

# Genomic polymorphism and protein changes of soybean mutant induced by space environment

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Soybean 194(4126) of excellent agricultural qualities such as high yield and rounder and wider leaf, was selected in six generation after abroad recoverable satellite 15 days in 1996 from Soybean 72163 (featured with long-leaf, white-blossom, grey-hair and infinitude-podding). To explore the mechanisms of plant mutation induced by space environment, we have experimented at genome and proteome level on Soybean 194(4126) and its control Soybean 72163. Amplified Fragment Length Polymorphism (AFLP) was used to identify mutated sites, and the result shows that 36 polymorphic bands, varying between 100 and 900 bp in 2022 DNA bands, varying between 100 and 1500 bp, have been amplified out of 64 pairs of primer combinations between mutant Soybean 194(4126) and the control plant. So the mutation degree of DNA is 3.56%.

The protein two-dimensional electrophoresis (2-DE) and peptide mass fingerprint (PMF) assays were used to investigate the difference of proteins in fruits and leaves between Soybean 194(4126) and its control. Results indicate that 62 protein dots specially appear in Soybean 72163 and 39 dots specially in the mutant Soybean 194(4126) by image analysis software PDQuest in the 2-DE maps of soybean seeds. Using PMF assay and protein data-base searching to investigate two distinct protein dots, we found that the protein specially expressed in the seed of mutant Soybean 194(4126) may be Dehydrin and the other protein specially expressed in the seed of the control Soybean 72163 may be maturation-associated protein MAT1. Because Dehydrin and MAT1 are both related with droughty resistance, it is necessary that further comparative study between Soybean 194(4126) and its control plant about it. In addition, we detected 60 protein dots specially expressed in the leaves of Soybean 72163 and 36 protein dots specially expressed in that of the mutant Soybean 194(4126) by the image analysis software PDQuest. Using PMF assay and protein data-base searching to investigate 1 protein dot specially in the mutant Soybean 194(4126), we suggested that it may be chloroplastic quinone-oxidoreductase homolog ceQORH. It exists in the inner membrane of chloroplast, and is concerned with the oxidation revivification chain. Its structure is similar with the quinone-oxidoreductase in the bacteria, epiphyte or animal. Whether it gets relationship with the high yield in the mutant Soybean 194(4126) should be further studied. Our experiments will ground for improving soybean breed and provide us the foundation for exploring the mechanism of the mutation induced by space environment.

This work was supported by 863 project of China (No. 2004AA231071) and the Scientific Research Foundation of Harbin Institution of Technology (No. HIT.200.00).