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Remodeling Hypothesis of ERV Elements for Host Genome

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ERVs are the unique exterior elements which had been originated from germ line infection of ancient infectious exogenous retroviruses. They had been regarded harmful elements for host genome. However, the results of human genome project gave rise to a question why human genome allowed many portions of ERV elements compared to coding regions. To reveal the specific role of ERV elements, bioinformatic and evolutionary analyses were conducted. Totally, 67 genes were provided the transcript start sites by the ERV elements. Among them, 23 genes have different splicing variants, 33 genes were modified by ERV elements, and 11 genes were created by the ERV elements. Comparison of ERV gene and non-ERV gene showed the different trend of function and process by gene ontology analysis. Possible gene data sets of human (28176 transcripts), orangutan (4611 transcripts), macaca (2103 transcripts), rat (9767 transcripts), and mouse (19508 transcripts) were compared for different usagesof ERV elements. Different ERV elements were applied in different species for supplying the transcript start sites. From our analysis, we proposed the "remodeling hypothesis of ERV elements for host genome". During the species differentiation from common ancestor, many kinds of viral agents could invade the host genome. However, winner who survived from a fierce struggle for existence under the invasion of infective elements could acquire the privilege of using the outside resources for the promotion of their fitness through the remodeling of ERV elements.

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Identification of molecular markers in tomato using RAPD analysis

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Cultivated tomato, *Lycopersicum esculentum*, is a veryimportant crop due to high value of its fruits both for fresh consumption. In the present study, 36 selected cultivars, representing variability for several morphological, physiological, and other characters, were studied for polymorphism employing random amplified DNA (RAPD) analysis with 80 oligonucleotide primers. Of the 80 only 36 primers (45.0%) were polymorphic. Detection of polymorphism in cultivated tomato opens up the possibility of development of its molecular map by judicious selection of genotypes that show DNA polymorphism. This approach will be useful for developing marker-assisted selection tools for genetic enhancement of tomato for desirable traits. We expected that the RAPD analyses assess the amount and structure of genetic diversity among cultivars of tomato in Korea. Lee et al. (2002) studied the relationships of some cultivars of cherry tomato in Korea. However, the genetic diversity and characteristics of some cultivars of tomato in Korea has not been studied. The basic question is it possible to detect the identification of cultivars using RAPD makers.