

File_S2 Global transcriptional analysis suggests *Lasiodiplodia theobromae* pathogenicity factors involved in modulation of grapevine defensive response

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The functional annotation was done through Blast2GO using all the sequences assembled of transcripts (all the conditions together). The gene ontology structure employs several levels to classify the relations among GOterms (Ashburner et al., 2000) using higher numbers for more specific categories. The three trunk classification was molecular function, biological process or cellular component (Ashburner et al., 2000).

Figure 1. Biological process in second level of gene ontology classification. Most of the transcripts are involved in metabolic processes (2,283) and cellular processes (1,750). Also a good number are classified as single-organism processes (801) and localization (607). And with a significant number also are represented process like biological regulation (351), response to stimulus (176) and signaling (87).

Figure 2. Biological process in third level of gene ontology classification. Most of the transcripts were distributed in primary metabolic processes (1316), organic substances metabolic process (1405), nitrogen compound metabolic processes (796), establishment of localization (603), single organism cellular (729) and metabolic (954) processes.

Figure 3. Biological process in fourth level of gene ontology classification. Most of the transcripts were involved in nitrogen metabolism (684), aromatic (665), organic cycles (689) and heterocycle (676) compounds metabolism. Also there are 589 transcripts involved in oxidation-reduction process.

Figure 4. Biological process in fifth level of gene ontology classification. Most of the transcripts were involved in cellular macromolecule metabolic process (103), nucleobase-containing compound metabolic process (66), gene expression (65) and macromolecule biosynthetic process (65).

Fig 1

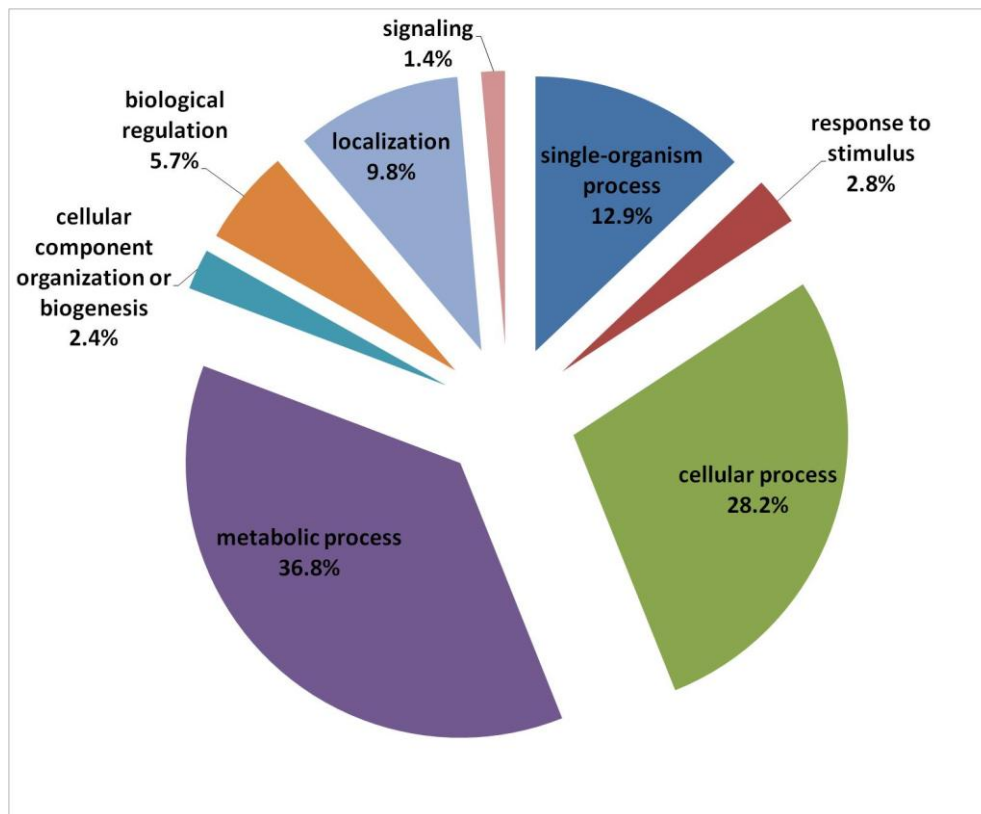


Fig 2

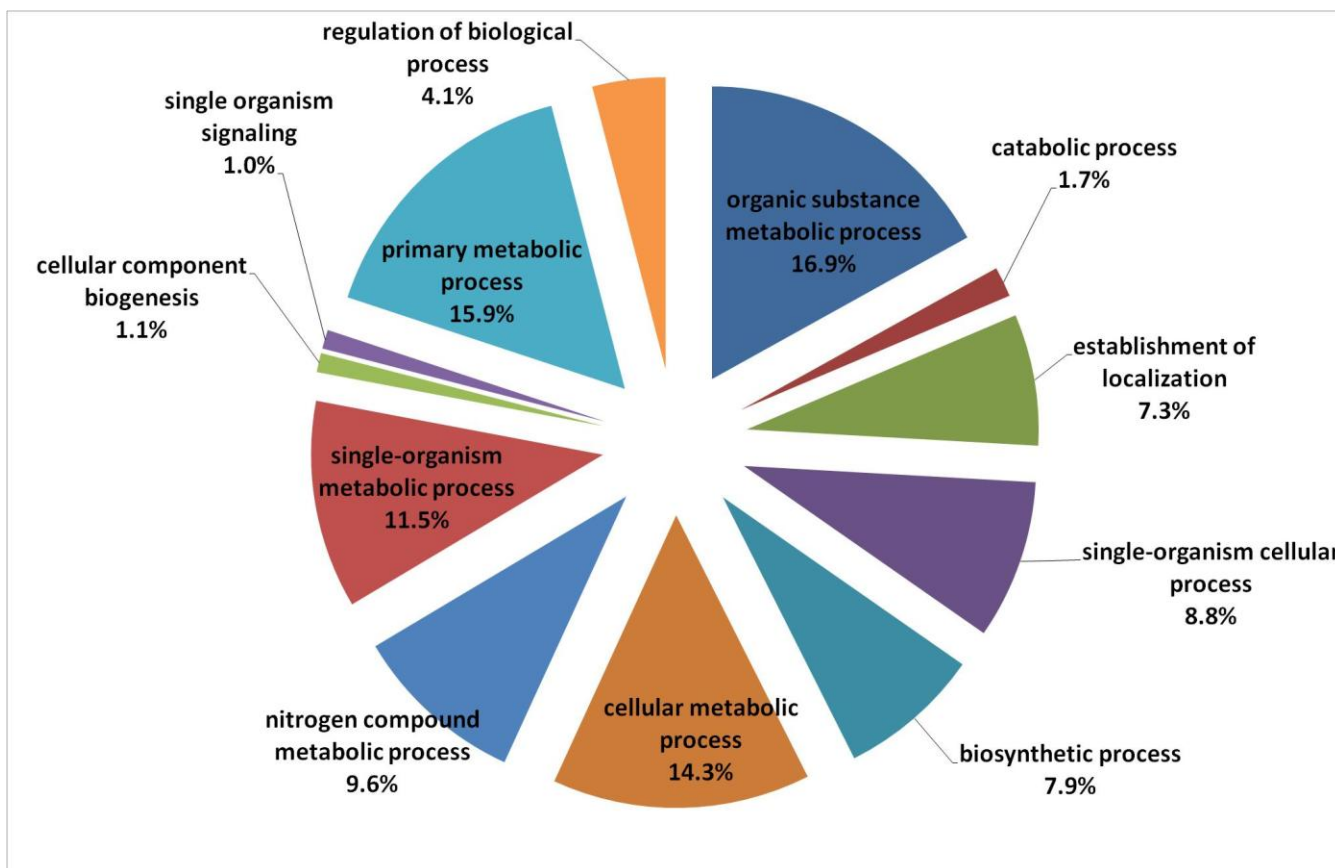


Fig 3.

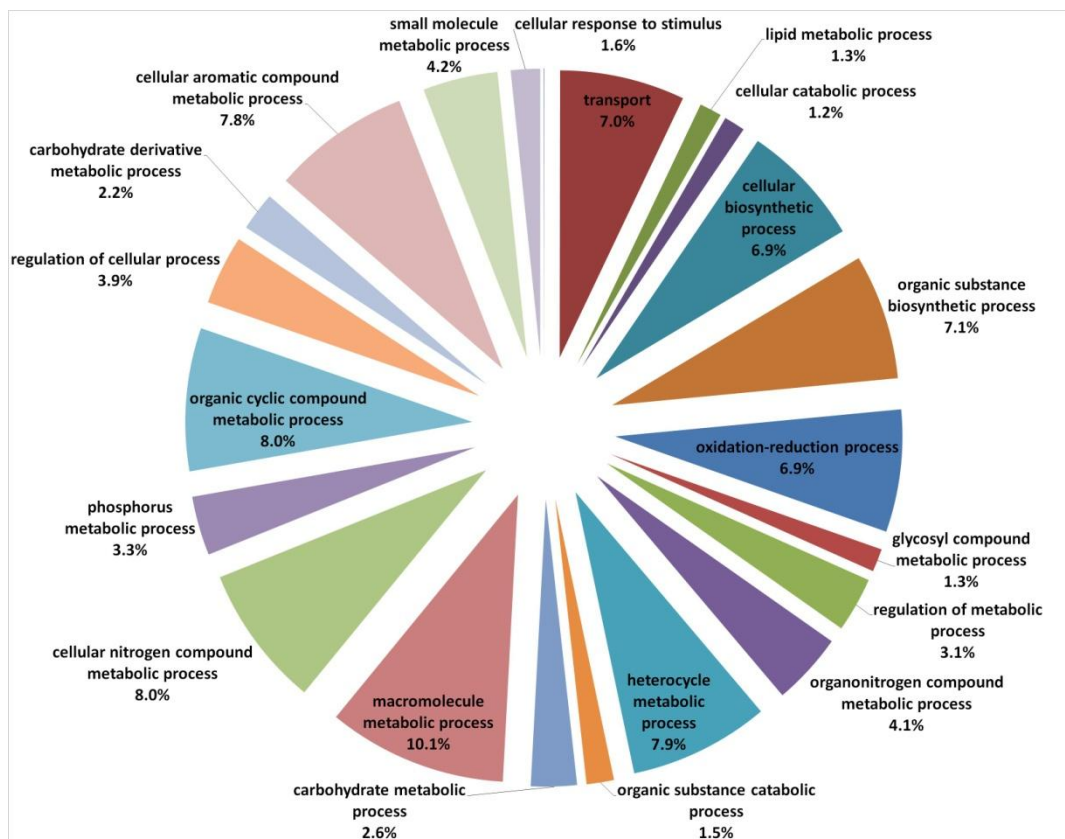
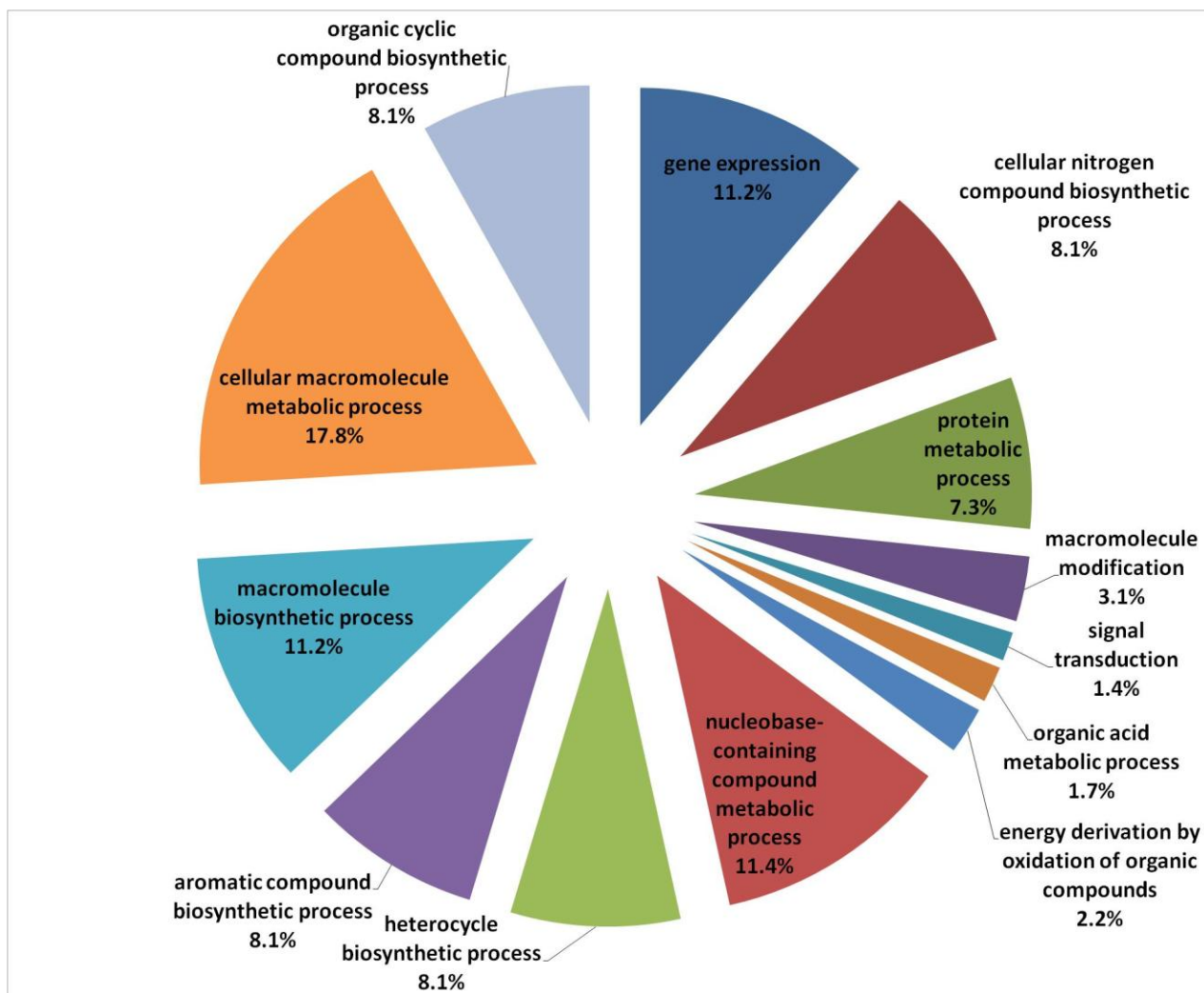


Fig 4



References

Ashburner, M., Ball, C. A., Blake, J. A., Botstein, D., Butler, H., Cherry, J. M., ... Sherlock, G. (2000). Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. *Nature Genetics*, 25(1), 25–9. doi:10.1038/75556