DNA barcoding should provide an accurate and automatable method for the genetic identification of plant species and varieties by using a standardized genic or integenic region as molecular tag. While in a range of animals, the mitochondrial genes such as the cytochrome oxidase subunit I (COI) have been proved to be suitable for DNA barcoding, in other organisms they are not useful. Land plants, especially angiosperms, seem to be problematic for DNA barcoding since most mitochondrial DNA regions have exceedingly low levels of variation to distinguish between taxa. Furthermore, the mitochondrial genome in plants undergoes significant rearrangement and horizontal transfer of genes, both at intra and interspecific levels. Consequently, it was suggested to use standard DNA regions from the chloroplastic genome that may offer for DNA barcoding in plants what the mitochondrial genome does for animals: it is an uniparentally inherited, nonrecombining and structurally stable genome. For phylogenetic purposes, the locus most commonly exploited in plants is that of the rbcL gene, encoding for ribulose 1,5 bisphosphate carboxylase-oxygenase. This gene was shown to be a good candidate also for genetic traceability. Some authors suggested to adopt an integrated approach of DNA barcoding consisting on the use of multiple genes for a quick and careful identification of species and varieties. Besides rbcL, other chloroplastic genes suitable for DNA barcoding include coding regions such as atpB, ndhF and matK exons and non-coding regions such as the trnL intron and the trnL-F intergenic spacer. Non-coding regions offer the advantages to have fast rates of evolution and to be short so they can be directly amplified and sequenced.

The potentials of the DNA barcoding in plants have not been investigated yet. Theoretically such strategy could be very useful also for assessing the distinctiveness of varieties and determining the relatedness among varieties of crop species, especially for mono-genotype varieties like pure lines, hybrids and clones. Our study deals with the use of DNA barcoding for the genetic recognition of plant species and varieties as well as their food derivatives. As plant materials, several pure lines of bean (Phaseolus vulgaris L.), commercial hybrids of corn (Zea mays L.) and clonal cultivars of grape (Vitis vinifera L.) were used for preliminary investigations of single gene polymorphisms in order to assess the genetic variability within species and the genetic traceability of single varieties. The three species were arbitrarily chosen because of the different reproductive and propagative mechanisms, i.e. sexual reproduction by seeds set through cross-pollination in corn and self-pollination in bean and vegetative propagation by cuttings in grape. Genomic DNA samples were isolated and purified from available plant materials of all species and characterized at the molecular level by amplifying and sequencing specific chloroplastic DNA regions, namely the rbcL gene exon, the intergenic spacer atpB-rbcL and the trnL gene intron. An extensive bioinformatic survey allowed us to preliminary retrieve nucleotide sequences of the selected
chloroplastic DNA regions from the NCBI databases in the *Fabaceae, Poaceae* and *Vitaceae* botanic families: 216, 161 and 26 entries for rbcL; 38, 50 and 28 entries for atpB-rbcL; 151, 103 and 36 entries for trnL, respectively. After serial local multiple sequence alignments, specific primer pairs were designed in highly conserved short stretches flanking the most variable regions in order to clone the orthologous sequences in bean, corn and grape species. The research is in progress with the main goal of discovering sequence-specific SNPs and haplotypes to be exploited for the precise identification of species and varieties.