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OA-01

## Genetic Allelism of Shrunken Endosperm in High-Lysine Barley : Is It Possible to Develop High-Lysine Barley Cultivars?

Hong-Sik Kim<sup>1\*</sup>, Sun-Lim Kim<sup>2</sup>, Seong-Bum Baek<sup>1</sup>, Hwa-Young Heo<sup>1</sup>, Kwang-Geun Park<sup>1</sup>, and Si-Ju Kim<sup>1</sup>

<sup>1</sup> Div. of Breeding Resource Development, National Institute of Crop Sci., RDA, Suwon 441-857, Rep. of Korea

<sup>2</sup> Div. of Post Harvest Technology, National Institute of Crop Sci., RDA, Suwon 441-857, Rep. of Korea

\* Corresponding Author Email: kimhongs@rda.go.kr

Most cereals are deficient primarily in lysine, one of the most important basic amino acids. Recently, a mutant line, 'M98', chemically induced from 'Chalssalbori' was developed and characterized by high nutritional value of lysine and other components. 'M98' had also an undesirable seed trait of shrunken endosperm, likewise other high-lysine barley mutant genetic stocks. All F<sub>1</sub> hybrids between 'M98' and high-lysine genetic stocks had plump endosperm except for GSHO2035 and GSHO2475 both of which had a dominantly inherited Lys4. The F<sub>1</sub> was lower than one or both parents in lysine content for each cross. Segregation of F<sub>2</sub> seeds from F<sub>1</sub> plants was fit to 9:7, plump:shrunken endosperm for only one cross of GSHO1784/M98, indicating the presence of independent non-allelic genes in crosses for shrunken trait. However, no typical segregation ratios of 9:7 or 1:1 was found in F<sub>2</sub> seeds from the other crosses where higher frequency of shrunken seeds was observed. Plump seeds were lower than the shrunken seeds in lysine in the F<sub>2</sub>. Seventy-three F<sub>4</sub>-bulk plump lines from the cross of 'Chalssalbori'/'M98' ranged from 0.43 to 0.58 in % lysine of total amino acid, and did not exceed in the average (0.64) of high-lysine genetic stocks. So far, F<sub>5</sub>-bulk plump lines from the same cross have been evaluated for lysine content.

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## Molecular diversity and relationships among diverse sources of maize inbreds

Suk-Ha Lee<sup>1\*</sup>, Da-Hao Zheng<sup>1,2</sup>, Kyujung Van<sup>1</sup>, Moon Young Kim<sup>1</sup>, Chunmei Cai<sup>1</sup>, and Taehun Jun<sup>1</sup>

<sup>1</sup> School of Plant Science, Seoul National University, Seoul 151-742, South Korea

<sup>2</sup> Department of agronomy, Yanbian University, Longjing 133400, Jilin, P.R. China

\* Corresponding Author Email: sukhalee@snu.ac.kr

With 36 elite maize inbreds from current China maize breeding, U.S. and CIMMYT populations, allelic diversity and cluster analysis was determined using SSR marker genotyping data. A total of 652 alleles at the 109 SSR loci were detected with an average of  $5.98 \pm 3.13$  alleles per locus. Among the alleles, 35.89% and 12.73% of alleles were unique to the inbreds from China current heterotic groups and American populations, respectively. Of the molecular variation, 34.14% was found among groups, and 65.86% was found within groups. Mean of alleles per locus in China current inbreds ( $5.22 \pm 2.46$ ) was significantly higher than that in American first-cycle inbreds ( $3.84 \pm 1.65$ ) ( $P < 0.00001$ ), and the genetic diversity of China current inbreds ( $0.654 \pm 0.158$ ) was significantly higher than that of American first-cycle inbreds ( $0.59 \pm 0.17$ ) ( $P < 0.00001$ ). Within various groups, genetic diversities in BSSS (0.35) and BSCB1 (0.29), BS11 (0.36) and Pool1 41 (0.35) were lower than those in TSPT (0.47), LDRC (0.41), Mo17Sub (0.45) and IR (0.52) groups. The inbreds from the domestic TSPT group had larger genetic distances compared with the inbreds from BSSS, BSCB1, BS11 and Pool41 (0.71 - 0.73). Nevertheless, the maximum distance was detected between BS11 and Pool41 (0.74). The relationships based on SSR marker data showed that BSSS, BSCB1, BS11 and Pool41 were diverged substantially from China current inbreds of TSPT, LDRC and LCS groups.