

# Comparative analysis of R-genes expression and transcriptomic profiles in potato tubers of selected potato genotypes after inoculation with virulent and avirulent races of *Phytophthora infestans*

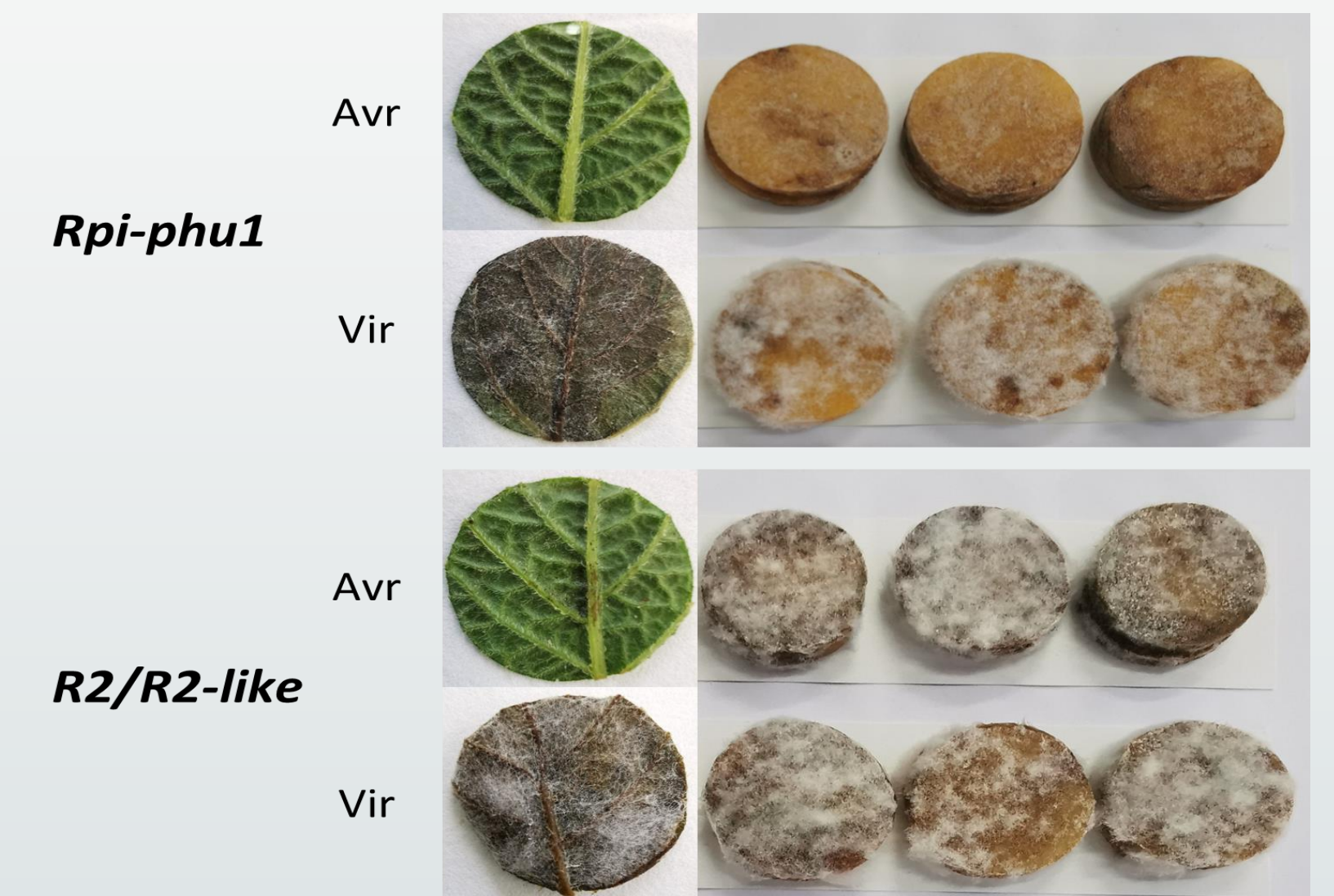


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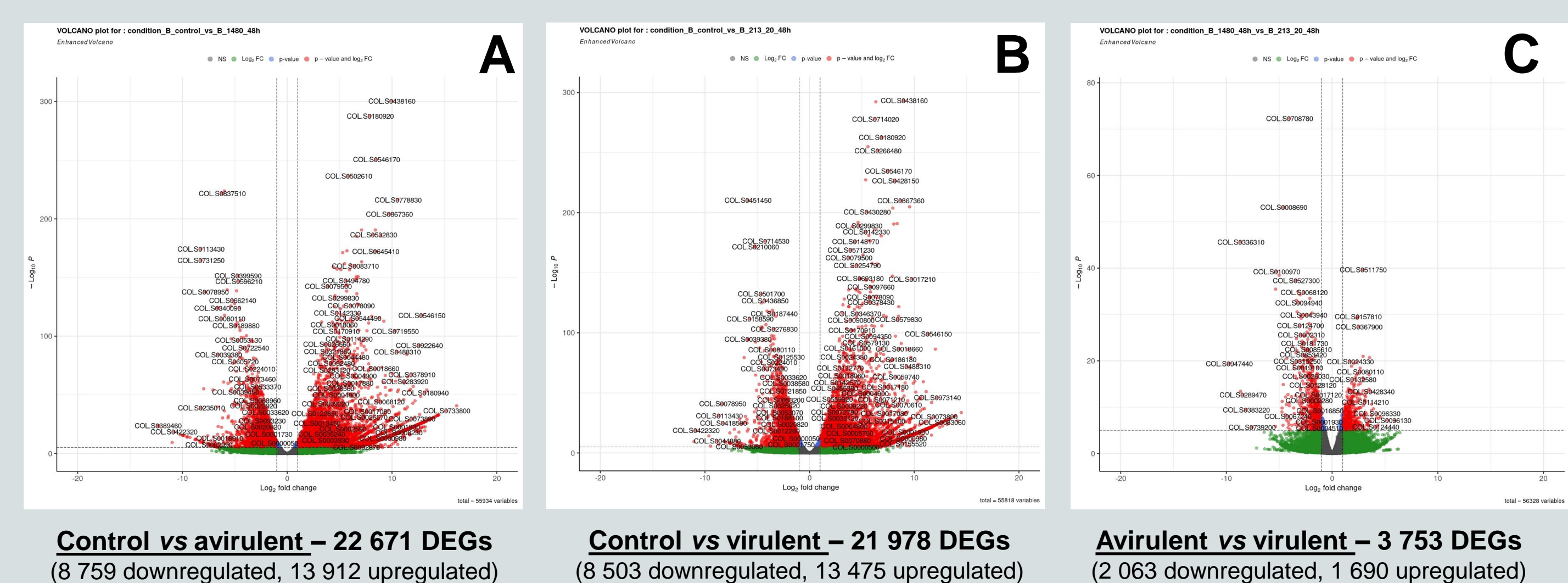
Late blight (LB) caused by *Phytophthora infestans* is the most destructive potato disease worldwide and there is consequently strong market demand for resistant cultivars. Resistance breeding is mainly based on the resistance genes (R-genes) identified in various wild *Solanum* species. However, some R-genes provides effective protection of foliage and tubers while other provide foliage but not tuber resistance. The most likely explanation of this phenomenon is different level of R-genes expression, but more general differences in the defense response can be also expected. In our study we plan to verify both these elements.

For our research we chose two R-genes: ***Rpi-phu1***, which provides effective protection of foliage and tubers, and ***R2***, which fails in tuber resistance. Tuber slices of non-transgenic cultivar Bzura (*R2*), potato clone TG 97-411 (*Rpi-phu1*) and DC 69 (*R2* and *Rpi-phu1*) were inoculated with virulent and avirulent races of *P. infestans* to assess its resistance and measure level of R-genes expression (work in progress). We performed also transcriptome analyses to study differences in expression of other genes, after inoculation with virulent and avirulent isolates of *P. infestans*. Here we present preliminary results of this part of experiment.

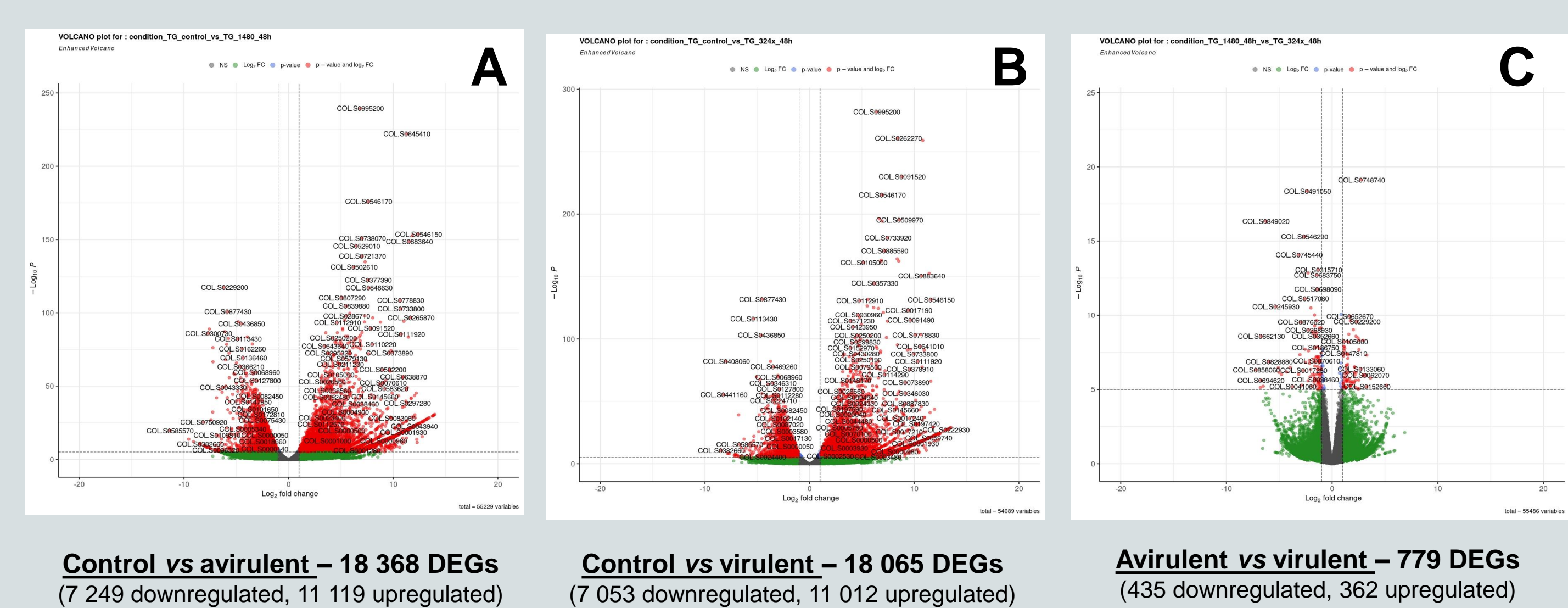


We compared transcriptome profile of RNA extracted from control samples (tuber tissue before inoculation) and samples collected 48 hpi. 'Volcano' plots illustrates numer of DEGs - differentially expressed genes (both, up- and downregulated) in case of comparisons: **A**) control vs samples inoculated with isolate MP 1480, which is avirulent to both genes; **B**) control vs samples inoculated with virulent isolates (MP 324x for *Rpi-phu1* and 213/20 for *R2* gene); and **C**) samples inoculated with avirulent MP 1480 vs samples inoculated with virulent isolates (MP 324x or 213/20).

**Bzura (*R2*)** Comparison of transcriptome profiles of control samples and samples inoculated with avirulent MP1480 (**A**) and virulent isolate 213/20 (**B**) result in identification of 22671 DEGs (8759 downregulated; 13912 upregulated); and 21978 DEGs (8503 downregulated; 13475 upregulated) respectively. Comparison of transcriptome profiles of samples inoculated with avirulent and virulent isolates (**C**) result in identification of 3753 DEGs (2063 downregulated; 1690 upregulated).



**TG 97-411 (*Rpi-phu1*)** Comparison of transcriptome profiles of control samples and samples inoculated with avirulent MP1480 (**A**) and virulent isolate MP324x (**B**) result in identification of 18368 DEGs (7249 downregulated; 11119 upregulated); and 18065 DEGs (7053 downregulated; 11012 upregulated) respectively. Comparison of transcriptome profiles of samples inoculated with avirulent and avirulent isolates (**C**) result in identification of 797 DEGs (435 downregulated; 362 upregulated).



**DC 69 (*R2+Rpi-phu1*)** Comparison of transcriptome profiles of control samples and samples inoculated with avirulent MP 1480 (**A**) result in identification of 19505 DEGs (7615 downregulated; 11890 upregulated). Comparison of control and samples inoculated with isolates 213/20 (**B1**) and MP 324x (**B2**) result in identification of: 20552 DEGs (7920 downregulated; 12632 upregulated); and 19705 DEGs (7562 downregulated; 12143 upregulated), respectively. Comparison of transcriptome profiles samples inoculated avirulent MP 1480 and avirulent isolate 213/20 (**C1**) and MP 324x (**C2**) result in identification of 16 DEGs (10 downregulated; 6 upregulated), and 288 DEGs (139 downregulated; 149 upregulated).

