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CONCLUSION

Genetic diversity of 47 *H. tuberosus* genotypes using SRAP markers

1. Genetic diversity of 47 *H. tuberosus* genotypes using a total of 9 different combinations of SRAP primers could be amplified 219 distinct bands which ranged from 95 to 2,000 bp. Of which 190 (86.8%) were polymorphic bands. Percentage polymorphism ranged from 53.9% (ME7-EM6), to a maximum of 100.0% (ME2-EM5), with an average of 86.0%. The Polymorphic information content (PIC) ranged from 0.90 to 0.96 with an average 0.95, revealed that all primer combinations had a high polymorphic DNA fragment of 47 *H. tuberosus* genotypes

2. The developed dendrograms through UPGMA clustering for Simple Matching was given highest cophenetic correlation as 0.88262 that evaluated as a convenient combination for detecting the genetic relationships between 47 *H. tuberosus* genotypes and 47 *H. tuberosus* were grouped into three clusters (coefficient = 0.67). The genotype groupings revealed agreement of the origin of *H. tuberosus* in Canada and USA.

Genetic diversity of *H. tuberosus* based on EST-SSR markers

1. 47 of 69 EST sequences homologous to disease resistance genes identified in *H. annuus* while 28 (40.6%) ESTs identified in *Arabidopsis*. These genes could be an important source of R-gene for enhancing resistant trait in Sunflower.

2. With SSR searching in only 69 ESTs of *H. tuberosus* homologous to disease resistance .A total of 41 ESTs contained SSRs which were 59.4%. The pentanucleotide repeat motifs were the most abundant SSRs, accounting for 65.2%, followed by 20.3%, 8.7%, and 5.8% for hexa-, tri- and tetra-nucleotide repeats, respectively.

3. 22 of 27 (81%) designed EST-SSR primers were able to amplify *H. tuberosus* with expected fragment size illustrated the interested genes were amplified

by EST-SSR primers. PCR product clone and sequencing have an alignment result was confirmed.

4. The developed dendrograms through UPGMA clustering for Simple Matching was given highest cophenetic correlation as 0.75884 that evaluated as a convenient combination for detecting the genetic relationships between 47 *H. tuberosus* genotypes and 47 *H. tuberosus* were clearly grouped into three clusters (coefficient = 0.75), but different than grouping by SARP technique.

5. The information will facilitate use of molecular marker for disease resistance in Jerusalem artichoke breeding program.

6. The SRAP techniques can be used for a wide range of genomic scan while the EST-SSR technique is narrower. Therefore, in the further study, this study information can be used in TRAP (Target region amplification polymorphism) technique. The TRAP technique uses two primers (18 nucleotides in length) to generate markers, one of the primers (fixed primer) is designed from the targeted EST sequence and the second primer is an arbitrary primer with either an AT- or GC-rich core to anneal with an intron or exon. As the TRAP technique can be used to generate markers for specific gene sequences, it is useful for genotyping germplasm, mapping QTL and generating markers associated with desirable agronomic traits in crop plants.