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Grant Title: Genetic Characterization of *Lophopyrum Elongatum* Salt Tolerance and Associated Ion Regulation as Expressed in Bread Wheat

Lophopurum elongatum is a highly salt-tolerant relative of wheat. Its salt tolerance is partially expressed in the amphiploid from a cross between wheat cv. Chinese Spring and *L. elongatum*. Genetic studies showed that the tolerance of gradually imposed salt stress is controlled by *L. elongatum* chromosomes 3E, 4E, 5E, and 7E and the tolerance of suddenly imposed salt stress by chromosomes 3E, 5E, 6E, and 7E. In wheat, rye, barley, and *Dasypyrum*, chromosomes of the same homoeologous groups, 3, 5, 6, and 7, were found to control the tolerance of these stress regimes. To gain insight into the physiological mechanisms of salt tolerance by wheat and *L. elongatum*, accumulation of Na and K, 20 protein amino acids, glycinebetaine, aminobutyrate, all TCA cycle intermediates, oxalate, glycerol-3-P, glyceraldehyde-3-P, pyruvate, lactate, ornithine, taurine, glucose, sucrose and other sugars was examined in the amphiploid and Chinese Spring by gas chromatography and H-NMR. The greater Na exclusion from the most recently expanded leaf blades of the amphiploid than Chinese Spring was found to be paralleled by greater accumulation of glycinebetaine in the young leave blades of the amphiploid. The amphiploid accumulated more asparagine in all leaves than Chinese Spring. Old leaves accumulated proline instead of glycinebetaine. There were no differences between the young leaves of the two genotypes in the proline concentrations. The proline concentrations in the old leaves were greater in Chinese Spring than in the amphiploid. This strongly suggests that the accumulation of proline is not a primary mechanism of salt stress tolerance in either *L. elongatum* or in wheat while glycinebetaine and asparagine are strong candidates.

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