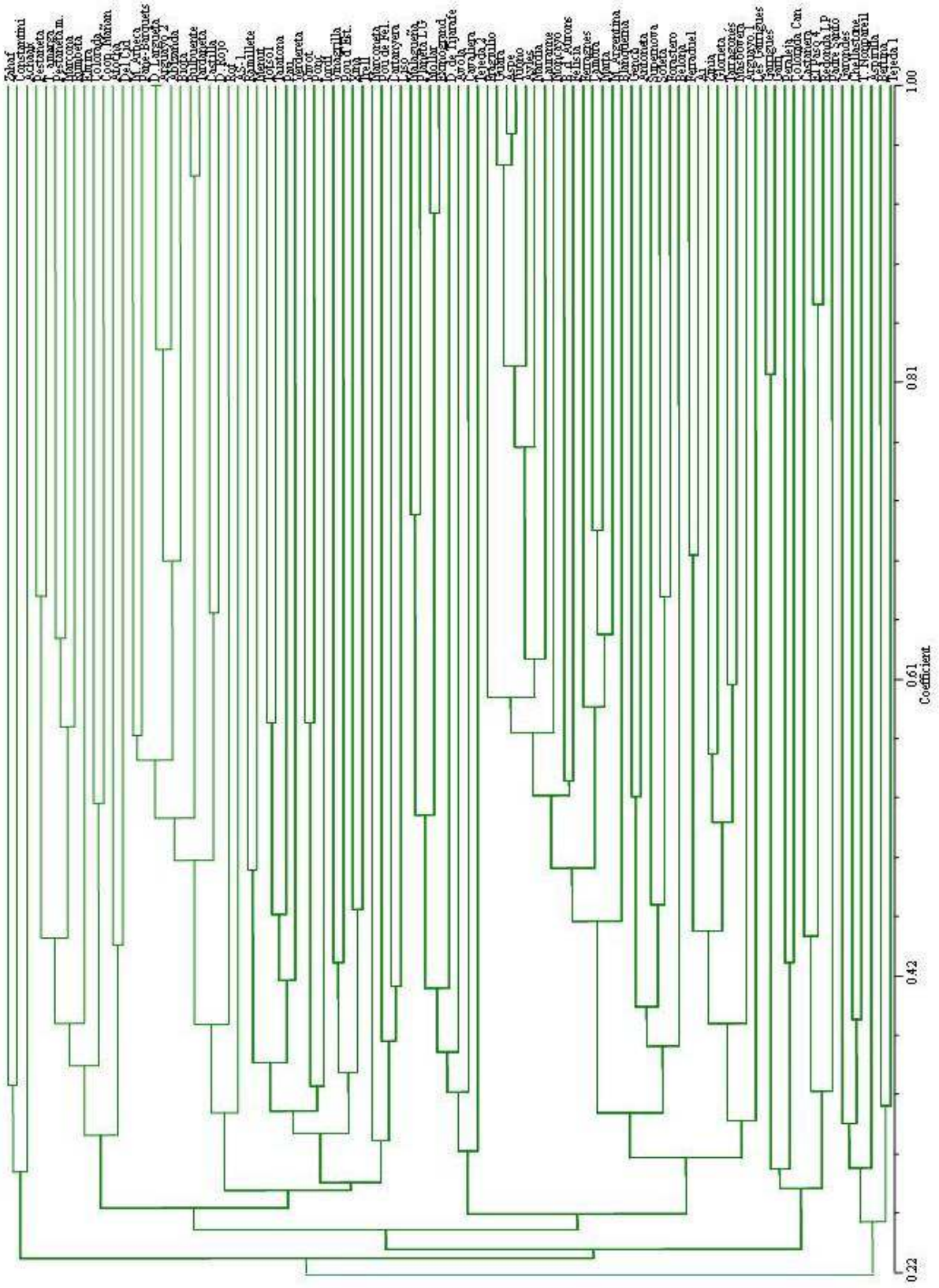

Fig. 1. Dendogram of 93 almond cultivars based on UPGMA analysis using the similarity matrix generated by the Nei and Li coefficients after amplification with 19 SSRs.