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DEVELOPMENT OF AN INFORMATIVE SET OF SSR MARKERS IN FENNEL

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Fennel (*Foeniculum vulgare* Mill.) is a species belonging to the *Apiaceae* family and is known for its nutritional and pharmacological properties. Despite the economic and agricultural relevance, genomic and transcriptomic data remain poor. The aim of this work was therefore to develop a set of Simple Sequence Repeat (SSR) markers. Microsatellites (SSRs) as codominant molecular markers are known to be a powerful tool for basic and applied research programs in crop plant species. In species for which genomic information are lacking or still poor, it is possible to perform a cross-amplification with markers developed in related species. This method has been proved to be a valid approach for starting analysis of a new species without sequencing analysis and consequently without the necessity to design *de novo* primers.

Here we present preliminary results of primer set developed for *F. vulgare* from a set of 300 *Daucus carota* SSRs for which the transferability value to 23 different *Apiaceae* species (not including fennel) was already tested and showed to be of 63%. Therefore, we started from the 39 primer sets with the highest transferability and tested the power of amplification in fennel. We tested the primer sets in 11 commercial varieties and 9 unknown accessions.

As expected, 7 loci did not give reliable amplicons and 7 others, amplified multiple bands. In these cases, we cloned the fragment of a length comparable to that for the SSR amplicon in the other *Apiaceae* species. These, together to the single-amplicon loci, for a total of 16 amplicons, were cloned and sequenced.

Sequence results showed that in 10 out of 16 loci an SSR motif was found with only 3 confirming the expected motif. These primer sets were then tested on our material and only six showed to be polymorphic. A total of 27 alleles were obtained for the 6 loci (avg of 3 alleles per locus), with a minimum of one and a maximum of eight. Two loci showed alleles very different in length and provided relevant observed heterozygosity (Ho). Data were also used for building a phylogenetic tree. Results will be reported and critically discussed.