

# Characteristics and genetic diversity of soybean genetic resources in Northeast China

N. YAMANAKA<sup>1</sup>, A. OKABE<sup>2</sup>, T. ADACHI<sup>1</sup>, C. YANG<sup>3</sup>, G. YANG<sup>3</sup>, Z. YANG<sup>3</sup>, X. MA<sup>3</sup>,  
L. CAI<sup>3</sup> and Z. SONG<sup>3</sup>

<sup>1</sup>Biological Resources Division, JIRCAS

<sup>2</sup>National Agricultural Research Center for Western Region, Japan

<sup>3</sup>Soybean Research Center, Jilin Academy of Agricultural Sciences, China

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## Objectives

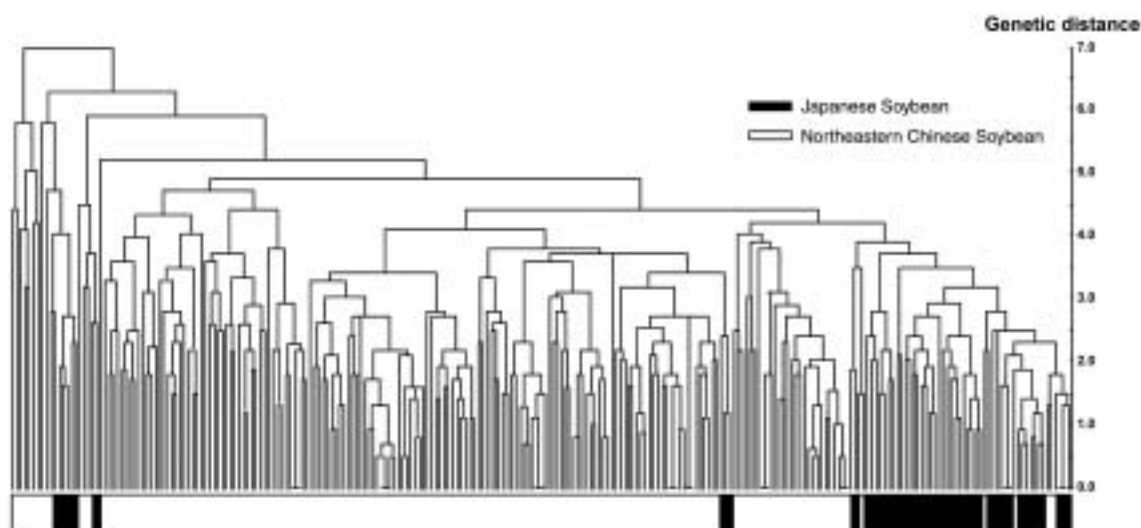
Northeast China is thought to be one of the regions from which soybean originated, due to the existence of a number of valuable soybean varieties in this region. Although these soybean varieties are important as genetic resources, their primary characteristics and genetic diversity have not yet been clarified. Therefore, we studied the main characteristics of some 3,000 soybean genetic resources and constructed a database, aiming to improve the efficiency of their utilization as breeding stock. In addition, we evaluated their diversity to clarify the usefulness of northeast Chinese soybean genetic resources.

## Results

In evaluation of primary characteristics, considerable variation was found in the quantitative and qualitative characteristics. For example, a large variation was found in main stem length, ranging from 7 to 277 cm, with a mean value of 86 cm. This measurement was somewhat longer than that of Japanese varieties, but the incidence of lodging tends to be small, except for climbing varieties. There were some varieties that were rich in protein content and low in oil content, while others had high oil content and low protein content. Highest and lowest protein contents were 59.4 and 11.5%, and highest and lowest oil contents were 23.6 and 10.3% , respectively. Chinese soybean genetic resources clearly showed a wide range of variation in protein and oil content. It is considered that many varieties would be useful as materials for various types of industrial processing. As these results show, soybean genetic resources in Northeast China harbor great diversity and differ in some traits from Japanese varieties. They may thus hold great potential as breeding materials.

In order to evaluate soybean genetic resources at the DNA level, utilization of soybean SSR markers to classify varieties and investigation of genetic diversity is necessitated. The plant materials that were used as subject matter for this research totaled 253 types: 194 varieties of Northeast Chinese soybean genetic resources and, for comparison, 59 Japanese soybean varieties. The evaluation of genetic diversity and classification of varieties were conducted through cluster analysis. Almost all varieties and most Japanese varieties can be classified into one cluster, as a subgroup of Chinese varieties (Fig. 1). These results indicate that the Northeast Chinese and Japanese soybean genetic resources are distantly related genetically and that Chinese genetic resources are clearly rich in diversity at the DNA level; thus, the incorporation of both Japanese and Chinese genetic resources into new soybean varieties will be effective for promoting enhanced breeding strategies.

The database of Chinese soybean genetic resources is available via Internet (<http://www.jircas.affrc.go.jp/DB/guide-eng.html>).



**Fig. 1.** A dendrogram (UPGMA) of Japanese and northeastern Chinese soybean varieties based on SSR markers. Black and white boxes denote Japanese and northeastern Chinese soybean groups, respectively.

## References

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**E-mail address:** naokiy@jircas.affrc.go.jp