Writing Results vs Discussions

One of the challenges of writing results and discussion is understanding the distinct difference between the two. The purpose of the results section is to describe your results using your analysed data as a skeleton. The discussion section, on the other hand, is to state your interpretations of the findings and to explain the implications of your findings in relation to your research aim(s), identify the strengths and limitations of your work and then make suggestions for future research. The main function of the discussion is to answer the questions posed in the introduction section of your paper, explain how the results support the research question(s) or not and, how these add to the existing knowledge on the topic or attempts to fill the research gap highlighted in the literature review section of your paper/report/thesis.

Results and discussion sections can be structured in different ways. For example, in a thesis you could have separate chapters for results and discussion, or you could structure each objective/finding as a paper that includes both results and discussion and have a separate conclusion chapter. For writing journal articles, the journal will have a specific structure that you will follow (reading current literature published in the journal can help as examples).

The results section is written up both in the past and present tense and so is the discussion section. The past tense is generally used to describe the findings in the results section and to summarise the findings making reference to figures and tables in your discussion section. Whereas present tense is used to interpret the results or to describe the significance of the findings in relation to the literature. Often, a combination of both the past and the present tense is used in sentences within the discussion section.

Example: *An elevated level of at least one risk factor was demonstrated in 63% of the children, indicating that children with obesity are at an increased risk of cardiovascular diseases.*

Note that the first part of the sentence refers to the results; hence the past tense has been used for this part. On the other hand, the present tense has been used for the second part as this part explains what the result may mean. You will also use the future tense in the discussion section when you are making recommendations for further research or providing future directions.

Writing results will entail using your analysed data to guide the descriptions. See our resource on figures and tables for formatting. You can also bring in your methods to remind the reader how the results were obtained.

Example:

Subcellular localization of SAG21

As *in silico* analysis of targeting predicted the presence of either a mitochondrial or a chloroplast targeting signal (Mitoprot II: 0.9856, TargetP: 0.555 for mitochondria; Claros & Vincens 1996; Emanuelsson *et al*. 2007), the subcellular localization of SAG21 was investigated by generating stable transgenic lines carrying a *SAG21*-YFP fusion driven by the 35S CaMV promoter (Fig. 7a). Confocal microscopy revealed that the YFP signal was associated with small subcellular compartments forming a punctate pattern suggesting mitochondrial localization (Fig. 7b). Time lapse imaging of these compartments in roots revealed that their appearance and behaviour is characteristic of mitochondria (Supporting Information Video S1).

In cotyledons, autofluorescence from chloroplasts clearly shows that the YFP signal is not chloroplast associated, and therefore a plastid localization for SAG21 can be excluded (Fig. 7b). The mitochondrial localization was confirmed with Mitotracker staining (Fig. 7c–e) of mature root epidermal cells.

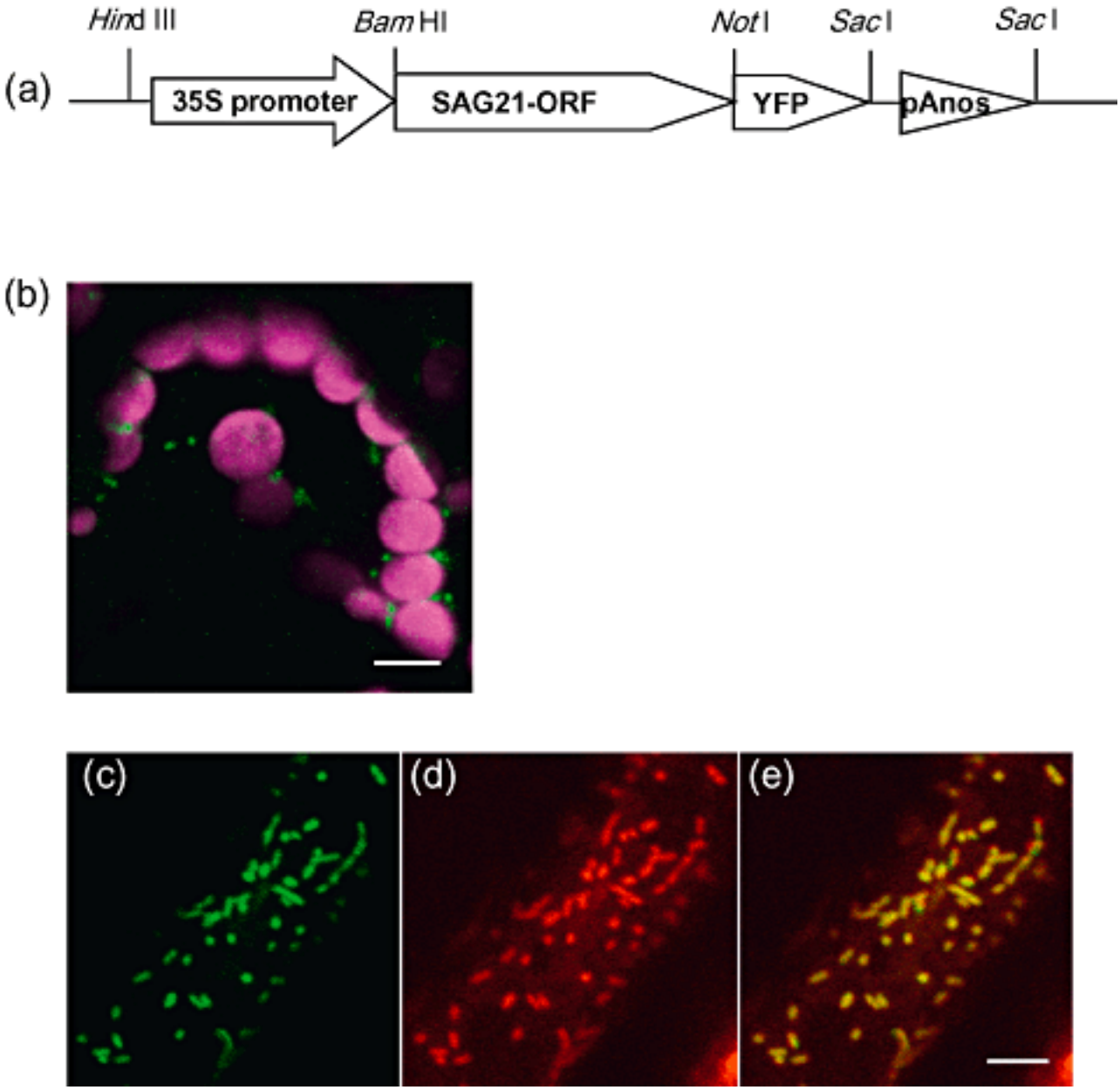

Figure 7: Subcellular localization of SAG21-YFP fusion protein.
(a) Schematic representation of the construct for stable expression in plants. SAG21-YFP localization in (b) cotyledon mesophyll of 5-day-old seedlings. YFP is indicated by green signal; magenta signal indicates autofluorescence from chloroplasts. (c) SAG21-YFP localization in a mature epidermal root cell, (d) mitotracker staining, (e) overlay of (c) and (d) (scale bars = 5 μm). YFP; yellow fluorescent protein.

A useful framework to write the discussion section is the 'look back' and 'look forward' approach.

Look back

- Start by reminding the reader what the aim of your study was and the contribution of your research
- Consider whether the results make sense in terms of
    - your expectation as expressed in the hypothesis?
    - what you read before beginning your research (literature)?
    - clinical practice?
- If your results agree with previous work, explain how this is a confirmation or extension of existing knowledge. If they do not, explain why not based on current literature or an informed opinion, or you may choose to leave it unresolved "We cannot account for the differences seen in..." in the latter case consider this an opportunity for future research.
- Have a separate section to state the strengths of your study and the limitations: Were there any limitations? Perhaps the sample size was smaller than expected, there were unexpected experimental delays. Were there any problems with carrying out the method as originally planned? Perhaps there was a low survey response rate?
- Are there any unsettled points in your results?

Example

LEA proteins are typically associated with protective functions, particularly in dehydrated tissues, where they are considered to act as chaperones, protecting other proteins from aggregation or desiccation (Tunnacliffe & Wise 2007). Although it has been implicated in growth and redox responses, its precise roles remain obscure. To address this problem, we characterized root and shoot development and response to biotic stress in *SAG21/AtLEA5* over-expressor (OEX) and antisense (AS) lines. *SAG21* was isolated via its ability to complement an oxidant-sensitive yeast mutant and this initial study linked *SAG21* over-expression to an increase in growth (Mowla *et al*. 2006). The data presented in the current manuscript build on this observation and enable us to draw the following conclusions.

Look forward

- Based on your limitations mentioned, turn these into future research recommendations so that the research can be continued afterwards.
- Suggestions for future research. "Future research could further investigate childhood obesity by… to broaden our understanding of ……". Be specific.

Example

The data presented here strongly implicate *SAG21* in the control of root hair growth. The short root hair phenotype of AS plants is similar to that of the *rhd2* mutant, which lacks the plasma membrane-located respiratory burst oxidase, *AtrbohC* (Foreman *et al*. 2003; Dolan & Davies 2004; Carol & Dolan 2006; Gapper & Dolan 2006). Root hairs of *rhd2* mutants are 20% shorter than WT and the primary root is also shorter, although interestingly, *RHD2* expression is absent from root tips, as is *SAG21* (Gapper & Dolan 2006). Not only are root hairs shorter in *SAG21* AS lines, but the OEX lines have a higher proportion of longer root hairs (Fig. 3d).

We conclude that *SAG21* plays a role in root hair elongation; moreover, its mitochondrial location suggests that this compartment has a controlling influence on this process. The pertinent question is: How can a mitochondrial protein participate in a pathway that leads to root hair expansion and does this involve *RHD2*, or is it a parallel pathway? Mitochondria are well established as sources of ROS (Rhoads *et al.* 2006; Noctor, De Paepe & Foyer 2007); and although we have not demonstrated a causal link with ROS and root hair growth in this study, *SAG21* expression is nevertheless linked to ROS (this study and Mowla *et al.* 2006). Both root hair elongation and the responses of plants to necrotrophic pathogens require the activation of different RBOH forms (Foreman *et al.* 2003; Miller *et al.* 2009). Thus, our data point to the possibility that *SAG21* plays a role in signalling pathways that involve RBOH. As a LEA protein, the most likely function of SAG21 is as an interacting protein that alters the function or stability of mitochondrial proteins involved in ROS production and/or signalling. This fascinating possibility awaits further investigation.

The following are some guiding questions to help frame the discussion section.

1. What are the major patterns observed from your results?
2. What are the relationships, trends and generalisations among these results?
3. Are there any exceptions to these patterns or generalisations?
4. What are the likely causes (mechanisms) underlying these patterns?
5. Is there agreement or disagreement with previous work and/or theories/hypotheses presented earlier in your paper/assignment/thesis?
6. Interpret results in terms of background laid out in the introduction. What is the relationship between the present results and the original question?
7. What are the implications of the present results?
8. Multiple hypotheses for quantitative research: There are usually several possible explanations for results. Consider the main relevant ones rather than simply pushing your favourite one.
9. Avoid bandwagons: Avoid jumping to a currently fashionable/widely accepted point of view unless your results does strongly support it.
10. What are the things we now know or understand that we didn't know or understand before the present work?
11. Include the evidence or line of reasoning supporting each interpretation.
12. What is the significance of the present results? Explain how the results and conclusions of this study are important and how they influence our knowledge or understanding of the problem being examined.

Reference: Salleh, F.M., Evans, K., Goodall, B., Machin, H., Mowla, S.B., Mur, L.A., Runions, J., Theodoulou, F.L., Foyer, C.H. and Rogers, H.J., 2012. A novel function for a redox-related LEA protein (SAG21/AtLEA5) in root development and biotic stress responses. *Plant, cell & environment*, *35*(2), pp.418-429.

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