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ITEMS FROM JAPAN

**NATIONAL INSTITUTE OF CROP SCIENCE (NICS) – NATIONAL AGRICULTURE
AND FOOD RESEARCH ORGANIZATION (NARO)**
Tsukuba, Ibaraki 305-8518, Japan.

A possible transmission route for common wheat to Japan by the distribution of high-molecular-weight glutenin subunit Glu-D1f; two transmission routes to Japan, a direct route via China and one via the Korean peninsula.

Hiro Nakamura.

High-molecular-weight (HMW) glutenin subunits make up a group of seed endosperm proteins of common wheat. This group has been extensively explored during the past 25 years, and its members have an important effect on the quality of bread and/or noodles made from wheat. HMW glutenin alleles, such as *Glu-D1*, are of particular significance for Japanese bread and/or udon products (Nakamura and Fujimaki 2002). The *Glu-D1f* allele has a major influence on Japanese common wheat. It is thus important to understand the genetic diversity of this allele in noodle-culture zones such as Asia compared with bread-culture zones such as Europe, Canada, and the USA (Nakamura 2001, Nakamura and Fujimaki 2001). Common wheat (2n=42, AABBDD) is thought to have originated about 7,000 years ago in the Middle

and Near East and was subsequently transported to Europe, Africa, southern Asia, and China. The cultivation of wheat can be traced back to 3,000 years ago in China (Zhang 1983), where it was a major crop at the time (Sun et al. 2000). Some common wheat cultivars were transported along the so-called Silk Road through China to the Far East, the Korean Peninsula, and finally Japan. Little is known, however, about the precise route of transmission of common wheat to Japan. Previous studies have concentrated on the variation in the HMW-glutenin *Glu-D1* allele, and the factors that have affected its distribution in different parts of the world (Nakamura 1999, 2000a, b, and c, 2001; Nakamura et al. 1999; Nakamura and Fujimaki 2001, 2002). Recently, a specific route of transmission for common wheat to eastern China and Japan was suggested (Nakamura 2002). Variation in the frequency of the *Glu-D1f* allele in different wheat varieties suggested a possible transmission route for common wheat to the Far East and Japan (Nakamura 2002). Distribution of the *Glu-D1* alleles throughout Asia, including the Korean Peninsula, was examined to estimate the route by which common wheat reached the most geographically remote regions of its production in the Far East, Japan.

The present study showed that carriers of the *Glu-D1f* allele were distributed across a limited region of Asia, comprising southern and northern Japan, Xinjiang in northwest China, Nanjing, and Zhejiang in southeastern China, Beijing in northeast China, the Korean Peninsula, and Afghanistan (Nakamura 2008). However, the allele was relatively rare in wheat cultivars from north Japan, the Korean Peninsula, China, and Afghanistan. The frequencies of *Glu-A1*, *Glu-B1*, and *Glu-D1* alleles in common wheat varieties are known to differ between Japan and other countries (Nakamura et al. 1999, Nakamura 1999). The HMW glutenin 2.2 subunit controlled by the *Glu-D1f* allele was frequently found among Japanese improved cultivars, as well as in Japanese landraces. However, only a few of the Korean, Chinese, and Afghani wheat cultivars possessed this allele. *Glu-D1f* was reported to be rare in previous studies of the worldwide distribution of *Glu-1* alleles (Nakamura and Fujimaki 2002). Moreover, this allele was found to be more common in wheat seed storage proteins from Japan than in those from bread-culture zones (Nakamura 2000a, b, c, 2001). The present study showed that the *Glu-D1f* allele was more common in Japan than elsewhere in Asia, including the Korean Peninsula. The frequency of this allele was shown to be in excess of 35% among improved Japanese cultivars and 25.3% among Japanese landraces, whereas it was found in only 1.4% of Chinese cultivars, 6.9% of Korean cultivars, and 9.5% of Afghani cultivars, respectively. This allele was identified in five Chinese cultivars (two in Xinjiang, one in Jiangsu, one in Zhejiang, and one in Beijing), in five cultivars from the Korean Peninsula, and in two Afghani cultivars. These results suggest that there are no other wheat cultivars possessing the *Glu-D1f* allele in any other region of Asia. In this study, the Far East implies only the Korean peninsula and Japan, not including eastern China (Nakamura 2008). The Far East, Japan is remote from most other wheat growing areas. In the course of its long journey and its adaptation to diverse local environments, Japanese common wheat appears to have depleted its genetic diversity. The frequency of the *Glu-D1f* allele differed between the Japanese and other Asian common wheat cultivars, including those from the Korean peninsula. Therefore, it is possible that all Japanese wheat cultivars have a common heritage. This hypothesis explains the similarities in *Glu-1* patterns among Japanese wheat cultivars. The distribution of an adaptively neutral character revealed by this study suggests two specific routes of transmission for common wheat to the Far East: either to eastern China and Japan, or to eastern China, the Korean Peninsula, and Japan. In the first scenario, wheat was introduced from Afghanistan, transported to Xinjiang in northwest China, to Shaanxi, Nanjing, and Zhejiang in southeast China, and then to southern Japan along the Silk Road. In the second scenario, wheat was introduced from Afghanistan, transported to Xinjiang in northwest China, to Shaanxi and Beijing in northeast China, to the Korean Peninsula, and then to southern Japan. During the course of its transmission and its adaptation to diverse local environments, Japanese common wheat has developed a unique set of glutenin alleles including the worldwide rare *Glu-D1f* allele, which is correlated with the quality of Japanese Udon products. Two possible transmission routes for common wheat through the Far East were detected in this study, a Chinese Route that was previously reported (Nakamura 2002b), and a new one via the Korean peninsula (Nakamura 2008).

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ITEMS FROM MEXICO

CIMMYT—INTERNATIONAL MAIZE AND WHEAT IMPROVEMENT CENTER Lisboa 27, Apartado Postal 6-641, 06600 México, D.F., México.

Wheat chemistry and quality improvement.

Roberto J. Peña.

Quality characterization/screening for wheat quality improvement. At CIMMYT, wheat experimental lines are tested for quality attributes and classified according to its potential end-use. Breeders and agronomists receive quality data, a classification of the lines according to their potential end use, and recommendations of the best sources of quality. This action helps breeders to identify lines to be used as quality sources in new crosses and allows screening and selection of quality-desirable lines throughout the breeding process. The wheat quality classification we use was developed based on observed and documented relationships between specific quality traits and end-use quality (bread, cookies, noodles, pasta, etc); actual observation of wheat-based food processing in different countries; and consultations with NARS.

Crop improvement, quality testing/screening. Approximately 18,700 entries were tested for wheat quality characterization using a few rapid small-scale tests to full-quality analysis. The tested materials included late-segregating lines (tested in Obregon), advanced lines (from both the spring and winter wheat programs), elite lines for candidates to international nurseries, and lines from national programs and special projects in breeding and agronomy (tested in El Batán).

Breeders received recommendations on the best quality sources (for diverse uses) to include in new crosses. We also suggested which lines to advance or include in international nurseries or to consider for cultivar registration (in the case of National programs).

In addition, SDS-PAGE to determine *Glu-1/Glu-3* glutenin composition and T1B·1R translocation status was applied to 8,000 bread and 4,175 durum wheat samples. The samples analyzed for glutenin composition were part of the wheat-improvement programs and special projects, including theses work of graduate students.

Sources of grain quality. Identifying the best sources of quality for new crosses has been an effective strategy to combine grain yield and quality. The proportion of lines having acceptable to excellent quality in the CBRF (2007–08) and CBBWIR (2007–08) populations were 40.2% and 27.1% , respectively. The top 10 best sources of gluten extensibility