

**Salt tolerance response revealed by RNA-Seq in a diploid halophytic wild  
relative of sweet potato**

Yan Luo<sup>1,2\*</sup>, Robert Reid<sup>3\*</sup>, Daniella Freese<sup>1,3</sup>, Changbao Li<sup>4</sup>, Jonathan Watkins<sup>5</sup>, Huazhong Shi<sup>6</sup>,  
Hengyou Zhang<sup>1</sup>, Ann Loraine<sup>3&</sup>, and Bao-Hua Song<sup>1&</sup>

1. Department of Biological Sciences, University of North Carolina at Charlotte, Charlotte, NC 28223, USA
2. Key Laboratory of Tropical Forest Ecology, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Kunming, Yunnan, 666303, China
3. Department of Bioinformatics and Genomics, University of North Carolina at Charlotte, Charlotte, NC 28223, USA
4. Breeding group, Monsanto Company, St. Louis, MO, 63141, USA
5. Department of Geography & Earth Sciences, University of North Carolina at Charlotte, Charlotte, NC 28223, USA
6. Department of Chemistry and Biochemistry, Texas Tech University, Lubbock, Texas 79409, USA

\* These authors contributed equally to this project  
&Corresponding authors:

Bao-Hua Song

Department of Biological Sciences,

University of North Carolina at Charlotte,

Charlotte, NC 28223

[bsong5@uncc.edu](mailto:bsong5@uncc.edu)

001-704-687-8670

Ann Loraine

Department of Bioinformatics and Genomics,

University of North Carolina at Charlotte,

Charlotte, NC 28223

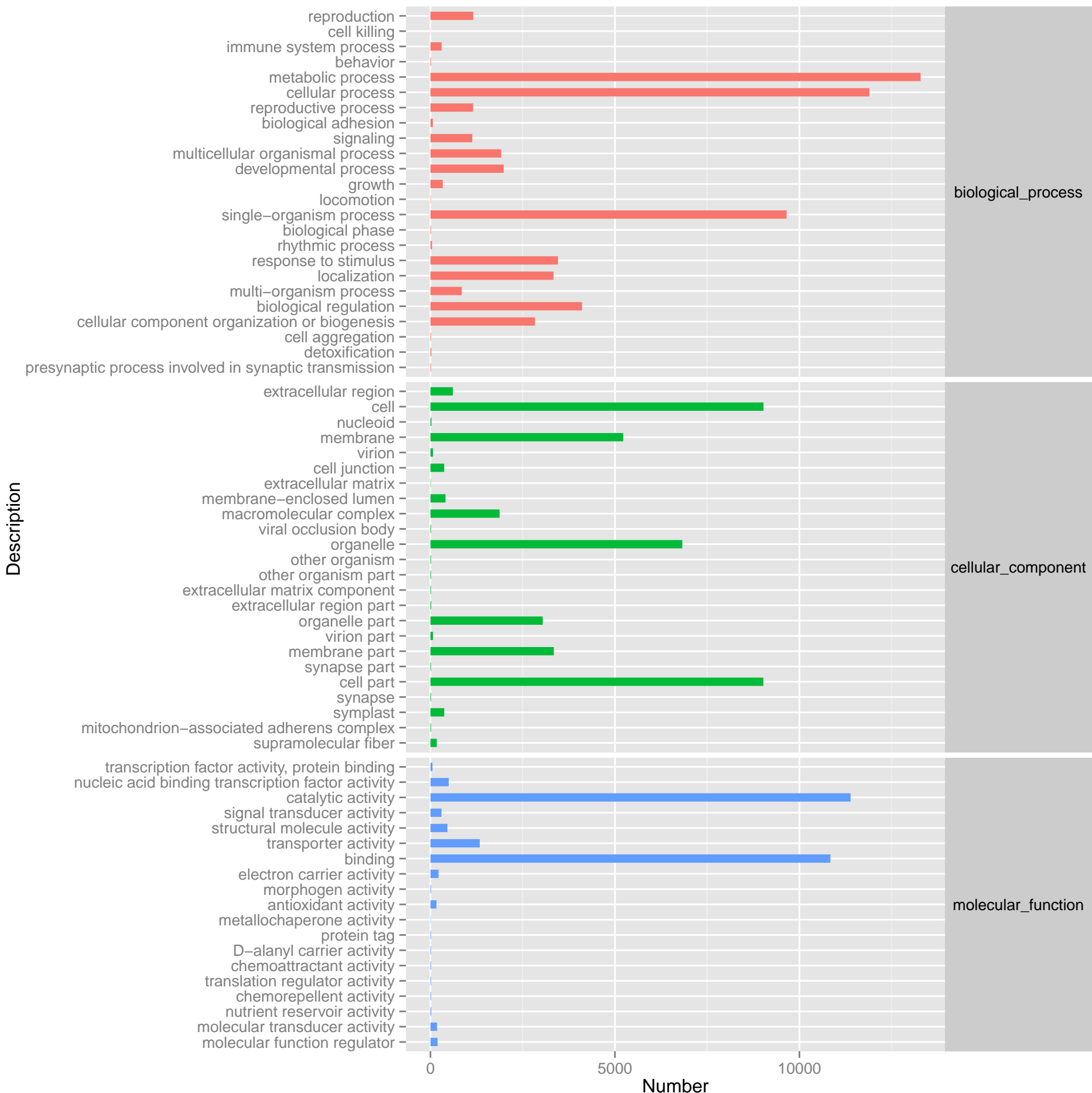
[aloraine@uncc.edu](mailto:aloraine@uncc.edu)

## Supplementary Figures

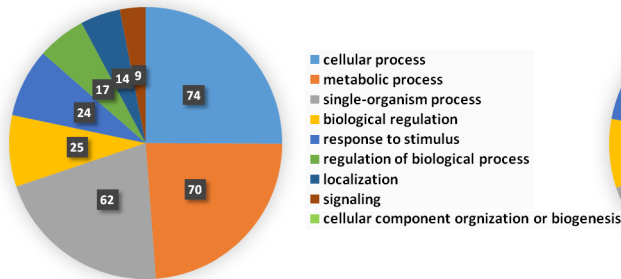
Figure S1. GO categories.

Figure S2. GO category of DEGs at the second level (A. Biological process categories; B. Molecular function categories; C. Cellular components categories) in roots and leaves in *I. imperati*. Different color blocks represent all kinds of GO categories. The number in color block indicates the DEG numbers in each GO term.

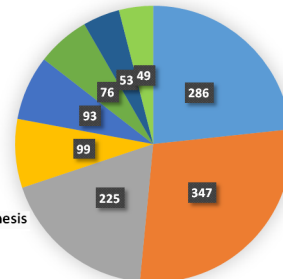
Figure S3. AgriGO analysis of DEGs enrichments of GO category (GO:0050896) “response to stimulus” in leaves (A) and roots (B). Each box shows the GO term number and GO term, an FDR in parenthesis. The pair numerals in the left represent the number of genes in input list associated with that GO term and number of genes in the input list. The pair of numerals in the right represents the number of genes associated with a particular GO term in the total *I. imperati* annotated genes. Box colors indicate levels of statistical significance: yellow=0.05; orange= $1e \times 10^{-5}$ ; and red= $1e \times 10^{-9}$ .



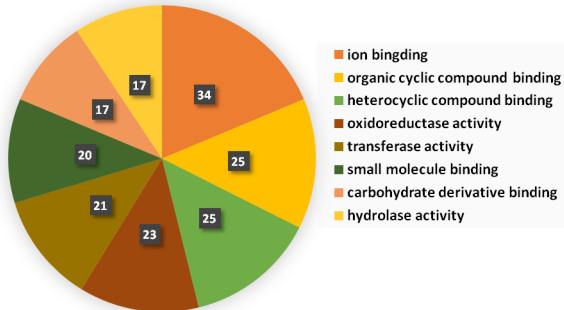
Biological process (Leaves 99)



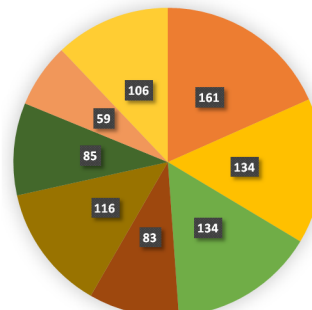
Biological process (Roots 421)



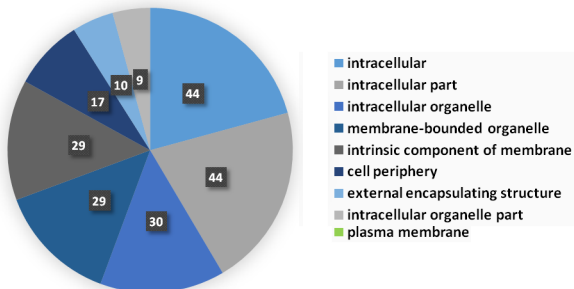
Molecular Function (Leaves 94)



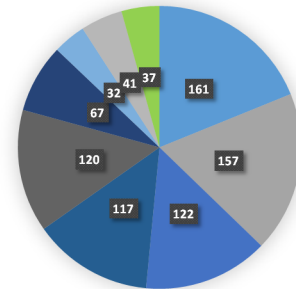
Molecular Function (Roots 430)

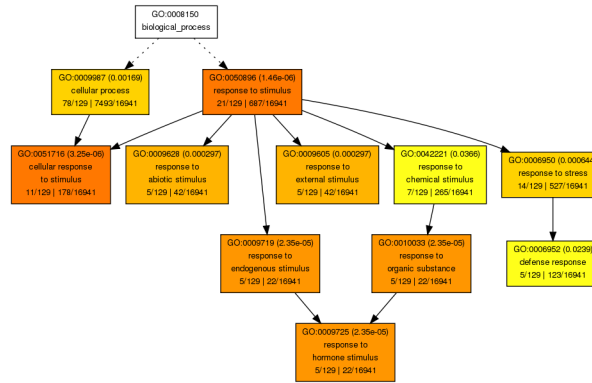


Cellular Component (Leaves 81)



Cellular Component (Roots 311)



**A****B**