



## Proteome analysis of tobacco leaves reveals dynamic changes in protein expression among different cultivation areas

L.M. Lu, K.Y. Ye, Z.X. Tang, L. Liu, Y. Chen, J. Luo and Y.B. Huang

Agronomy College, Sichuan Agricultural University, Chengdu,  
People's Republic of China

Corresponding author: Y.B. Huang  
E-mail: yubihuang@sohu.com

Genet. Mol. Res. 14 (4): 15276-15284 (2015)  
Received September 15, 2014  
Accepted February 19, 2015  
Published November 30, 2015  
DOI <http://dx.doi.org/10.4238/2015.November.30.3>

**ABSTRACT.** The leaves of tobacco plants were used to analyze differences in protein content of tobacco grown in the four main flue-cured tobacco-producing areas of Sichuan Province, China. An improved protein extraction method, isoelectric focusing/sodium dodecyl sulfate-polyacrylamide gel electrophoresis two-dimensional gel electrophoretic separation, was used to extract and separate total protein from tobacco leaves. Proteomic maps with relatively high resolution and repeatability were produced. At isoelectric points 4 to 7 and molecular weight ranging from 20-100 kDa, we detected 1032, 1030, 1019, and 1011 clearly visible protein spots in tobacco leaves from the four study areas. Proteome comparison between these protein spots showed that 119 spots with a greater than 2-fold change in expression quantity contributed to the variation in expression. Of which, 115 were successfully identified and annotated. According to the annotation results, these proteins participate in photosynthesis, energy metabolism, mineral nutrition, terpene metabolism, defensive reaction, and other physiological and biochemical processes. This study preliminarily explains the effects of ecological conditions on

the physiological metabolism of tobacco leaves and how such effects directly or indirectly contribute to tobacco leaf quality.

**Key words:** Flue-cured tobacco; Proteome; Ecology; Leaf quality; Two-dimensional electrophoresis