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Phylogenetic study of the genus *Rosa* (Rosaceae)

Xinfen Gao, Marie Fougere-Danezan, Zhangming Zhu and Yundong Gao
Chinese Academy of Sciences, China

There are about 150-200 species of the genus *Rosa* L which is widely distributed in the northern hemisphere. We have been studying this genus in following three aspects. The first is the phylogenetic study of *Rosa*. We analyzed the sequences data from the nrDNA ITS region and GAPDH gene, the plastid psbA-trnH spacer, trnL intron, trnL-F spacer, trnS-G spacer and trnG intron, the results showed molecular trees are not accordance with the species tree based on the morphological data. The ancestral area reconstruction suggests that despite an early presence on the American continent, most extant American species are the results of a later re-colonization from Asia, probably through the Bering Land Bridge. The results suggest more recent exchanges between Asia and western North America than with eastern North America. Secondly, we explored the hybrid origin of some species by both nrDNA and cpDNA fragments confirmed the wild rose hybrid occurred not only between species of the same section but also between the different sections. The third is studying the origin and differentiation of species complex, gene flow between populations and gene introgression. In the present study, *Rosa sericea* complex as an example, we detected the chloroplast DNA trnL-trnF, ndhF-rpl32 and ndhJ-trnF and nuclear mic*rosa*tellite (nSSR) on eight sites from 763 individuals of 62 populations preliminarily obtained 42 haplotypes. The result reveals the evolutionary lineage of this complex, the demographic history of R. sericea which diverged in the middle Pleistocene, was mostly affected by climatic oscillations instead of by geographical barriers.

xfgao@cib.ac.cn

miRNA alternation in adipose-derived stromal cells during differentiation towards nucleus pulposus cells

Zhen Sun
Fourth Military Medical University, China

The application of stem cell therapy has made tremendous strides in intervertebral disc regeneration. Adipose-Derived Stromal Cells (ADSCs) were found to differentiate to Nucleus Pulposus (NP) cells following co-culture with NP cells. However, it remains unknown in the change of miRNA of the ADSCs during differentiation. Accordingly, the present study is aimed to clarify the miRNA alternation in ADSCs following co-cultured induction. Human ADSCs were co-cultured by Traswell with NP cells obtained from non-degenerate human NP tissue at 50:50 ratios for 7 days. Differentiation of ADSCs was measured and changes of miRNA in ADSCs were assessed by microarray. The ADSCs was showed to differentiate to the NP cell phenotype with an increased expression of related extracellular matrix. Importantly, it was found that 29 miRNAs were differentially expressed in the ADSCs following differentiation. The expression of miR-29a-5p, miR-4725-5p and miR-190a were up-regulated whereas miR-802, miR-345-3p and miR-3201 were down-regulated (Fold Change>=2.0, $p<0.05$). In conclusion, this study provides an essential understanding and expands our knowledge of ADSCs differentiation in disc regeneration in miRNA level.

fmmusunzhen@126.com