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# Does C 4 Photosynthesis Occur in Wheat Seeds?

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# **Does C<sub>4</sub> Photosynthesis Occur in Wheat Seeds?**

Dear Florian and Graham,

Our recent report of new evidence for C<sub>4</sub> photosynthesis in wheat seeds (Rangan et al., 2016) has been met with skepticism (Busch and Farquhar, 2016), maybe because this has been such a long-running controversy. Much of the confusion has been because early work did not distinguish photosynthesis in the pericarp of the seed (Fig. 1) from that in the covering glumes. Glumes, like leaves in wheat, capture  $CO_2$  from the atmosphere by C<sub>3</sub> photosynthesis. However, RNA-Seq analysis demonstrates the expression of a complete  $C_4$  pathway in the seed with a  $C_4$ -specific form of PEP carboxylase expressed specifically in the pericarp and aleurone capturing carbon released by respiration in the endosperm. Decarboxylation by a  $C_4$ -specific malic enzyme in the inner pericarp supplies  $CO_2$  to a  $C_3$  pathway. The decarboxylation of malate specifically in the pericarp is suggested by comparison of the levels of C<sub>4</sub>-specific malic enzyme expression in the pericarp with the low levels in the endosperm. This provides a source of concentrated carbon dioxide for Rubisco in the pericarp, acting like the  $C_4$  pathway in leaves that effectively concentrates  $CO_2$  at the bundle sheath chloroplast for fixation in a  $C_3$  process. Unlike the situation in wheat leaves, high concentrations of  $CO_2$  in the endosperm cannot be fixed through photosynthesis due to the lack of light penetration, but capture as malate allows processing to generate higher CO<sub>2</sub> concentrations for the Rubisco expressed very specifically in the photosynthetic pericarp.

Analysis of the genome shows specific genes encoding the  $C_4$  enzymes that are distinct from those encoding the  $C_3$  pathway. These genes are expressed in a highly tissue-specific way in the pericarp and endosperm. Analysis of the specificity of wheat seed enzymes supports this interpretation. Labeling studies using <sup>14</sup>C-labeled CO<sub>2</sub> provide overwhelming support for the capture of carbon as malate in these tissues and the flow of this carbon into  $C_3$  photosynthesis (Nutbeam and Duffus, 1976; Singal et al., 1986). Confusion on this issue has been deepened by a labeling study (Bort et al., 1995) that did not recognize the difference between glumes capturing external CO<sub>2</sub> and the inner seed capturing respired carbon. This study claimed evidence against C<sub>4</sub> photosynthesis based upon feeding  $CO_2$  to the intact ear rather than respired carbon diffusing outwards from the endosperm despite very early work establishing the later as the source of carbon. Further misinterpretation may have resulted from an expectation that seed photosynthesis would use free CO<sub>2</sub> as a substrate. The endosperm of the developing seed maintains a high pH with a drop in pH only happening

during germination. The native substrate in the developing seed tissues would be bicarbonate acting as a substrate for the large amounts of  $C_4$ -specific PEP carboxylase found in the aleurone and pericarp.

We therefore propose that there is no credible evidence opposing these reports of  $C_4$  activity in wheat. Study of tissues outside the pericarp and a lack of recognition by some of respiration in the endosperm as the source of carbon have confused the issue.

Sincerely,

Robert, Parimalan, and Agnelo

Dear Robert, Parimalan, and Agnelo,

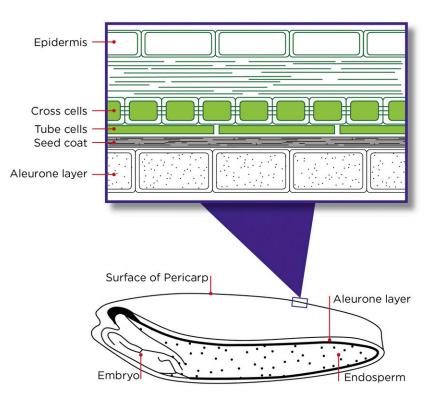
In your recent paper, you report interesting transcript profiles of wheat leaves and seeds, showing that the leaves express variants of genes encoding enzymes necessary for  $C_4$  photosynthesis that resemble those found in  $C_3$  plants, while the variants expressed in the seeds resemble those found in  $C_4$  plants (Rangan et al., 2016). This is novel information that warrants a renewed and deeper look into the issue of whether wheat grains employ a  $C_4$ -type carbon concentrating mechanism, or more generally, why  $C_3$  and  $C_4$  plants have different isozymes of key photosynthetic proteins to begin with. In our commentary (Busch and Farquhar, 2016), we tried to raise the point that these expression profiles alone, however, are not sufficient to conclude on the existence of a functioning  $C_4$  photosynthetic pathway.

Previous studies on this topic have been, as you pointed out, contradictory, and to discuss each of their virtues and flaws would go beyond the scope of this discourse. But whatever technique one chooses to establish the existence of a C<sub>4</sub> photosynthetic pathway, in our opinion the gold standard (and really the only standard) has to be to provide evidence of a flux through that pathway. As Hibberd and Furbank (2016) noted in their commentary, all the genes coding for proteins necessary for C<sub>4</sub> photosynthesis already exist and are expressed in C<sub>3</sub> plants, but are usually not used for that purpose. Just because a gene is expressed more highly does not imply it is translated more, or produces a higher activity of that protein, or, most importantly, that the protein catalyzes a reaction that directly contributes to a certain biochemical pathway.

Unfortunately, experimental evidence for or against a  $C_4$  pathway in the wheat seed is scarce. Despite its shortcomings, in our view the most rigorous of these experiments support the idea that PEP carboxylase facilitates anaplerotic reactions and is not involved in a  $C_4$  pathway (Bort et al., 1995). Furthermore, some of the data you presented in your recent work (Rangan et al., 2016) itself go against the existence of a  $C_4$  pathway in the seed: The expression level of the gene for a critically important enzyme for  $C_4$  photosynthesis, Rubisco, is almost negligible. If we assume for the moment (as you have) that expression of genes directly relates to protein

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**Figure 1.** Schematic of a wheat seed with the outer layers detailed. The magnification of the pericarp shows the epidermis, cross cells (photosynthetic), and tube cells (photosynthetic) surrounding the endosperm with the outer (aleurone) layer depicted.

activity, most of the  $CO_2$  fixed by PEP carboxylase would therefore have to be metabolized in a biochemical pathway other than photosynthesis.

Another aspect conflicting with a  $C_4$  pathway in the seed is related to the compartmentation you mentioned: The CO<sub>2</sub> concentration is high in the endosperm but relatively low in the Rubisco-containing pericarp. One unifying feature of the  $C_4$  pathway is the enrichment of  $CO_2$  at the site of Rubisco relative to where the initial fixation occurs by PEP carboxylase. Why invest in an energy-intensive  $C_4$  pathway if the CO<sub>2</sub> diffusing outward along its concentration gradient would arrive in the pericarp for free? In this sense, a  $C_4$  carbon pump in the seed goes against intuition and therefore would need good experimental support based on carbon-flux measurements. To date, this evidence is lacking.

Sincerely,

Florian and Graham

#### Dear Florian and Graham,

The "gold standard" has been satisfied here by demonstration of flux through malate to  $C_3$  intermediates in barley (Nutbeam and Duffus, 1976) and wheat (Singal et al., 1986). The  $C_4$  versions of key genes have not only been shown to be expressed, but the proteins have been isolated and characterized as having the required specificity (Singal et al., 1986). Enzymes catalyzing the same reactions (e.g. PEP carboxylase) are found in both  $C_3$  and  $C_4$  plants, but the genes in  $C_4$ plants encode versions with  $C_4$  specificity. In wheat, we have demonstrated both  $C_3$  versions expressed in the leaves and  $C_4$  versions very specifically expressed in the seeds. The Rubisco level in the pericarp is far from negligible. The concentrations of Rubisco transcripts we reported were for the whole caryopsis including the endosperm. Our analyses of published data (Pearce et al., 2015) shows that Rubisco is very specifically expressed in the pericarp tissues of the caryopsis and not significantly in the endosperm, suggesting high concentrations of Rubisco in pericarp cells. The study of Bort et al. (1995) was designed largely to test glume photosynthesis as this seemed to be the most likely site of ear photosynthesis at the time. As a consequence, it could not have supplied significant labeled carbon via respiration to the pericarp and cannot be used to infer the pathway in the pericarp. However, it has erroneously been interpreted by some as evidence against  $C_4$  in the pericarp.

The CO<sub>2</sub> concentrations in seed show very different patterns to those in a leaf. The leaf has light throughout, so it can use  $C_4$  to capture low concentrations of  $CO_2$ move the carbon inwards, and concentrate it for capture by Rubisco. The high CO<sub>2</sub> concentrations in the seed need to be moved out to a place that the light can reach. In the seed, the very active pericarp-specific decarboxylation of malate delivers concentrated CO<sub>2</sub> specifically at the site of the high concentrations of Rubisco in the pericarp with light penetrating the outer clear tissues to reach this point. If CO<sub>2</sub> was merely allowed to diffuse out, it would not reach the pericarp at a high concentration and could escape past this site during times of the day when sufficient light was not available. Indeed, the pathway of C<sub>4</sub> activity in seeds does act just like  $C_4$  in leaves in that it delivers the required concentrations of CO<sub>2</sub> to Rubisco although the flux is outwards not inward.

We now have evidence at the gene (Rangan et al., 2016), transcript (Rangan et al., 2016), protein (Meyer et al., 1982), and metabolite (Nutbeam and Duffus, 1976) level for  $C_4$  photosynthesis in wheat seeds. Many more aspects of these processes need to be explored. For example, it has been shown that wheat genotypes expressing higher levels of  $C_4$  enzymes in the seed give a higher yield under stressed conditions, although the implications have not been recognized (Jia et al., 2015). The wide variation in the level of expression we have found suggests potential for selection of wheat genotypes for improved performance in hot or dry environments during grain filling.

### Sincerely,

Robert, Parimalan, and Agnelo

Dear Robert, Parimalan, and Agnelo,

Previous studies estimating the carbon flux through a  $C_4$  pathway in the seed have been contradictory, with a flux through malate to  $C_3$  intermediates shown initially (Nutbeam and Duffus, 1976; Singal et al., 1986) but later refuted (Bort et al., 1995). The more recent study focused on photosynthetic pathways in the glume, although they also tested for <sup>14</sup>C-labeling of metabolites in the seed and found a similar labeling pattern to the  $C_3$ flag leaf blade. You do have a valid point that the <sup>14</sup>CO<sub>2</sub>labeling from the outside of the grain may result in different labeling patterns from what one would expect of labeled CO<sub>2</sub> released by respiration in the endosperm. However, Nutbeam and Duffus (1976) used isolated pericarps lacking the aleurone and endosperm with all its PEP carboxylase that could potentially be involved in C<sub>4</sub> photosynthesis. Consequently, their experiments also provide limited insight into a potential photosynthetic  $C_4$  acid transport from the inside of the grain to the pericarp. The PEP carboxylase that does exist in the pericarp should fix CO<sub>2</sub> regardless of where it comes from as it lies on the periphery of the grain. It is therefore remarkable that Bort et al. (1995) did not find any involvement of PEP carboxylase in a  $C_4$  pathway.

In addition—we have to emphasize this point again—the CO<sub>2</sub> respired in the endosperm that is not assimilated there via anaplerotic reactions would follow Fick's law and diffuse outwards, having to pass through the pericarp on its way. This means that the rate of CO<sub>2</sub> moving through the pericarp is equal to the rate of CO<sub>2</sub> release, independent of whether this happens via active transport as malate with subsequent release of  $CO_2$  in the pericarp or via simple diffusion of  $CO_2$ . Therefore, the  $CO_2$  concentration in the pericarp in both cases would equally be determined by the rate of CO<sub>2</sub> leakage from the pericarp to the outside air, which is the difference between the rate of seed respiration and that of  $CO_2$  uptake by Rubisco, multiplied by the resistance to leakage of CO<sub>2</sub>. This result is independent of whether malate transport occurs or not. The main difference between these two scenarios, corresponding to a C<sub>4</sub> pathway and a C<sub>3</sub> pathway, respectively, is the cost of two ATP per CO<sub>2</sub> fixed by PEP carboxylase in the former case (Hatch, 1987). It is not obvious how this investment would pay off, especially since the ATP and NADPH involved in this reaction have to be provided, as you pointed out, via respiratory processes due to lack of light in the endosperm. In this regard, it is also important to determine whether a potential  $C_4$  pathway in the grain shuttles  $CO_2$  from the cross cells in the periphery that have access to light to the tube cells, as you describe in your paper (Rangan et al., 2016), or from the inside of the endosperm outward, as you argue here.

This brings us back to the earlier statement that we still have much to learn about the photosynthetic properties of the wheat grain before reaching a definite conclusion about its photosynthetic type. With the gene expression analysis in your recent paper, you provided an exciting new piece of the puzzle as to how wheat grains may maximize their carbon gain. To turn this into solid evidence for or against C<sub>4</sub> photosynthesis, it needs to be supplemented by experiments that unequivocally determine the magnitude of the carbon flux through a potential  $C_4$  pathway. Experiments that may help quantify this flux include thorough labeling studies as well as in vivo physiological measurements, such as the response of the  $CO_2$  compensation point to the  $O_2$  concentration. A detailed quantification of enzyme activities and in particular their location would significantly add to that understanding. We encourage evervone to look for this evidence with great scientific rigor.

Sincerely,

Florian and Graham

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