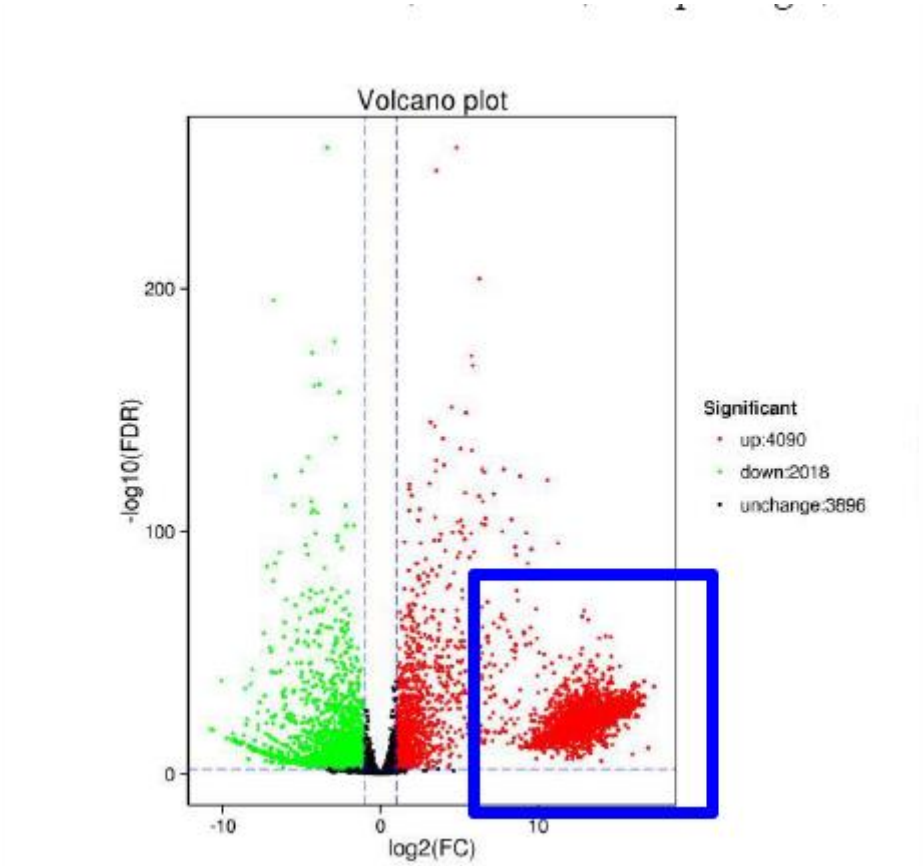
Major comments

The article sent by the authors is very interesting, deals with such a relevant topic as studying the response of spruce to infection by rust fungi, uses various modern methods such as transcriptome analysis and electron microscopy, and will be useful in phytopathology, especially as similar data are accumulating for other plants. The authors have done the work at a fairly high technical and scientific level. There are a few comments to improve the manuscript.

Detail comments

1. This is a mostly formal remark, but references in the text should be arranged in accordance with the requirements of the journal, i.e. their numbers should be written in bold coloured font in square brackets, it is better to clarify this on the site. Now there are only numbers in the text, and this should be corrected.
2. It is also a formal point, but the names of species and genera should always be written in italics. It is necessary to make amends to “Phytophthora infestans” (line 40), “Populus euphratica” (line 52), “Pinus massoniana” (line 63), “Picea cracifolia” (line 83 and line 99, line 390) and possibly something else. Please check the manuscript again.
3. Similarly, when referring to genes rather than proteins, they should be written in italics. For example, MEKK1, GH3, NDK/NME, whose expression changes were discussed in Section 3.8. The text should also be checked for such errors.
4. In Section 2.1, it is highly desirable to indicate at what time of day each sample was collected, if such data are preserved. Circadian rhythms can strongly influence transcriptomes. It is also desirable to indicate the coordinates at which the biomaterial was collected.
5. What is written in Section 2.2 should probably be moved to the Results section, as it describes what was identified rather than the identification process itself. There are also some notes about the results obtained. Can the pathogen be identified more accurately than to the family level (e.g., by ITS-region sequencing)? According to NCBI Taxonomy, *Melampsora* is the only genus in the family Melampsoraceae, and the family itself belongs to the phylum Basidiomycota, subphylum Pucciniomycotina, class Pucciniomycetes, order Pucciniales. And I suppose it is better to use modern names of taxa.
6. In Section 2.4, it is worth describing in as much detail as possible all the programmes used in the analysis, including their versions. For example, fastqc for assessing the quality of reids, STAR/HISAT2/kallisto for mapping them, DESeq2/edgeR for finding differentially expressed genes, etc. The reference gene or transcriptome used should also be specified.
7. Section 2.5 should detail all reagents and equipment used, including their manufacturer. A similar section should describe the process of RNA isolation, library preparation, and sequencing.
8. It is highly desirable to specify how the raw sequencing data from the study can be accessed. For example, to provide the accession number in the SRA repository if the data are hosted there.
9. The captions to Figures 2, 3, 4, 5 should be made more detailed, indicating by what methods each part of the image was obtained.
10. Figures 6, 7, 8, 9 should be made larger and in higher resolution. Currently, it is necessary to zoom in on the document or strain vision to see signatures, especially in Figure 7.
11. The left volcanic plot has a region of points that behave atypically for volcanic plots, being far away from log2(FC)=0 with high density. Is it possible to explain what this behaviour is related to? Could it be interesting in terms of process biology or is it an artefact of the study? In the screenshot below I have highlighted them with a blue square.



12. The explanation for the differential expression of hormone-related genes may differ from what is written in the article. In very brief, plants have 2 blocks of immune response regulation: an SA-regulated response against biotrophic pathogens (as noted in the article, it is associated with systemic acquired resistance and hypersensitive response) and a JA/ET module active against necrotrophs. Moreover, in *Arabidopsis*, wheat and rice, they are in antagonistic relationships and inhibit each other (since, for example, reactive oxygen species may be useful against biotrophs but, conversely, will help necrotrophic pathogens) (https://doi.org/10.3390/ijms20030671). For trees such as poplar, current evidence refutes this - perhaps these hormones act synergistically (https://doi.org/10.1111/nph.18148). *Melampsora* is a well-known example of a biotrophic pathogen. So perhaps suppression of JA signalling is linked to suppression by SA. I would advise the authors to analyse the expression of as many genes related to SA signalling as possible (all *PRs*, *NRP1*, *3*, *4*, *defensin*, etc.) as well as JA and ET. Perhaps the fungus is indeed suppressing the plant's immune response.
13. The data obtained in this study are in any case very valuable. But I would ask the authors to specify more clearly why the L group was analysed. As far as I understood, it is related to the fact that in the second year plants are less susceptible to rust due to a denser and differently structured cover. But it would be better to state this more explicitly, preferably both in the abstract and in the introduction.