On the conservation of the endangered European crab apple (Malus sylvestris): threats from hybridization with domesticated apple (Malus ×domestica).

1 Background

Malus sylvestris is a small tree of the Rosaceae family. Its natural distribution range covers the British Islands and continental Europe except for northern Scandinavia and the southern part of the Iberian Peninsula (Fig. 1). The species is influenced severely by habitat modifications and potentially exposed to interspecific hybridization with cultivated relatives (Klinitzsch et al., 2000). Because of its widespread distribution and early flowering, it is a promiscuous species to hybrids by means of both pollen and seeds (Wagner, 1996). Interspecific hybridization between wild species and their domesticated relatives are likely to reduce the fitness of the wild populations in question and might even lead to their extinction (Brynhild & Stokkehold, 1994). The numerous occurrences of phenotypic intermediacy of the two hybridizing species, M. ×domestica and M. sylvestris, has led to the hypothesis, that the range of closely related Eurasian species actually one panmictic species (Klinitzsch et al., 2000).

In the present study, a total of 176 wild individuals from four Danish populations were studied along with a reference sample of 29 old cultivars. Hybridization and genetic variation was studied using ten microsatellite marker loci. A morphological analysis was performed in order to 1) to identify hybrid occurring in the wild and 2) test for correspondence between phenotype and genotypes of the wild individuals.

3 Microsatellite markers

Large variation was found at the ten microsatellite loci studied as defined by either allele count at a given diversity (Table 1). Great overlap in allele identities were found between the two species, leaving no chance of identification of hybrids by means of private alleles. Therefore ordination (non-metric multidimensional scaling based on Bierwisch et al.'s (1996) allele-sharing distance) and the correspondence analysis were applied to the data set. The result was that two genetically distinct clusters could be identified, ranging from wild and cultivated individuals respectively (Fig. 3 and 4). Only few individuals could be identified as hybrids. In general there was rather poor correspondence between genotypic and morphological indices of hybridization when testing individual genotypes whereas the correspondence was great at the population level. This is taken to be indicative of geographically stable introgression from M. ×domestica.

Table 1 Distribution of alleles studied and number of alleles detected for each locus are shown... (M. ×domestica).

5 Phenology

In addition to genetic incompatibility, differences in flowering phenology is another potential hindrance to interspecific hybridization under natural conditions. In the present study, flowering was observed in two wild populations of M. sylvestris along with two nearby orchards of M. ×domestica in the same area. The later represent a range of early to late flowering cultivars. Beside relatively large variation in individual flowering time within populations of M. ×domestica, a marked difference between the two species was observed (Fig. 7).

4 Morphology

Analyses of hybridization between M. ×domestica and M. sylvestris has to date been dominated by morphological studies (eg. Remmy & Gruber, 1993) and a wide range of characters has been suggested for the differentiation between the two species and their hybrids (Wagner, 1996). In the present study phenotypic evidence of the broad lat of long shoots and the inferior surface of leaves from long and spur shoots was described in August on a scale from 0 to 4 (0 to 3). Hairiness in (5) leaflets where visible above (1) (usually hairy; hairs restricted to the main nerves is indicative of hybrid orchards and 4) is typical for M. ×domestica. Presence data was combined into a phenology index, where (1) indicates hybrid character at one or more of the studied organs and (0) means wild type. Fruits were registered as being of either wild or hybrid type.

From the phenology index a total of 18 individuals out of the 176 studied were identified as possible hybrids. Fruit characters could only be obtained from ca 40% of the individuals. Both investigations found the proportion of morphologically identified hybrids to vary strongly among the four studied populations (Fig. 5 and 6).

6 Conclusion

Based on molecular data, the present study found individuals of M. ×domestica from wild Danish populations and cultivars of M. sylvestris to form two distinct clusters. This indicates that pronounced admixture between the two species is not present. At the population level, a high correspondence was found between geographic isolation from M. ×domestica and genotypic and morphological indices of hybridization. As expected, isolated populations appeared least affected by hybridization than poorly isolated populations. Isolated ‘pure’ M. sylvestris populations could thus be identified indicating that genetic isolation of its progenitor populations is both possible and advisable. However, morphological and molecular evidence of hybridization was found to be emergent in the individual level. This is suggestive of some historical introgression into the M. ×domestica gene pool and indicates that relying exclusively on either morphological or molecular characters as diagnostic markers in studies of hybridization between M. ×domestica and M. sylvestris might lead to falsifiable results. Difference in flowering phenology was observed and can in part explain the low level of contemporary hybridization under Danish conditions.

For further information about hybridization between M. ×domestica and M. sylvestris in an ecological perspective.

References