Characterisation of naturalised populations of *Thinopyrum ponticum* Podp through indexes obtained under saline stress

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Introduction Argentina has 2.5 million hectares considered marginal for agriculture, with salinity problems that limit productivity. Among the adapted species, *Thinopyrum ponticum* is one of the perennial grasses worth mentioning because of its adaptation to lowland and salty soils. On soils with low osmotic potentials, available water is reduced, and toxicity due to ion concentration arises. Salt tolerance is genetically determined and its improvement is similar to any other character in that requires genetic variability and evaluation methods to identify superior genotypes. Due to the essentially low-intensity livestock production in Argentina, and the soil limitations in marginal environments, the characterisation and evaluation of germplasm is important in order to have a higher genetic diversity. The knowledge of parameters, procedures and methodologies for the evaluation of genetic diversity would help to plan future collection efforts aiming to add divergent populations. The objectives of this work, were to characterise *T. ponticum* germination under saline stress in ten naturalised populations through the Relative Index of salt Tolerance (RIT) (Pearen *et al*., 1997) and to quantify population diversity through the Shannon-Wiener index (**H**)(Pielou, 1969).

Materials and methods The seeds were sown in plastic trays, paper substrate, and wetted with NaCl solutions, with conductivity at 0, 6, 12 y 18 decisiemens per meter (dS/m). The osmotic potential of these solutions were 0; -0,26; -0,6 y –1,0 MPa. The conditions for germination were: 20-30ºC, 16L:8D), in a completely randomised block design, with 4 replicates and counts up to 25 days. For each population the RIT was calculated, values close to 1 indicate higher tolerance. The Hi were calculated as: $\mathbf{Hi=-}\sum_{i=1}^{n} \mathbf{pi \cdot log_2\, pi}$; where **pi= nji/nj**.; **nji**= germinated seeds of the j population at each salinity level (i), and **nj** = germinated seeds at the three levels. This H value indicates niche breadth regarding tolerance for each population. This breadth has both genetic and phenotypic components; the lower the value, the more restricted the response range. This index allows for comparing populations. The H by salinity level is, $\mathbf{Hsk=-}\sum_{i=1}^{n} \mathbf{pk \cdot log_2\, pk}$; where **pjk=nk/n.1** indicates germination diversity for all the populations taken together at a given level (s). A low value indicates that there are few populations that germinate well at that level.

Results The results allowed the identification of more tolerant populations both in quantity and germination time. At the higher stress levels (12 y 18 dS/m) populations were more susceptible but three of them showed tolerance to all the salinity levels tested. The Hi ranged from 1.56 to 1.37, with some populations differing significantly (Table 1). The Hsk were lower at higher salinity levels ranging from 3.46 to 3.36. The contribution to the total diversity was 70% for salinity level, and 30% for niche breadth.

Table 1. Estimates of the diversity index (Hi) and Relative Index of salt Tolerance (RIT) for each population over salinities of 6, 12 and 18 dS/m. Based on germinated seeds data. Duncan Test, significant at 0.05 level.

Populations	Hi	RIT	Populations	Hi	RIT
1	1.45 bc	0.31	7	1.47 ab	0.34
2	1.44 c	0.27	8	1.43 bc	0.27
3	1.56 a	0.64	9	1.53 ab	0.48
4	1.49 bc	0.36	10	1.55 a	0.57
5	1.52 ab	0.47	11	1.42 c	0.27
6	1.37 c	0.21			

The RIT would be an effective tool for salinity tolerance evaluation. Along with the Shannon-Wiener index it could provide new tools for the collection, characterisation and evaluation of genetic resources.

References

Pearen, J.R.; Pahl, M.D.; Wolynetz, M.S.; Hermesh,R. 1997. Canadian Journal of Plant Science. 77:81-89.
Pielou, E. C. 1969. An Introduction to Mathematical Ecology. Wiley. New York.