

CHARACTERISATION OF APPLE-PEAR HYBRIDS (*MALUS DOMESTICA* x *PYRUS COMMUNIS*)

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Apple (*Malus x domestica*) and pear (*Pyrus communis*) are two economically important fruit crops of the temperate zones that have been cultivated in Europe for more than 2.000 years. They belong to the Pyrinae, the former subfamily Maloideae of the Rosaceae. Both are well known for their unique texture and flavors but also by their nutritional qualities. The identical chromosome number ($2n = 2x = 34$) and similar genome size (apple 1,57 pg/2C; pear 1,11 pg/2C), as well as their supposed recent divergence date (33,9 to 55,8 million years ago) and DNA-marker analyses led to the assumption that their genomes might be highly co-linear. Recently, a putative hybrid between *M. domestica* and *P. communis* including five F1 seedlings became available giving a unique perspective not only for genomic, transcriptomic and metabolomic studies but also for advanced breeding strategies. Based on the recent (*Malus*, *Pyrus*) genome projects comparative genomic approaches were applied to identify the genetic differences of the putative hybrid and its five offsprings. Various SSR marker and characteristic ITS sequences gave clear evidence for a hybrid plant. The use of genomics and other -omics technologies (metabolomics, transcriptomics) gave further insight into the genetic reorganization of the hybrid but also enhance and accelerate the breeding process for the development of superior crops for producers and consumers by introducing the gene pool of *Pyrus* into *Malus* traits.