

Chapter 3

Carbon Isotope Fractionation in Plant Respiration

Camille Bathellier*

Research School of Biology, ANU College of Science, Australian National University, Canberra 2601, ACT, Australia

Franz-W. Badeck

Council for Agricultural Research and Economics, Research Centre for Genomics and Bioinformatics, via San Protaso 302, Fiorenzuola d'Arda 29017, Italy

and

Jaleh Ghashghaie

Laboratoire d'Ecologie, Systématique et Evolution (ESE), UMR 8079, Université Paris-Sud, CNRS, AgroParisTech, Université Paris-Saclay, 91400 Orsay, France

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*Author for correspondence, e-mail: camille.bathellier@anu.edu.au

e-mail: franz@badeck.eu

e-mail: jaleh.ghashghaie@u-psud.fr

Summary

Carbon isotopes have long been used to dissect metabolic pathways. More recently, stable isotopes have become an important tool in modeling global fluxes in the biosphere, and notably CO₂ isofluxes. The accuracy of these models relies partly on the knowledge of fractionations associated with each individual flux component. This has led to the observation that carbon isotope fractionation occurs during respiration in plants, and exhibits large temporal and spatial variations. Despite important advances in the area, metabolic features underlying such variability remain to be fully elucidated. The present chapter summarizes available data on plant respiratory fractionation, and presents a critical discussion about the metabolic origin of its variation, in the light of recent developments in understanding the compartmentation and plasticity of plant respiration. It emphasizes the need for refining existing frameworks, and points out knowledge gaps that need to be filled so as to achieve a more quantitative modeling of respiratory fractionation.

I. Introduction

Both stable and radioactive isotopes are used as tracers in a wide range of domains, either at natural abundance or using labeling approaches (e.g. hydrology, geophysics, geochemistry, forensics, criminology, medicine, and different fields of biology, ecology and agronomy). In particular, they have a wide range of applications related to respiration. For example, radioactive ¹⁴C can be used as a tracer to study carbon residence time in plants before it is released through respiration (see Chap. 12; e.g. Carbone et al. 2007). Also, electron partitioning between cytochrome and alternative pathways of mitochondrial respiration can be measured using the natural ¹⁸O abundance in oxygen exchange flux (Guy et al. 1989; Ribas-Carbo et al. 1995; McDonald et al. 2002). Furthermore, the combined effect of respiratory and photorespiratory discriminations against ¹⁸O is one of the major causes of the Dole effect (natural ¹⁸O-enrichment of atmospheric O₂ relative to oxygen in seawater) and thus needs to be understood in order to explain isotopic fluxes (isofluxes) of oxy-

gen at the global scale and use this knowledge for the reconstruction of past environments (Bender et al. 1994; Angert and Luz 2001).

In this chapter, we will focus on the use of stable carbon isotopes, ¹²C and ¹³C. Carbon forms the backbone of biomolecules and represents the major fraction of plant dry mass (generally around 40%). The natural ¹³C abundance in metabolites and CO₂ exchange fluxes can thus be used to trace the fate of carbon within plants and ecosystems (Buchmann et al. 1998; Schnyder et al. 2003; Bowling et al. 2008), and to help disentangling the contribution of the different components of the carbon cycle in the biosphere (Ciais et al. 1995; Yakir and Wang 1996; Fung et al. 1997).

However, this requires a sufficient knowledge of isotopic fractionations associated with the different components of the CO₂ exchange flux, and how they vary. Photosynthesis has been known for now more than 50 years to discriminate against ¹³C so that the organic matter is naturally ¹³C-depleted compared to atmospheric CO₂. Photosynthetic discrimination has been

satisfactorily modeled and explains most of the isotopic signal of net fixed CO₂ (as measured in organic matter). However, it is only relatively recently that it has been recognized that further fractionations do occur in the metabolism downstream carbon assimilation, especially during respiration. Ghashghaie and coworkers have thus shown that the CO₂ evolved by leaves in the dark exhibited an isotopic composition systematically different from that in organic matter (Duranceau et al. 1999), providing evidence for the so called ‘apparent respiratory fractionation’. Since this pioneering work, respiratory fractionation has been shown to be widespread amongst plants, although being highly variable between taxa, organs and environmental conditions. This has facilitated the understanding of metabolic fluxes associated with respiration in different plant tissues, but to date, a complete understanding of the mechanism underlying these variations is still lacking.

In most cases, more than 25% of the carbon fixed by photosynthesis is subsequently released by respiration at the whole plant level (although it can vary widely throughout plant development; Thornley 2011). The annual ratio of carbon released through plant respiration relative to photosynthesis determined experimentally was 0.53 to 0.69 during boreal forest post-fire succession (Goulden et al. 2011), and varied between 0.17 and 0.78 as reviewed by DeLucia et al. (2007) for evergreen and deciduous forest stands. In the latter study, it was shown that the respiration/photosynthesis ratio varies with biome, stand age and leaf mass ratio. For sunflower, the ratio was 0.42 throughout the crop growth cycle (Cheng et al. 2000) and it varied between 0.23 and 0.38 in two *Plantago* species at a daily time scale depending on species and growth temperature (Atkin et al. 2007). When a respiratory

fractionation exists, it must then influence the isotopic composition of plant organic matter, impairing its accuracy as a proxy for photosynthetic discrimination.

Part of the problem lies in the somewhat ambiguous nature of respiration, even at a cellular level. In the simplest case respiration consists in the stoichiometric oxidation of glucose in the presence of oxygen to yield CO₂ and water through the action of glycolysis and the tricarboxylic acid (TCA) pathway (i.e. Krebs cycle when the pathway is cyclic). This definition is not easily applicable to the carbon isotope fractionation associated with respiration. In fact, these two central pathways are intimately interconnected to the other branches of metabolism (see also Chaps. 1 and 14), through intermediates that can engage in biosynthesis (e.g. amino acids, fatty acids, nucleotides...). Therefore, (i) other substrates than glucose can fuel respiration depending on the physiological status of cells, and (ii) additional carboxylating/decarboxylating steps can participate in the net respiratory CO₂ flux measured experimentally. In other words, the knowledge of fluxes in anabolic and catabolic processes (within different plant cell types) is required to fully understand the metabolic origin of the observed isotope composition in CO₂ evolved by plants (see Fig. 3.1 for metabolic pathways associated with respiration).

In the present Chapter, the current knowledge about the variability of respiratory apparent fractionation in plants will be reviewed. Besides, we will make an attempt to describe metabolic features (fluxes, isotope effects) that underpin such variations as far as they are now understood. Finally, a rapid survey of areas where additional knowledge is needed to improve the understanding of respiratory carbon isotope fractionation will be provided.

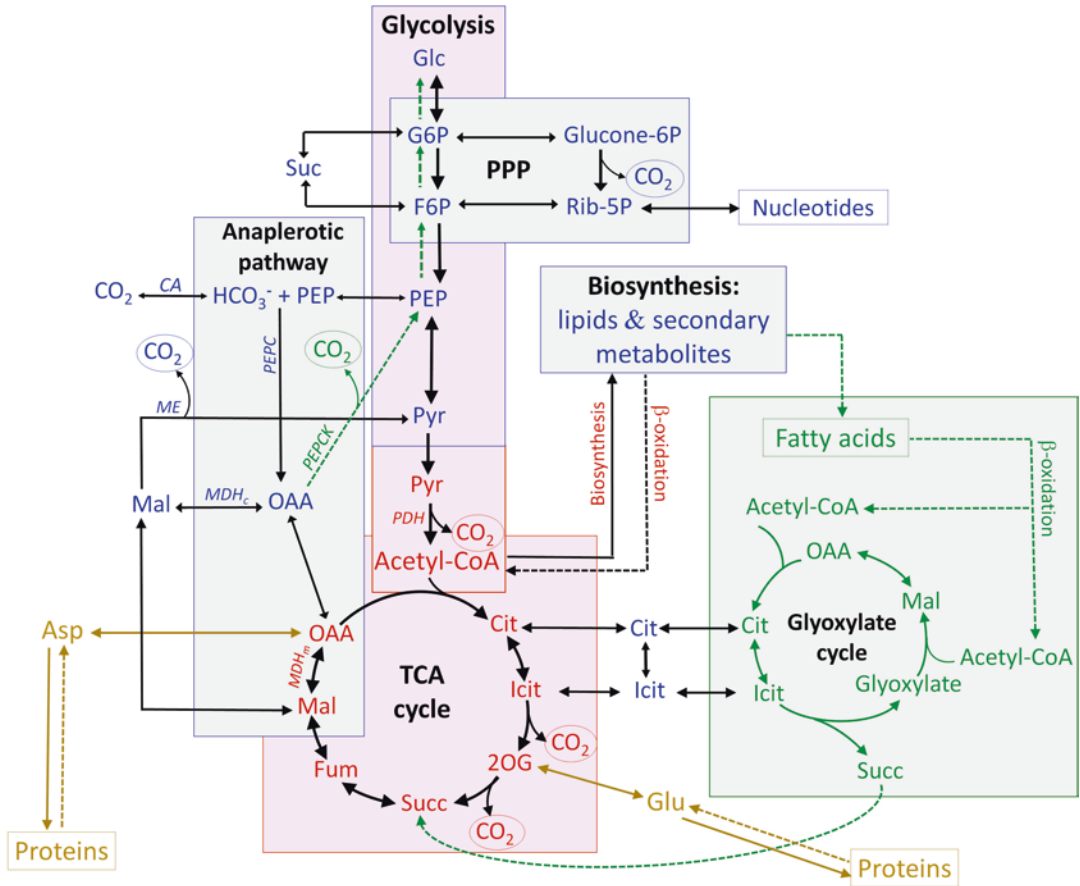


Fig. 3.1. Simplified metabolic scheme of main respiratory pathways (pink boxes including glycolysis, translocation and decarboxylation of pyruvate and Krebs cycle) and associated pathways (grey boxes including pentose phosphate pathway, anaplerotic pathway, biosynthesis of lipids and secondary metabolites, and green box including glyoxylate pathway). Biosynthesis of proteins linked to the tricarboxylic acid (TCA) pathway are shown in light brown. Metabolites involved in processes occurring in the cytosol, mitochondrion, and glyoxysomes are shown in blue, red and green, respectively. Anabolic pathways are shown with solid-line arrows, and catabolic ones with dashed-line arrows, i.e. degradation of lipids, β -oxidation of fatty acids, and gluconeogenesis [from the incorporation of succinate (Succ) coming from the glyoxylic cycle into TCA pathway, and transformation of resulting OAA to PEP and finally to sugars (dashed-line arrows in green)]. The degradation of proteins to amino acids is also indicated by dashed-line arrows. Evolved CO_2 molecules are shown in ellipses. Pathways and enzymes are in bold letters: *PPP* pentose phosphate pathway, *PEPC* phosphoenolpyruvate carboxylase, *PDH* pyruvate dehydrogenase, *PEPCK* phosphoenolpyruvate carboxykinase, *MDH* malate dehydrogenase, *ME* malic enzyme, *CA* carbonic anhydrase

II. Stable Carbon Isotopes and Photosynthesis

A. Carbon Isotopes, Abundance and Fractionation Definitions

The fundamental definitions required for the use of stable isotopes in biological or geochemical studies have already been extensively reviewed in previous contributions

(e.g. Kendall and McDonnell 1998), which the unaccustomed reader can refer to for further details. In what follows, the main features are briefly addressed, and points particularly relevant to metabolic studies are underlined.

Chemical elements naturally occur in various forms named isotopes, which differ only in their mass number. Forms that do not decay with time (i.e. non-radioactive forms)

are referred to as stable isotopes. The lightest forms are always the most abundant (Meija et al. 2016). The atomic mass difference between the heavy and light isotopes of a given element comes from the number of neutrons in the nucleus. Heavy isotopes have one, two or more additional neutrons compared with the light isotope. There are 15 known carbon isotopes with mass numbers ranging from 8 to 22 (https://en.wikipedia.org/wiki/Isotopes_of_carbon). Among them, only ^{12}C and ^{13}C are stable, with an average natural abundance of 98.9% and 1.1%, respectively. All other carbon isotopes are radioactive, and only ^{14}C (half-life of 5730 years) is found in nature. The most stable artificial carbon isotope is ^{11}C with a half-life of 20.334 min. Besides stable carbon isotopes, radioactive ^{14}C (e.g. Dieuaide-Noubhani et al. 1995) and ^{11}C (e.g. Bloemen et al. 2015) have also been applied as tracers in physiological studies.

The relative abundance of stable isotopes can be expressed as an isotope ratio (R), defined as the molar ratio of the heavy to light isotope, e.g. for carbon, $R = ^{13}\text{C}/^{12}\text{C}$. Because these ratios are very small, it is generally more practical to express them as a deviation relative to an international standard, the isotopic composition δ . For carbon:

$$\delta^{13}\text{C} = (R_S - R_{\text{PDB}}) / R_{\text{PDB}} = (R_S / R_{\text{PDB}}) - 1 \quad (3.1)$$

where, R_S and R_{PDB} are the isotope ratios of the sample and the PDB standard, respectively. PDB is a belemnite fossil coming from the geological formation Pee Dee in South Carolina, USA. Since the PDB is only slightly ^{13}C -enriched ($R_{\text{PDB}} = 0.0112372$) compared to almost all organic and inorganic materials, the $\delta^{13}\text{C}$ of biological samples are generally very small (expressed in per mil, ‰) negative values. Different combinations of light and heavy isotopes within a given molecule are defined as ‘isotopologues’ (e.g. $^{12}\text{C}^{16}\text{O}^{16}\text{O}$, $^{13}\text{C}^{16}\text{O}^{16}\text{O}$, $^{12}\text{C}^{18}\text{O}^{16}\text{O}$ are three isotopologues of CO_2).

The atomic mass difference between the heavy and light isotopes of a given element leads to differences in physical (e.g. coefficients for diffusion, dissolution, evaporation, etc.) and chemical properties (e.g. rate constants of reaction) forming the basis for isotopic fractionation processes occurring in the biosphere and during metabolism (e.g. during enzymatic reactions involving bond formation or cleavage). Fractionating processes are at the origin of the observed natural differences in heavy-to-light isotope ratios between different compartments of the biosphere (both organic and inorganic compartments), between metabolites, but also between the atoms within molecules (see Fig. 3.2).

For a (bio)chemical reaction converting a substrate S into a product P, the isotope effect can be expressed as:

$$\alpha = R_S / R_P \quad (3.2)$$

In the case of kinetic reactions (i.e. irreversible reactions), the isotope effect (α_k) corresponds to the ratio of kinetic rate constants of the light to the heavy isotope (e.g. for carbon, $\alpha_k = ^{12}k/^{13}k$) and R_S and R_P are measured at the beginning of the reaction. The light isotopologue generally reacts faster than the heavy one, so that $\alpha_k > 1$ and the product is depleted in ^{13}C compared with the substrate. For reversible reactions (i.e. operating close to the thermodynamic equilibrium), the isotope effect (α_e) is then defined as a ratio of equilibrium constants (e.g. for carbon, $\alpha_e = ^{12}K/^{13}K$). Quite often for reactions involving the making of a C-C bond, $\alpha_e < 1$ (i.e. the product is ^{13}C -enriched compared with the substrate).

Biologists use more frequently the isotope fractionation (or discrimination), defined as:

$$\Delta = \alpha - 1 \quad (3.3)$$

In fact, the isotope discrimination can be conveniently rearranged using δ values:

	Compounds S1, S2, S3, ... internal (int) or external (ext)	Changes in $\delta^{13}\text{C}$ of:	
		Compartments	Bulk OM
Exchange across compartments boundaries with Fractionation		Yes	Yes/No
Exchange across compartments boundaries without Fractionation		No	Yes/No
Enzymatic Fractionation at metabolic branching point		Yes (S2 opposite to S3)	No
Thermodynamic Fractionation		Yes (S1 opposite to S2)	No
Fragmentation Fractionation		Yes (S2 opposite to S3)	No

Fig. 3.2. Fractionation processes that affect the carbon isotope composition of compounds within or between compartments of a biological system. Pink rectangles represent compartments that can range from organelles, through tissues, organs up to the whole organism. S1, S2, S3 denote compounds (metabolites or components of structural mass) that are involved in reactions or transport associated with fractionation processes and/or exchange with other compartments. Metabolic or transport fluxes denoted by blue arrows can proceed without fractionation or be associated with thermodynamic (α_e), kinetic (α_k) or fragmentation fractionation. The two columns on the right hand side indicate isotope effects on individual compounds and/or on bulk organic matter (OM) and thus leading to a difference in isotope composition between the compartments and the external environment. Note that only processes involving trans-boundary transport can have an effect on the bulk isotope composition of the compartment considered. Reactions limited to within compartments will increase or decrease the heterogeneity of isotopic signatures between compounds within the compartment. Thus, they may cause a change in the bulk isotope composition only if reactants are exchanged across the compartment boundaries

$$\Delta = (\delta_s - \delta_p) / (1 + \delta_p) \quad (3.4)$$

Because δ values are negligible compared to 1, Δ can be approximated by the difference in the isotopic composition between the source and the product (i.e. $\Delta = \delta_s - \delta_p$). It is thus a convenient parameter to manipulate in biological and ecological systems where fractionating processes can be very diverse (Fig. 3.2).

When dealing with *in vivo* isotopic discrimination (Δ) in a metabolic context (like

respiration), it is important to keep in mind that observed kinetic isotope effects will vary with the fraction of substrate that is consumed by the reaction under consideration. If all of the substrate is converted to the product, then Δ will be equal to zero. It is only when the substrate is partially consumed by the enzymatic reaction under consideration and/or another fraction of the substrate has an alternative fate (i.e. metabolic branching occurs) that the kinetic isotope effect will be expressed. The observed magnitude of the fractionation will depend

on the relative fluxes in competing reactions (for a detailed analysis see Hayes 2001). A typical example is the photosynthetic discrimination against ^{13}C .

B. Setting the Stage for Respiration: Photosynthetic Carbon Isotope Fractionation

Plants discriminate against ^{13}C during photosynthetic CO_2 assimilation. Therefore, plant organic matter (OM) is naturally ^{13}C -depleted compared to atmospheric CO_2 by on average around 20‰ in C_3 and 4‰ in C_4 plants. Net photosynthetic carbon isotope discrimination has been extensively studied and robust models have been developed and validated for many C_3 and C_4 species (Farquhar et al. 1982, 1989). It results mainly from the interplay between two contrasted fractionating processes: the diffusion of CO_2 from the air into the leaves through stomata and its subsequent carboxylation by ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco), which discriminate against ^{13}C by 4.4‰ and 29‰ (Roeske and O’Leary 1984; Guy et al. 1993; McNevin et al. 2006; Tcherkez et al. 2013), respectively. Diffusion occurs across the leaf boundary layer, stomata, intercellular air spaces, and cellular medium to the site of carboxylation. Hydration, facilitated by carbonic anhydrase, supplies HCO_3^- for carboxylation by phosphoenolpyruvate carboxylase (PEPC) and feeds the pool of $\text{CO}_2/\text{HCO}_3^-$ present in a given compartment, functioning as a buffer for internal carbon dioxide.

Photosynthetic discrimination can be estimated using either the $\delta^{13}\text{C}$ of bulk OM (integrated value during plant growth), $\delta^{13}\text{C}$ of sugars (integrates about 2–3 days of photosynthetic discrimination) or measured on-line during leaf CO_2 exchanges (instantaneous net photosynthetic discrimination under fixed conditions). However, the photosynthetic discrimination and thus the ^{13}C content in photosynthetic products vary between plant species, plant developmental stages

and environmental conditions. While the instantaneous discrimination value (net photosynthesis) is physiologically the most relevant, values obtained from organic materials should be viewed as average values. Thus, their biological significance is different since they also result from differences in residence times of different metabolites.

In addition, in C_3 plants, there is a competition between CO_2 and O_2 at the active site of Rubisco, which can catalyze both the carboxylation and oxygenation of ribulose-1,5-bisphosphate (RuBP), so that the relative rates of photosynthesis *versus* photorespiration (carboxylation-to-oxygenation ratio) depend on the relative concentration of CO_2/O_2 at carboxylation sites. CO_2 production by photorespiration has been shown to discriminate by up to 12‰ against ^{13}C (i.e. with an isotopic difference between released CO_2 and net fixed C of 12‰) thus blurring the on-line photosynthetic discrimination measurements (Lanigan et al. 2008). It is the combination of all these concomitant processes which determines the overall fractionation between CO_2 and primary photosynthetic products. Note that net photosynthetic discrimination against ^{13}C is also influenced by anaplerotic CO_2 fixation (by PEPC) as well as (photo)respiratory release of CO_2 and as such can be impacted by high fluxes through PEPC, feeding malate into the TCA pathway that operates in a non-cyclic manner in the light (Tcherkez et al. 2012).

Variations in photosynthetic discrimination values in C_3 plants have been shown to be mainly due to changes in stomatal closure caused by changes in environmental factors, thereby limiting the CO_2 supply to Rubisco. In C_4 plants, the lower discrimination value is due to the CO_2 concentrating mechanism involving PEPC. Variations in the discrimination value of C_4 plants are mainly driven by the proportion of CO_2 leaking from the bundle sheath to mesophyll cells rather than by stomatal closure (for a review, see Brugnoli and Farquhar 2000). CAM plants

can exhibit either a C₃ or C₄ photosynthetic metabolism depending on the environmental conditions. The integrated discrimination, as measured in the $\delta^{13}\text{C}$ value of total organic matter, may thus vary in between the typical signatures of these two metabolic types, but quite usually, is observed to be intermediate between the characteristic values of C₃ and C₄. The isotopic composition of plant OM can thus be used to identify the prevalent photosynthetic pathway (C₃, C₄ or CAM).

III. Respiratory Carbon Isotope Fractionation

As recalled above, the $\delta^{13}\text{C}$ of leaf bulk OM has been first considered to reflect net photosynthetic discrimination. However, inter-organ isotopic differences have been repeatedly observed in plants that cannot be accounted for by photosynthetic discrimination only (Badeck et al. 2005). In fact, leaves have been shown to be generally ¹³C-depleted compared to all other organs, suggesting that fractionating mechanisms do occur after CO₂ fixation (reviewed by Cernusak et al. 2009). Such differences imply that (i) fractionating processes occur in the metabolism downstream photosynthesis, so that metabolic pools can have contrasted isotopic compositions, but also that (ii) some of these pools are either lost or transported differentially between organs. There are several processes in plants where carbon is lost to the environment such as volatile organic compounds (VOC) emission, ablation of waxes, exudation, etc. Among those, respiration is certainly the most important in terms of flux. In what follows, we will focus on the carbon isotope fractionation during respiratory processes, and how it can be explained by interactions in the metabolic network. Yet, to understand possible origins of the isotope composition in CO₂, the end product of respiration, we must first have a deeper look into how car-

bon isotopes are distributed within the potential substrates, before they are oxidized.

A. Origin of Non-statistical Intramolecular Distribution of ¹³C in Carbohydrates

One of the first post-carboxylation fractionation steps occurs in the Calvin cycle during aldolase reaction (i.e. synthesis of fructose-1,6-bisphosphate from triose phosphates), enriching in ¹³C the C-3 and C-4 atom positions of hexoses while leaving behind the light triose-phosphates at the equilibrium (Gleixner and Schmidt 1997). Rossmann et al. (1991) experimentally showed that the C-3 and C-4 positions of glucose molecules extracted from both C₃ (sugar beet syrup) and C₄ (maize flour) plants are effectively heavier (¹³C-enriched) while other carbon atom positions (C-1, C-2, C-5 and mainly C-6) are lighter (¹³C-depleted) than the average of the molecule. A simple model developed by Tcherkez et al. (2004) based on the isotope effects of both aldolase reported by Gleixner and Schmidt (1997) and transketolase (estimated values) fits well the reproducible non-statistical ¹³C distribution in hexose molecules reported by Rossmann et al. (1991), although not properly accounting for the ¹³C-depletion in C-6. More recently, however, the refinement of quantitative ¹³C-NMR techniques has allowed the intramolecular isotopic distribution to be measured on natural glucose and sucrose without the need for prior chemical degradation (Gilbert et al. 2011). While globally confirming the isotopic pattern initially described by Rossmann et al. (1991) in glucose from beet sugar, this work clearly demonstrated that (i) the glucosyl and fructosyl moieties of sucrose have contrasted ¹³C distributions, especially in C-2 and C-3 atom positions, but also that (ii) the intramolecular pattern in glucose could exhibit significant variations depending on its origin (starch/sucrose from either source or sink tissues), that cannot be accounted for by the sole action of aldolase and transketolases. Interestingly, the addition in the model cited

above of the isotope effects associated with (i) the interconversion of glucose-6-phosphate (G6P) by phosphoglucose isomerase, and (ii) the breakdown of sucrose by invertase, have led to reasonably good predictions of the observed distributions, notably for the ^{13}C -depletion in the C-6 atom position of glucose (Gilbert et al. 2012). Importantly, it means that the intramolecular ^{13}C pattern of glucose, generally the main substrate for respiration, can be modified downstream the Calvin cycle by starch and sucrose metabolism, which are variable both spatially (among the different tissues of the plant) and temporally (day/night cycle, and seasonal cycle). Besides, it shows that different patterns can be found amongst carbohydrates.

Intramolecular isotopic heterogeneity has long been documented in other compounds such as amino acids (Abelson and Hoering 1961; Melzer and O'Leary 1987) and lipids (Monson and Hayes 1980, 1982), and is

likely to be a general feature among all classes of metabolites (e.g. in alkaloids; Romek et al. 2015, 2016). Certainly then, the expected developments in that area in the near future will be of great help to improve our understanding of the spatial and seasonal variability in the isotopic composition of respired CO_2 (see also Sect. III.C). In fact, the isotope composition in specific carbon atom positions that are decarboxylated during respiratory processes is crucial to anticipating the overall $\delta^{13}\text{C}$ of evolved CO_2 , as discussed in what follows.

B. Differences in Isotopic Composition Among Metabolites

Enzymatic fractionations in metabolic pathways not only produce intramolecular heterogeneities, but also lead to substantial isotopic differences between metabolite classes. The updated survey of available data (Fig. 3.3) confirms the trend described

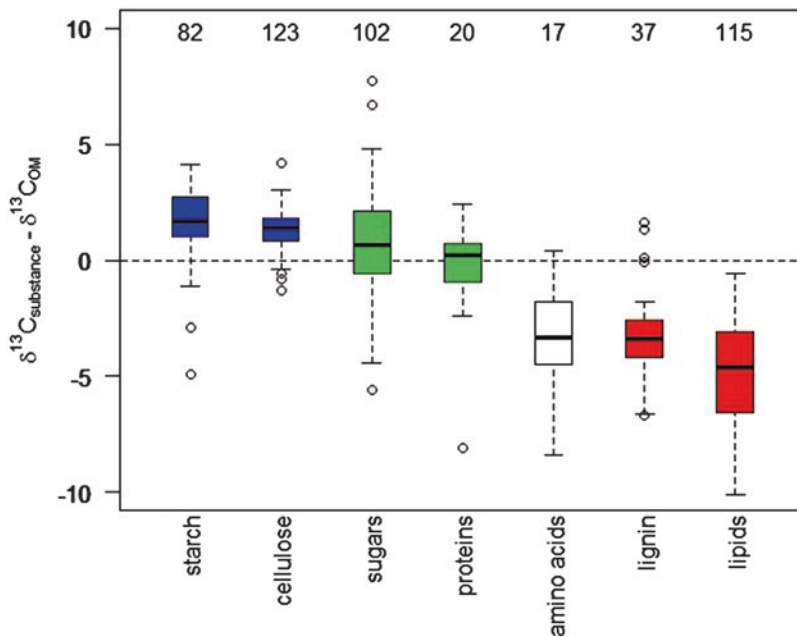


Fig. 3.3. Difference in $\delta^{13}\text{C}$ value (in ‰) between compound classes ($\delta^{13}\text{C}_{\text{substance}}$) within plant organs and total organic matter ($\delta^{13}\text{C}_{\text{OM}}$), assembled from literature data. Numbers on top indicate the number of measurements. Compounds that are significantly ^{13}C -enriched compared to bulk OM are indicated in blue, those that are not significantly enriched or depleted in green, and significantly depleted compounds in white (amino acids with low sample number) or red. Note the higher variance for the compound classes of shorter residence time (e.g. sugars and amino acids), that is likely due to dynamic changes in the photosynthetic discrimination with fluctuating environmental conditions

by Schmidt and Gleixner (1998). Compared to OM, a large ^{13}C -depletion is observed in lignin and lipids (around 3‰ and 5‰, respectively). Conversely, sugars, starch and cellulose are generally slightly ^{13}C -enriched due to the equilibrium isotope effect of aldolase described above. The depletion in lipids have been attributed to the fractionation against ^{13}C of chloroplastic pyruvate dehydrogenase complex (PDH) (Melzer and Schmidt 1987), while that in lignin has been proposed to originate from phenylalanine ammonia lyase activity (Butzenlechner et al. 1996). Interestingly, amino acids are also found to be substantially ^{13}C -depleted (by about 3.5‰), but this isotopic signature does not seem to be conserved in proteins (Fig. 3.3).

It must also be noted that the isotope composition in metabolites can vary temporally, as found in starch. In fact, aldolase favors ^{13}C in hexoses, thereby forming ^{13}C -enriched transitory starch in chloroplasts, while leaving behind ^{13}C -depleted triose phosphates, which are then converted to sucrose in the cytosol. Accordingly, phloem sugars are ^{13}C -enriched during night-time (because they come from transitory starch degradation), while day-time sugars originating from trioses are ^{13}C -depleted. Such a diel change in the ^{13}C content of phloem sugars modeled by Tcherkez et al. (2004) was measured by Gessler et al. (2008) on *Ricinus communis* (castor bean) plants.

C. Metabolic Branching and General Causes for Respiratory Fractionation

There is now a strong body of evidence that the isotope composition in CO_2 respired by different organs of the plant often differ from that in either bulk organic matter or carbohydrates (Fig. 3.4). This clearly illustrates the fact that respiratory metabolism and anabolic pathways are strongly interconnected, so

that not all glucose molecules entering glycolysis are eventually fully oxidized in the mitochondria (therefore, isotope fractionations can be expressed), and/or other substrates (with contrasted isotope compositions) can be oxidized. However, data that have accumulated in recent years also show a large variability of the apparent respiratory fractionation in plants (more than 10‰; Fig. 3.4). Understanding the origin of such a large range is a challenge that has triggered a renewed interest in the plasticity of respiration. Specifically, it has highlighted the need for a better understanding of metabolic fluxes, which ultimately determine the extent to which potential fractionations are expressed throughout the metabolic network (Hayes 2001).

Some important features driving variations in respiratory fractionation have been put forward. In what follows, we will try to present them based on specific examples, but also highlight their limits based on experimental evidence currently available, so as to point out where, in our view, further research efforts are needed.

1. Apparent Respiratory Fractionation

Because the mixture of substrates effectively sustaining respiration (and its isotope composition) is in general not known when measuring the isotope composition of respired CO_2 in gas exchange systems, respiratory fractionation has to be expressed relative to a somewhat arbitrary reference, and thus the term ‘apparent fractionation’ is used. One can choose to use the isotope composition of total organic matter, or that of a subset representative of a putative respiratory substrate, when available.

In typical conditions, dark respiration in plants exhibits a respiratory quotient (RQ) close to 1, suggesting that the main substrate is generally carbohydrates. Although the RQ

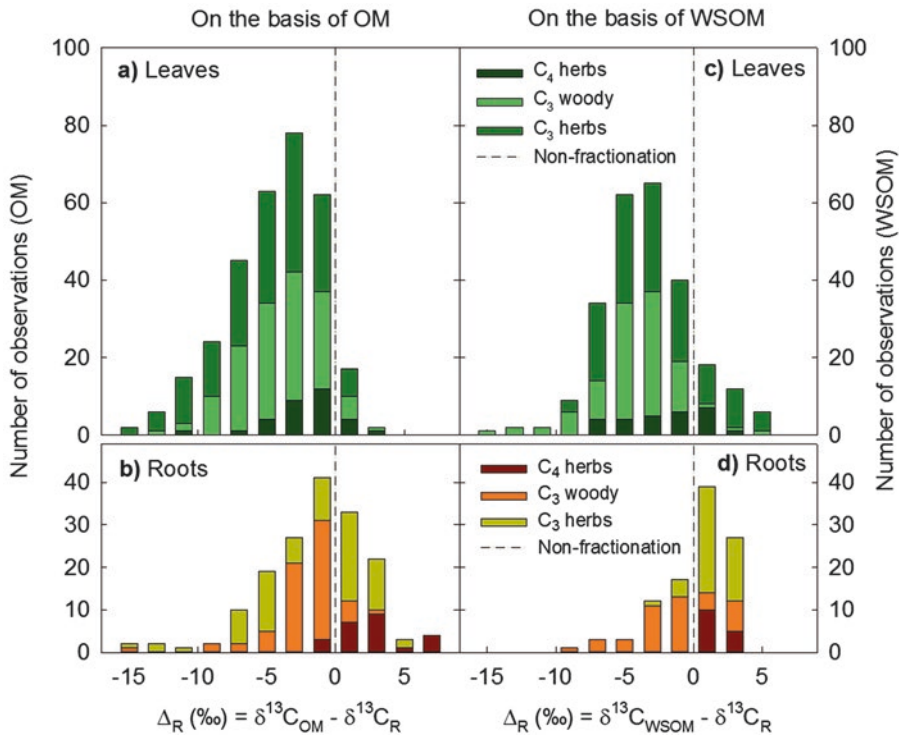


Fig. 3.4. Frequency distribution of apparent respiratory fractionation values (Δ_R) in leaves (a, c) and roots (b, d) of C_3 herbs, C_3 woody plants, and C_4 herbs under varying growth conditions and measured in the dark at different day or night time using different methods. For leaves, only data under non-LEDR conditions are presented (measured during either the night or the day but after at least 15 min darkness). Leaf data from the literature are from 32 herbaceous C_3 , 29 woody C_3 (including 7 coniferous) and 12 herbaceous C_4 species, and root data are from 20 herbaceous C_3 species, 9 woody C_3 species (including 3 coniferous) and 5 herbaceous C_4 species. Δ_R is calculated as the difference between the carbon isotope composition of leaf or root material available in the literature [bulk organic matter (OM, left side panels) or water soluble fraction (WSOM, right side panels), considered as respiratory substrates], and that in leaf- or root-respired CO_2 ($\delta^{13}C_R$) as the product of respiration. Negative Δ_R values correspond to a ^{13}C -enrichment and positive Δ_R values to a ^{13}C -depletion in respired CO_2 compared to the substrate. Vertical dashed lines indicate no respiratory fractionation (i.e. $\Delta_R = 0$)

may be different from 1 or an RQ of 1 may result from a mixture of respiratory substrates of different oxidation level (as will be discussed later), in this section we chose to refer to the apparent fractionation defined against the isotope composition of the carbohydrate pool (generally measured as the water soluble fraction, WSOM) as a reference point. Apparent respiratory fractionation may be expressed relative to the whole organic matter when assessing the role of respiration in driving the observed differences in isotopic

composition between autotrophic and heterotrophic organs (see Ghashghaie and Badeck 2014 for a discussion). However, when looking into the variability of respiratory fractionation from a metabolic point of view, anchoring the discussion to the most probable main substrate is preferable. WSOM is generally slightly heavier than OM (1–3‰), so that the ^{13}C -enrichment in respired CO_2 is artificially exaggerated when compared to OM. Besides, the isotope composition of WSOM can exhibit variations on short time

scales (diel range of up to 3‰, Werner and Gessler 2011) that are not apparent in OM. Also, it must be emphasized that WSOM is not only composed of carbohydrates, so that large variations of other compounds, (e.g. organic acids or sugar alcohols) can influence its isotopic composition. Ideally, the isotope composition in sucrose (which is generally found to be close to that of WSOM) would be a better reference to express respiratory apparent fractionation in this context, but it is not available in many of the studies reviewed here.

2. Dark Respiration in Leaves: PDH-TCA Imbalance and Beyond

First systematic investigations of the isotopic composition of respired CO₂ in darkened mature leaves of herbaceous C₃ plants have shown that released CO₂ is on average heavier than sucrose by about 3–6‰ (Duranceau et al. 1999; Ghashghaie et al. 2001). Subsequent studies suggested that the systematic enrichment in leaf respired CO₂ compared to WSOM is a widely distributed feature in plants, but also demonstrate that, as pointed out earlier, the range of variation can be quite large (Fig. 3.4).

The ¹³C-enrichment in leaf respiratory CO₂ has been attributed to the so called ‘fragmentation fractionation’ (see Tcherkez et al. 2004). Glycolysis produces pyruvate, which can enter mitochondria and subsequently be decarboxylated by PDH to produce acetyl-CoA. The C-1 atom position of pyruvate decarboxylated in the process originates from positions C-3 and C-4 of glucose that are ¹³C-enriched by about 4‰ compared to the average isotopic composition of the molecule. Accordingly, acetyl-CoA carries the four other carbon atoms of glucose into the TCA (C-1, C-2, C-5, and C-6), which are relatively ¹³C-depleted (see Sect. III.A). If a large amount of acetyl-CoA is diverted to various anabolic pathways (e.g. fatty acid biosynthe-

sis, secondary metabolites...) instead of fueling the TCA cycle, the respiratory CO₂ efflux will be dominated by PDH activity, and therefore substantially ¹³C-enriched. It is thus generally accepted that the degree of imbalance between PDH and TCA decarboxylations in the respiratory flux is an important driver of the variability in the isotopic composition of respired CO₂ (Ghashghaie et al. 2003; Badeck et al. 2005; Cernusak et al. 2009; Werner and Gessler 2011; Ghashghaie and Badeck 2014). An important assumption here is that pyruvate is fully committed to acetyl-CoA, so that the isotope effect of PDH (1.023), which would deplete respired CO₂ in ¹³C, is not expressed. This is probably valid in darkened leaves where pyruvate entering mitochondria does not have obvious alternative fates to decarboxylation.

In this framework, however, accounting for the commonly observed respiratory fractionation in leaves (around –4‰, the negative value showing that it is ¹³C-enriched) requires that the commitment of acetyl-CoA to TCA remains very low (around 5%, see Tcherkez 2010). This is because (i) for one fully oxidized pyruvate molecule, two CO₂ are released by the TCA when only one arises from PDH, and (ii) citrate synthase (CS) exhibits a kinetic isotope effect of about 1.020 during the formation of citrate, further ¹³C-depleting TCA intermediates when acetyl-CoA is not fully committed.

Yet, such a large imbalance seems unlikely to occur *in vivo*, especially in the dark. Most biosynthetic processes probably occur predominantly in the light, and in particular, fatty acid synthesis has been shown to take place mainly in chloroplasts (Schmid and Ohlrogge 2002) during the day, when light energy can provide the required ATP and NADPH, and chloroplastic PDH is activated (Tovar-Mendez et al. 2003). It is still possible that acetyl-CoA in the cytosol can be involved in lipid chain elongation and biosynthesis of various secondary metabolites

(isoprenoids, flavonoids, etc...), even in the dark. However, these fluxes are unlikely to exceed 5–10% of the respiratory flux of PDH. In addition, the accepted view is rather that the cytosolic pool of acetyl-CoA is fueled by citrate exported from the mitochondria and cleaved by citrate lyase (Oliver et al. 2009). In other words, there is very little evidence that large fluxes of acetyl-CoA can escape the TCA pathway. Consistently, no acetyl-CoA mitochondrial membrane carrier has been identified in *Arabidopsis thaliana* (Lee and Millar 2016). In fact, if a very low proportion of acetyl-CoA were to enter the TCA pathway, one would expect CO₂ production to largely exceed O₂ consumption by mitochondria, as the latter is coupled to the TCA pathway through NADH dehydrogenases and succinate dehydrogenase (regardless of complications that would arise in imbalances in ATP/ADP and NAD/NADH pools). This does not seem to be the case since (i) the RQ of darkened leaves is generally close to 1 (Noguchi and Terashima 1997; Tcherkez et al. 2003), and (ii) their respiration rate matches reasonably well the estimated ATP demand for sucrose export and protein turn-over (Noguchi et al. 2001).

It is also worth noting that the observed range of leaf respiratory fractionation spans values up to at least –8‰ (Fig. 3.4), which largely exceeds the theoretical maximum that can be attained based on fragmentation fractionation. Other explanations thus need to be found to explain the general ¹³C-enrichment in dark-evolved CO₂.

In fact, if both pyruvate and acetyl-CoA were nearly fully committed, one would expect very little respiratory fractionation to occur upon oxidation of carbohydrates (Werner et al. 2011). Interestingly, some clues to try and solve this conundrum can be sought in recent progresses toward an integrated view of respiratory metabolism and the plasticity of the TCA cycle (Sweetlove et al. 2010; Tcherkez et al. 2012). Thus, because organic

acids of the TCA pathway contribute to several anabolic pathways, but also to redox and pH regulation within the cell, the cyclic nature of the pathway can vary considerably. This is clearly the case in illuminated leaves (as will be discussed later), where a non-cyclic flux mode of the TCA have been demonstrated using isotopic tracers (Tcherkez et al. 2009; Gauthier et al. 2010).

In the dark, cells largely rely on mitochondrial ATP production, so that such non-cyclic flux modes are less likely to occur. However, this does not preclude some intermediates to be withdrawn from the cycle for other metabolic purposes, as long as these leaks are compensated for in some ways. In fact, it is known that citrate, and to a lesser extent malate, can be accumulated in the vacuole of plant cells in the dark (Gout et al. 1993). Consistent with these observations, a recent diel flux balance model applied to C₃ leaf metabolism has predicted that up to 15% of citrate produced by CS at night is stored in the vacuole, before being remobilized during the day to support glutamate synthesis (Cheung et al. 2014). This has consequences regarding the isotopic composition of the CO₂ evolved in the TCA during the night.

To understand these implications, we first need to come back to the fate of each individual carbon atom position of glucose that is decarboxylated in the TCA pathway (positions C-1, C-2, C-5 and C-6), which, as pointed out earlier (Sect. III.A), are not isotopically equivalent. When glucose is converted into pyruvate by glycolysis, positions C-1 and C-6 get pooled in the C-3 atom of pyruvate (corresponding to C-2 in acetyl-CoA), while positions C-2 and C-5 end up in the C-2 atom of pyruvate (corresponding to C-1 in acetyl-CoA). Complication then arises because the 2 carbon atoms of acetyl-CoA incorporated into citrate by CS are not immediately decarboxylated in the TCA pathway. None of them is decarboxylated upon first turn, and it is only during the sec-

and turn that the C-1 position of acetyl-CoA is lost. But from then on, because of the symmetry of the succinate molecule, the C-2 position of acetyl-CoA has only 50% chance to be decarboxylated at each subsequent turn. In other words, it means that in conditions where a substantial flux of organic acids (e.g. citrate) is withdrawn from the TCA, glucose atom positions C-1 and C-6 will be underrepresented in the CO₂ efflux, so that any isotopic disequilibrium between these positions and positions C-2/C-5 will be expressed in respiratory fractionation. Glucose atoms C-2/C-5 are ¹³C-enriched in comparison to positions C-1/C-6. Intramolecular data suggest that the difference is generally around 2‰, but might vary with environmental conditions (Gilbert et al. 2012). However, it has been shown to be substantially larger in the fructosyl moiety of sucrose (8‰), where the C-2 atom is strongly ¹³C-enriched (Gilbert et al. 2011). If, as hypothesized by these authors, this enrichment is due to the equilibrium isotope effect of glucose-6-phosphate-isomerase, it is likely to be expressed in fructose-6-phosphate entering glycolysis in darkened leaves, where the glucose-6-phosphate pool is constantly utilized for sucrose export.

The explanation given just above can be summarized with a simple numerical example. As discussed, both pyruvate and acetyl-CoA are supposed to exhibit high commitments (>95%) to PDH and CS, respectively, so that the isotope effects of these enzymes are probably negligible *in vivo*. The isotope composition in respired CO₂ can thus be calculated with an isotopic mass balance, summing the contribution of each pyruvate atom position to the total CO₂ efflux (i.e. meaning that three different pools of glucose carbon atoms are considered: C-3/C-4, C-2/C-5, and C-1/C-6). The relative contribution of positions C-2/C-5, and C-1/C-6 to the overall efflux from the TCA pathway can then be varied in order to illustrate the effect of the C-1/C-6 trapping

when intermediates of the TCA pathway are being withdrawn. Starting from the experimentally measured isotopic distribution in glucose carbon atoms, it yields slightly negative respiratory fractionations (i.e. ¹³C-enriched CO₂ compared to glucose), ranging from 0 to -0.5‰, while the values of sucrose fructosyl extend that range to up to -2‰. This illustrates that the CO₂ produced by the TCA pathway does not necessarily have to be ¹³C-depleted, as often assumed. We nevertheless recognize that the above calculation does not capture the whole complexity of the system. Notably, even relatively small leaks (between 5 and 15% of the flux) of pyruvate, acetyl-CoA, and/or 2-oxoglutarate could suppress this enrichment, and lead to slightly positive apparent fractionations (easily up to 5‰), because PDH, CS and 2-oxoglutarate dehydrogenase (2OGDH) can all discriminate against ¹³C by up to 20‰ or more (See Tcherkez et al. 2011a for details on isotope effects). Overall, it suggests that in a respiratory system where all commitments are high (85% and above), the mere interplay of glycolysis and TCA pathway can only account for apparent fractionations roughly in between 5‰ and -2‰. Clearly then, other processes must occur in darkened leaves where the respiratory CO₂ has commonly been found to be heavier than WSOM by 3‰ to 8‰ (Fig. 3.4).

In that perspective, we must consider how the organic acid leaks discussed previously can be compensated for in order to keep the cycle running. The first possibility is a sustained flux of cytosolic oxaloacetate (OAA), derived from PEP by the action of PEPC, into the mitochondria. The anaplerotic function of PEPC in leaves in the light has been known for some time (Melzer and O'Leary 1987), and it has been shown that it can carry substantial fluxes in heterotrophic organs (around 10% of the respiratory efflux, Dieuaide-Noubhani et al. 1995; Bathellier et al. 2009). Yet, its quantitative contribution

in darkened leaves remains poorly documented, despite early reports of $^{14}\text{CO}_2$ incorporation into organic acids in tobacco and avocado leaves in the dark (Kunitake et al. 1959; Clark et al. 1961) and in other species (Nalborczyk 1978). Accounting for the isotope effect of the equilibrium between CO_2 and HCO_3^- , carbon fixation by PEPC discriminates in favor of ^{13}C by about 5.7‰ (Farquhar 1983). When operating during the day, it would fix mostly atmospheric CO_2 , thus strongly enriching OAA and its derivatives (malate, fumarate, aspartate; Melzer and O’Leary 1987; Tcherkez et al. 2011b; Lehmann et al. 2016). Nevertheless, at night, when stomata are closed, PEPC will merely reflux CO_2 from respiration. No matter how large the flux is, its net isotope contribution will thus be negligible, unless a large proportion of the OAA produced is not subsequently decarboxylated, in which case it should slightly deplete respired CO_2 in ^{13}C .

Alternatively, TCA cycle intermediates could be fed by stored pools of organic acids. In *Arabidopsis*, both malate and fumarate have been shown to exhibit large diel variations, accumulating to substantial amounts (up to $10\ \mu\text{mol g FW}^{-1}$) during the day, while decreasing sharply during the night (Chia et al. 2000; Pracharoenwattana et al. 2010). As noted above, accumulation of organic acids in the light is strongly supported by PEPC activity, so that they can be quite substantially enriched in ^{13}C , especially in carbon atom positions C-4 and C-1, which can be decarboxylated by the TCA cycle. Considering the enrichment of about 20‰ observed in the C-4 of aspartate (Melzer and O’Leary 1987), it follows that even a relatively modest contribution of these pools to the respiratory CO_2 efflux (i.e. 10–20%) could suffice to account for the most frequently observed fractionations (–3‰ to –6‰) during dark respiration.

Currently, no direct experimental evidence is available to confirm such a hypoth-

esis, and further work is clearly needed so as to clarify the contribution of organic acids to dark respiration. However, if correct, it implies that the extent of the ^{13}C -enrichment in leaf respired CO_2 in the dark will largely depend on (i) the degree of accumulation of organic acids (such as malate or fumarate) during the day, which should in turn change their contribution throughout the night, and (ii) the degree of enrichment that they will exhibit. A recent model of *Arabidopsis* leaves predicts that the partitioning of assimilates between carbohydrate and organic acids should exhibit a tight trade-off that will be modulated by the energy and redox status of photosynthesizing cells (Cheung et al. 2015). In the studies cited above (Chia et al. 2000; Pracharoenwattana et al. 2010), fumarate accumulation in *Arabidopsis* leaves was tightly linked to nitrogen availability. Besides, one can expect that varying physiological conditions will influence the relative contribution of PEPC to organic acid synthesis in the light, but also the isotope composition of its substrate, HCO_3^- . Overall, it could thus offer a promising framework toward a better understanding of the variability of respiratory fractionation in leaves during the night.

An interesting observation in that context is the general trend for a reduction of the ^{13}C -enrichment in respiratory CO_2 between the beginning and the end of the night illustrated in Fig. 3.5. It is indeed possible that the contribution of organic acids would decrease throughout the night as the vacuolar pool shrinks. The direction of malate flux, to or from the vacuole in protoplasts, has been shown to be dictated by a threshold value of the cytosolic pool (Gout et al. 1993). Note however that other processes are probably involved, such as the increasing contribution of recycled proteins and/or lipids, as suggested by the slight decrease that has been observed in the RQ during the night (Noguchi and Terashima 1997, see also Sect. III.D).

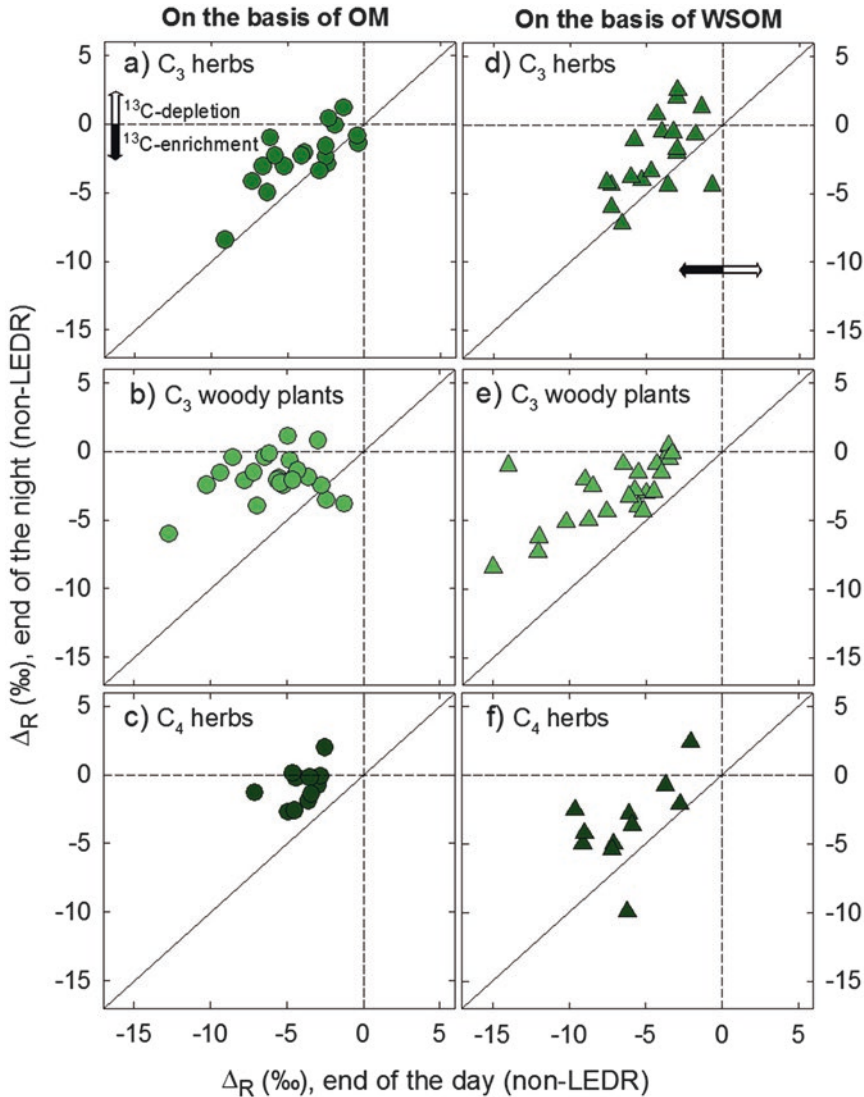


Fig. 3.5. Apparent respiratory fractionation (Δ_R) of leaves from C_3 herbs (a, d), C_3 woody species (b, e) and C_4 herbs (c, f) measured at the end of the night *versus* Δ_R values determined at the end of the day (or beginning of the night) from literature when both day and night data were available. Data reported under LEDR conditions are not used. Δ_R is calculated as the difference between carbon isotope composition in leaf bulk organic matter (OM, circles) or water soluble fraction (WSOM, triangles) considered as potential respiratory substrates and that of leaf-respired CO_2 ($\delta^{13}C_R$). Negative Δ_R values correspond to a ^{13}C -enrichment and positive Δ_R values to a ^{13}C -depletion in respired CO_2 compared to plant material, shown by black and white arrows, respectively. Solid lines correspond to 1:1 relationships and dashed lines indicate no respiratory fractionation (i.e. $\Delta_R = 0$)

3. The Special Case of Light-Enhanced Dark Respiration (LEDR)

A phenomenon which seems to unequivocally illustrate the impact of organic acids on respiratory fractionation is LEDR. LEDR corresponds to a transient increase in respi-

ration rates (both CO_2 release and O_2 consumption) that occurs within the first 15–25 min after darkening. It needs to be distinguished from the post-illumination burst (PIB). The latter occurs within the first minute after darkening and is presumably related to the decrease in the photorespira-

tory glycine pool, while LEDR sets on after the end of PIB and attains maximal rates around 3–4 min after darkening (Atkin et al. 1998, and earlier work cited therein). During that transient time, respired CO_2 has been found to exhibit large ^{13}C -enrichments that decreased exponentially to reach a steady state when respiration rate stabilizes (reviewed in Werner and Gessler 2011). LEDR has been attributed to the rapid consumption of an excess malate pool upon darkening, which triggers the activity of light inhibited NAD-dependent malic enzyme (NAD-ME) and PDH in the mitochondria. Consistently in *Ricinus*, the transient enrichment in respired CO_2 could be satisfactorily explained by a 22% contribution of the decarboxylation of the strongly enriched C-4 atom of malate (see above) by NAD-ME, which matched the reduction of the malate pool (Gessler et al. 2009).

Yet, it is worth noting that LEDR time frame is probably rather loosely defined. Most studies of the phenomenon, done on dark adapted protoplasts or leaves subjected to very short pre-illumination periods (10–15 min, Heichel 1971; Reddy et al. 1991; Igamberdiev et al. 1997; Atkin et al. 1998), show a rapid bell shaped transient (within 25 min or less). However, when measured on leaves taken after a longer photoperiod (>6 h), the pattern is slower (up to 1 h), and strongly temperature dependent (Azcon-Bieto and Osmond 1983). Besides, the bell shape only appears when non-photorespiratory conditions are applied 20 min before darkening. When continuously recorded overnight, after a full photoperiod, leaf respiration decrease looks more like a single exponential decay, except for C_4 plants (Byrd et al. 1992). A clear-cut distinction between LEDR and steady state respiration might thus be difficult to achieve in practice, and in fact, the isotope composition in respired CO_2 during LEDR, and after 1 h in the dark, exhibits a rather good correlation, with a consistent offset (Fig. 3.6).

Highly ^{13}C -enriched leaf respired CO_2 has been reported for many C_3 species (fractionation of up to -13‰) after 4–5 min in the

dark measured rapidly with TDLS (Barbour et al. 2007) or by rapid in-tube incubation (Priault et al. 2009; Werner et al. 2009; Wegener et al. 2010; Lehmann et al. 2015). Similarly, strikingly high $\delta^{13}\text{C}$ values of up to -4‰ (i.e. heavier than atmospheric CO_2) are observed in respired CO_2 in C_4 maize leaves even after about 20 min in darkness, thereafter declining relatively slowly to reach stable values (around -14‰) only after 1h30 in darkness, together with a decrease of leaf malate content (Ghashghaie et al. 2016). Recently, Lehmann et al. (2015) found that the $\delta^{13}\text{C}$ of leaf respired CO_2 (potato plants), for both LEDR and steady-state conditions, was better correlated with that of malate than with soluble sugars, suggesting that variations in malate consump-

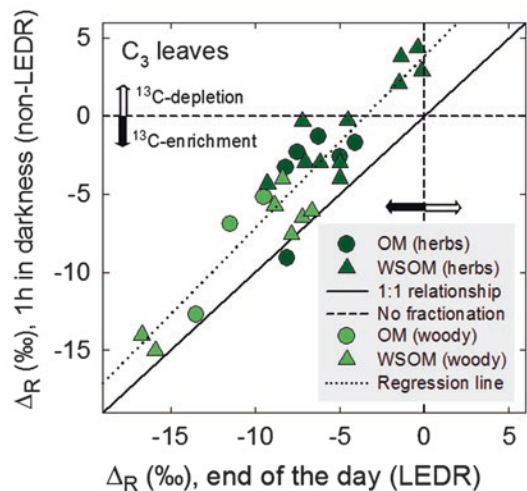


Fig. 3.6 Apparent respiratory fractionation (Δ_R) of leaves from C_3 herbs (dark symbols) and C_3 woody species (light green symbols) from the literature, determined after 1 h in darkness (i.e. non-LEDR conditions) versus values obtained at the end of the day after a few minutes in darkness (under LEDR conditions). Δ_R is calculated as difference between the carbon isotope composition in leaf bulk organic matter (OM, circles) or water soluble fraction (WSOM, triangles) and that of leaf-respired CO_2 ($\delta^{13}\text{C}_R$). Dashed lines indicates no respiratory fractionation (i.e. $\Delta_R = 0$). Negative Δ_R values correspond to a ^{13}C -enrichment and positive Δ_R values to a ^{13}C -depletion in respired CO_2 compared to plant material (shown by dark and white arrows, respectively). The solid line corresponds to the 1:1 relationship and the dotted line to the linear regression ($y = 3.86 + 1.10x$, $r^2 = 0.85$)

tion (remobilized or synthesized *de novo*) could strongly influence the isotope composition in respired CO₂ throughout the night.

Further work is thus needed to clarify the metabolic adjustments occurring upon darkening. It is possible that pathways other than malate decarboxylation are involved, considering the strong effect of non-photorespiratory conditions just prior to switching to darkness. It cannot be excluded that the early phase of LEDR is influenced by the consumption of metabolic pools linked to photorespiration that built up in the light. In this regard, it is worth noting that serine has been shown to be strongly ¹³C-enriched in *Pelargonium* leaves (Tcherkez et al. 2011b). However, photorespiration can also significantly impact the redox status of the cell, and thus malate pools in different cell compartments. In fact the subcellular origin of the malate pool involved in LEDR is uncertain. In spinach, the drop in total malate content during the first 15 min after darkening cannot be accounted for by the decrease measured in both the vacuole and the chloroplasts, while the cytosolic pool remained rather constant (Gerhardt et al. 1987), suggesting that inter-organelle regulations are involved.

4. What About Leaf Respiratory Fractionation in the Light?

Experimental assessment of respiratory fractionation in leaves in the light is a difficult task since (i) CO₂ photosynthetic fixation largely dominates the net flux, and (ii) CO₂ efflux is a mixture of both photorespiratory (i.e. glycine decarboxylation) and respiratory processes *per se*. Indirect estimations of each component are possible by fitting observed net photosynthetic fractionation values to predicted values using an extended model for Δ (Lanigan et al. 2008; Tcherkez et al. 2010). Using such an approach, it has been calculated that respiratory CO₂ efflux from illuminated *Pelargonium* leaves is ¹³C-depleted as compared to organic matter by 0–10%, con-

sistent with previous theoretical argument (Tcherkez et al. 2004, 2011b).

In the light, contrasted fractionating processes can be suspected to occur. Both glycolysis and mitochondrial TCA decarboxylating enzymes (PDH, IDH, and 2OGDH) are thought to be strongly down-regulated, so that day respiratory flux is probably dominated by a combination of chloroplastic PDH activity, and non-cyclic TCA pathway decarboxylations, with a potentially large involvement of cytosolic bypasses (Sweetlove et al. 2010; Tcherkez et al. 2012). PDH in the chloroplast is fueled by triose-phosphates, which are slightly ¹³C-depleted (Gleixner et al. 1998), and will probably further fractionate against ¹³C since pyruvate is likely to be diverted for a range of biosynthetic processes in the light (e.g. pyruvate derived amino acids and their derivatives). Similarly, a large part of the 2OG pool can be used to form Glu to sustain nitrate assimilation, so that the isotope effect of 2OGDH (probably close to 1.020) can be expressed, although the flux it carries might be rather small. On the other hand, labeling experiments suggest that a substantial proportion of respired CO₂ in the light comes from stored carbon pools (40–86%, Pärnik and Keerberg 2006; Tcherkez et al. 2010, 2011b), which could be organic acids accumulated in the night (e.g. citrate or malate, see above). Depending on their degree of enrichment, their contribution can partly compensate for the depleting effects of decarboxylases. Still, one might expect organic acids accumulated at night to be less ¹³C-enriched than those accumulated in the light, since PEPC activity likely refixes an important proportion of ¹³C-depleted respired CO₂ in the dark.

5. The Role of the PPP as Illustrated in Roots

Heterotrophic organs of plants entirely rely on the constant export of photosynthetic products from autotrophic organs (leaves)

through the phloem. Respiration is their main source of energy to sustain cellular functioning and biosynthesis (except in conditions that favor fermentation), so that it exhibits much less diurnal variability than in leaves. In roots, where it has been the most extensively studied, the isotopic composition of respired CO_2 is also less variable than in leaves, and on average, slightly ^{13}C -depleted compared to WSOM (Fig. 3.4).

Labeling experiments on French bean have shown that the organization of the respiratory metabolic network in roots shares some similarities with that of darkened leaves described above (Bathellier et al. 2009). The TCA pathway functions as a cycle, and the commitment of mitochondrial acetyl-CoA to CS is probably relatively high. In fact, fatty acid synthesis also occurs in plastids in roots (at low rates), which possess their own PDH, supplied directly from cytosolic pyruvate (Fisher and Weber 2002). A substantial part of TCA intermediates are also abstracted from the cycle mostly to form glutamate and aspartate for nitrogen assimilation. This feature would be further amplified in conditions where organic acid exudation is high. Accordingly, an important flux through PEPC has been found to occur, compensating for the abstraction of TCA intermediates. Following the arguments exposed for darkened leaves, root respiration would thus be expected not to be associated with a large fractionation, potentially slightly negative (i.e. in favor of ^{13}C) because of both the trapping of positions C-1/C-6 of glucose in abstracted TCA intermediates, and the activity of plastidial PDH. Yet, these effects are probably counterbalanced by the isotope effect of 2OGDH (which can be expressed due to a branching point at 2OG, used for both Glu and succinate synthesis).

That said, a significant proportion of respired CO_2 in roots is believed to come from the activity of the oxidative pentose phosphate pathway, PPP (20–25%; Dieuaide-Noubhani et al. 1995; Bathellier et al. 2009). Oxidative PPP activity is important in pro-

viding NADPH for nitrate reduction and fatty acid synthesis (Bowsher et al. 2007). During the oxidative phase of PPP, 6-phosphogluconate dehydrogenase (6PGDH) decarboxylates 6-phosphogluconate to form ribulose-5-phosphate, releasing the C-1 atom of glucose as CO_2 . 6PGDH has been shown to exhibit a kinetic fractionation against ^{13}C of around 9.6‰, while being also capable of reversible catalysis thereby giving an equilibrium fractionation in favor of ^{13}C of about 4‰ (Rendina et al. 1984). The classical textbook view is that the reactions of the oxidative phase of the PPP are mostly irreversible *in vivo* (Tobin and Bowsher 2005). However, a recent estimate of the standard Gibbs free energy of reaction (ΔG_r^0) for the decarboxylation of 6-phosphogluconate (using the component contribution method; Noor et al. 2013) predicts a rather high *in vivo* value of around +8 kJ/mol (Tepper et al. 2013). It is likely then that 6PGDH must exhibit quite a substantial degree of reversibility *in vivo*, which will vary depending on the relative concentration of 6-phosphogluconate to ribose-5-phosphate. The effective isotope effect at this step can thus be expected to be rather small. However, the first enzyme of the PPP, glucose-6-phosphate dehydrogenase (G6PDH) fractionates by 16.5‰ against ^{13}C in the C-1 atom position of glucose (Hermes and Cleland 1984), which is subsequently decarboxylated by 6PGDH. G6PDH thus tends to deplete in ^{13}C the CO_2 released by the PPP. Still, it must be pointed out that in a specific case where oxidative PPP would be predominantly active in plastids, the commitment of Glc-6-phosphate to chloroplastic G6PDH can be high (provided little starch synthesis occurs), so that the isotope effect is not expressed. Therefore, if 6PGDH operates close to equilibrium, the oxidative PPP would then contribute ^{13}C -enriched CO_2 (up to 4‰ compared to Glc C-1) to the respiratory efflux.

Taken all together, the isotopic contributions of PDH, TCA and oxidative PPP in

roots fit reasonably well the range of observed respiratory fractionations (-4‰ to 4‰ ; Fig. 3.4). We nevertheless recognize that occurrence of more negative respiratory fractionations (below -4‰), if they were to be confirmed, cannot easily be accounted for without the consumption of ^{13}C -enriched substrates. Since organic acids accumulated in leaves in the light are the only obvious ^{13}C -enriched pool, it would imply transport processes. Such processes are possible (e.g. Peuke et al. 1996), but further work would be required to establish their implication in respiration of heterotrophic organs. The existence of other ^{13}C -enriched pools in the roots is still possible, but remains to be demonstrated. Notably, in respiring heterotrophic organs, the isotopic composition of $\text{CO}_2/\text{HCO}_3^-$ in cells should be much less influenced by atmospheric CO_2 than in illuminated leaves with open stomata, especially in underground organs such as roots, as many respiring organisms contribute to the overall CO_2 pool in the soil. Thus in these tissues there is less room for carboxylases like PEPC to produce strongly ^{13}C -enriched metabolites, although this will be dependent on their specific conductance to CO_2 and respiration rates.

D. Variations in the Substrate Mixture Sustaining Respiration

The above discussion was focused on conditions where respiration oxidizes carbohydrates, so that the RQ is close to 1. Although this is certainly the most common situation, there are both environmental and developmental circumstances that lead plant respiration to consume alternative substrates to sustain ATP production in mitochondria. This has been clearly illustrated in French bean leaves under prolonged darkness (up to 2 weeks; Tcherkez et al. 2003). As the carbohydrate pool collapses, lipids and proteins

are remobilized (providing acetyl-CoA, TCA intermediates, and/or pyruvate) and maintain mitochondrial activity. This switch in respiratory substrates is accompanied by a marked decrease of the RQ, which correlates with a ^{13}C -depletion in respired CO_2 , reaching values consistent with the isotopic composition of lipids and proteins. A switch similar to that artificially induced by prolonged darkness can be expected during plant senescence. Also, as discussed earlier, respiration decreases throughout the night (together with the carbohydrate pool), suggesting that the contribution of the constant turn-over of proteins and membranes probably increases, thus depleting respired CO_2 in ^{13}C (Fig. 3.5).

Switches between substrates can also be expected across ontogenetic developmental stages, especially when seeds contain non-starchy reserve types. In peanut seeds (which contain about 50% lipids), lipid remobilization starts progressively during the early stages of germination. Consistently, the isotopic composition of respired CO_2 in the emerging radicle and leaves becomes progressively ^{13}C -depleted as lipid contribution increases in the respiratory substrate mix (Ghashghaie et al. 2015), while it remains rather constant in the case of the starch-containing French bean seeds (Bathellier et al. 2008). However, the depletion in respired CO_2 is not accompanied by a change in respiratory apparent fractionation, because lipids reserves are converted to carbohydrates through the glyoxylate cycle and gluconeogenesis before being exported to developing organs. In oil-containing seeds, the glyoxylate cycle converts two acetyl-CoA molecules, resulting from fatty acid breakdown, to succinate (Fig. 3.1). Succinate leaving the glyoxylate cycle transports the relatively ^{13}C -depleted carbon stored in lipids to the mitochondrion where (after being converted to malate and oxaloacetate) it can be either directly used by the TCA pathway, exported to the cytosol (malate-oxaloacetate

shuttle), or used to fuel gluconeogenesis. Despite the likely contribution of ^{13}C -depleted lipids as substrates, peanut cotyledons exhibited a negative respiratory fractionation (i.e. in favor of ^{13}C) during the heterotrophic phase of germination, suggesting either that inverse fractionations are associated with the metabolism of lipid remobilization, or that their respiration is also fuelled by stored carbohydrates (see Ghashghaie et al. 2015 for a more detailed discussion).

It is worth noting that the time course of the respiratory fractionation in growing organs during ontogeny is so that the isotope composition in respired CO_2 eventually reaches the typical values observed in mature plants after the onset of autotrophy, in both C_3 and C_4 plants (see Bathellier et al. 2008 and Ghashghaie et al. 2015 for C_3 legumes, and Ghashghaie et al. 2016 for C_4 maize), and this effect cannot be accounted for by a simple switch in respiratory substrates (i.e. from remobilized reserves to photosynthetic assimilates). Rather, it must reflect flux changes in primary carbon metabolism that occur when leaves become photosynthetically active.

IV. Conclusions

The recently renewed interest in studying the isotope signature of respired CO_2 arises from the non-invasive nature of isotopic measurements of CO_2 . In fact, it allows monitoring metabolic activities in systems which cannot be replicated and destructively sampled, including the entire biosphere (Ciais et al. 1995; Fung et al. 1997; Kaplan et al. 2002) or entire ecosystems (Yakir and Wang 1996; Buchmann et al. 1998; Ogée et al. 2003; Knohl et al. 2005; Tu and Dawson 2005; Bowling et al. 2008; Wehr and Saleska 2015). At the single plant level between-species differences in Δ_R might be related to

the growth rate (Ocheltree and Marshall 2004) and the production of secondary aromatic metabolites (Werner et al. 2007) suggesting other potential applications for *in vivo* diagnosis. A better knowledge of fractionation steps and respiratory metabolism will be instrumental to better understand the origin of the $\delta^{13}\text{C}$ value in respired CO_2 and its physiological significance.

Data accumulated in the past 15 years on the isotope composition of CO_2 respired by plants clearly demonstrate that a respiratory fractionation does occur, but it is strikingly variable. Throughout this chapter, we have provided hypotheses to explain the origin of the isotope composition in respired CO_2 but refinements are to be expected, after having integrated more knowledge on respiratory metabolic fluxes and metabolic compartmentalization within cells. Difficulties have to be anticipated to fully explain the very wide range of isotopic variation that is observed, highlighting the complexity and plasticity of the underlying metabolic network. Particularly striking is the fact that the respiratory fractionation (in autotrophic organs) is more often found to be in favor of ^{13}C , while most decarboxylating enzymes discriminate against ^{13}C , and most metabolites analyzed so far are ^{13}C -depleted as compared to carbohydrates. This simple observation leverages two comments. First, energetic imperatives of respiratory metabolism might require a rather linear organization of catabolism, i.e., with limited metabolic branching, so that enzyme kinetic isotope effects are not expressed *in vivo* to a significant extent. Second, isotopically heavier yet unknown metabolites may exist, or there is a systematic ^{13}C -enrichment in C atom positions that are decarboxylated. In any case, a more thorough investigation of the intramolecular isotopic distribution in different classes of metabolites is needed in order to move one step further in the understanding of respiratory fractionation in plants.

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