Opportunities and limitations related to the application of plant-derived lipid molecular proxies in soil science

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Abstract

The application of lipids in soils as molecular proxies, also often referred to as biomarkers, has dramatically increased in the last decades. Applications range from inferring changes in past vegetation composition, climate and/or human presence to unraveling input and turnover of soil organic matter (SOM). Molecules used include extractable and non-extractable lipids, including ester-bound lipids. In addition, the carbon or hydrogen isotopic composition of such molecules is used. While holding great promise, the application of soil lipids as molecular proxies comes with several constraining factors the most important of which are: i) variability in the molecular composition of plant-derived organic matter plant-internally and in between plant individuals; ii) variability in (relative contribution of) input pathways into the soil; and iii) transformation and/or (selective) degradation of (some of) the molecules once present in the soil. Unfortunately, the information about such constraining factors and their impact on the applicability of molecular proxies is fragmented and scattered. The purpose of this study is to provide a critical review of the current state of knowledge with respect to the applicability of molecular proxies in soil science, specifically focusing on the factors constraining such applicability. Variability in genetic, ontogenetic and environmental factors influence plant *n*-alkane patterns in the way that no unique compounds or specific molecular proxies pointing to e.g. plant-community differences or environmental influences, exist. Other components such as *n*-alcohols, *n*-fatty acids, cutin- and suberin-derived monomers have received far less attention in this respect. Furthermore, there is a high diversity of input pathways offering both opportunities and limitations for the use of molecular proxies at the same time. New modelling approaches might offer a possibility to unravel such mixed input signals. Finally, transformation and turnover of SOM offer opportunities when tracing such processes is the purpose of applying a molecular proxy, whilst posing limitations when they obliterate molecular proxy signals linked to other phenomena. For *n*-alkanes several modelling approaches have recently been developed to compensate for (selective) degradation. Still such techniques are in their infancy and information about their applicability to other classes of components than *n*-alkanes is lacking yet. All constraining factors considered can have a significant influence on the applicability of molecular proxies in soil science. The degree of influence strongly depends on the type of molecular proxy as well as the environmental context in which it is applied. However, the potential impact of the constraining factors should always explicitly be addressed whenever molecular proxies are applied in a soil scientific context. More importantly, there is still a serious lack of available information in particular for compound classes other than the *n*-alkanes. Therefore, we urgently call for the consideration of more holistic approaches determining various factors during sampling as well as using as many compound classes as possible.

1 Introduction

Since more than a century, various compounds deriving from the substance class of lipids, have been investigated in plant and soil science. Some of the earliest publications in plant science date back to the first half of the 19th century (Liebig et al., 1837; Wöhler F. and Liebig, 1839) and in soil science to the early 20th century as already reviewed by Stevenson (1966). One of the main interests to study lipids was the large heterogeneity of compounds included in this substance class. Some of the individual compounds have been described as ‘biomarkers’ or ‘biogenic markers’, i.e. compounds that *“may be diagnostic of specific organisms, classes of organism, or general biota that contribute organic matter to the atmosphere, aqueous or sedimentary environment”* (Peters et al., 2005). In addition,, in environmental sciences also anthropogenic and petroleum markers were highlighted that have the ability to be preserved with “no or only minor change” (Tissot and Welte, 1984; Peters et al., 2005).. Because *sensu strictu* the term biomarker has been used for the differentiation of biological tissues of different origin in environmental matrices, recently the term ’molecular proxy’ has come in vogue. This term allows for an inclusion of biomarkers *sensu strictu* as individual compounds characterizing specific biogenic sources, but also individual compounds acting as specific proxy e.g. for anthropogenic impact or thermal alteration. Furthermore, it accommodates the use of groups of compounds used in the before mentioned way. Finally, it implies the use of molecular ratios of compounds like the carbon preference index (CPI) or the average chain length (ACL) that could also be indicative for biogenic sources, alteration or overprint of organic matter. Therefore, in the present work we use the term molecular proxy rather than biomarker.

In its broadest sense, molecular proxies allow determination of the presence, absence, or certain characteristics of a (set of) molecule(s) that are indicative for a process in, or state or composition of a system of interest. For instance, in the clinical sciences molecular proxies among other applications are used as indicators of the presence of a disease or response to treatment (Brennan et al., 2013; Van Bon et al., 2014); in toxicology to assess the effect of toxicant exposure on biota (Clemente et al., 2014); in the forensic sciences to link suspects to a crime scene (Concheri et al., 2011); in limnology to examine past lacustrine environmental conditions (Castañeda and Schouten, 2011); and in organic geochemistry to follow oil formation and translocation in source and reservoir rocks (Curiale, 2002).

Also in soil science, molecular proxies have been used for decades, and their application has exponentially increased in the last decade as indicated by the number of related articles published in Web of Science indexed journals (Table 1). The types of molecular proxies used are as diverse as the field of soil science itself. They range from the use of phospholipid fatty acids to estimate bacterial and fungal biomass in soils (Frostegard and Bååth, 1996), to the application of preserved retene/caldalene ratios to infer palaeoecological vegetation shifts (Hautevelle et al., 2006). Also the archives of the molecular proxies in soil sciences that are used are diverse and, in addition to soils themselves, include lacustrine and terrestrial sediments, peat deposits, as well as paleosols (Zhang et al., 2006; Bai et al., 2009; Andersson et al., 2011; Berke et al., 2012). However, in spite of this large variety a limited number of scientific topics can be discerned that encompass the great majority of molecular proxy application in the soil sciences. These are:

- Changes in vegetation composition inferred from extractable and/or ester-bound lipids of plant origin, and/or their carbon isotopic composition (e.g. Huang et al., 1996; Zech et al., 2009; Le Milbeau et al., 2013).

- Changes in climate, i.e. mean annual temperature and/or precipitation inferred from bacterial membrane lipids and/or the hydrogen isotopic composition of plant-derived lipids (e.g. Weijers et al., 2006; Krull et al., 2006; Rao et al., 2009).
- Changes in palaeoelevation inferred from bacterial membrane lipids and/or the hydrogen isotopic composition of plant-derived lipids (e.g. Sachse et al., 2006; Bai et al., 2011; Ernst et al., 2013).
- Changes in human impact or settlement inferred from compound-specific N isotope analysis or transformation products of plant-derived lipids, e.g. through burning, or manure derived lipids (e.g. Bull et al., 1999; Eckmeier and Wiesenberg, 2009; Zocatelli et al., 2012).
- Contribution of fossil fuel-derived carbon to soil assessed by lipid molecular composition and compound-specific isotopes (e.g. Lichtfouse et al., 1995; Lichtfouse et al., 1997; Rethemeyer et al., 2004).
- Input, transformation and/or decomposition of soil organic matter inferred from or traced through extractable and/or ester-bound lipids of plant origin and/or bacterial membrane lipids and/or their carbon isotopic composition. (e.g. Nierop et al., 2001; Amelung et al., 2008; Hamer et al., 2012).

In Table 1 an overview is given of the classes of molecules frequently used as molecular proxies in soil archives in relation to their application as well as total and recent (last ten years) publications including the respective keywords.

When using molecular proxies to answer research questions in any of the areas identified, in particular when soils are used as an archive, several constraining factors have to be taken into account that vary with the type of application and research question to be answered. The most important ones are:

i) Variability in the source of plant-derived organic matter, i.e. abundance and composition of the molecular proxies in different plant species, plant specimens and plant parts as a result of genetic or life stage variations and/or external factors such as climate, seasonality or exposure to the sun (e.g. Nødskov Giese, 1975; Lockheart et al., 1998; Shepherd and Griffiths, 2006).

ii) Variability in (relative contribution of) input pathways into the soil, in particular microbial versus vegetation input, and root versus aboveground biomass input (e.g. Jackson et al., 1996; Schefuß et al., 2003; Mambelli et al., 2011).

iii) Transformation and/or (selective) degradation of (some of) the compounds once present in the soil, when it is not the aim of the study to use the molecular proxies to study such transformations (e.g. De Leeuw and Baas, 1986; Nguyen Tu et al., 2004; Andreetta et al., 2013).

However, the information about such constraining factors and their impact on the applicability of molecular proxies is fragmented and scattered over different publications inside and outside the scientific discipline of soil sciences. For instance, much of the available information about variation of leaf wax lipid composition is presented in the plant physiological literature in studies that were not conducted with the application of such lipids as molecular proxy for past vegetation composition from soil archives in mind (e.g. Tulloch, 1973; Avato et al., 1984; Kim et al., 2007). The fragmentation of the information makes it difficult for researchers to assess the potential influence of constraining factors on the application of molecular proxies. It also hinders the identification of hiatuses in the available knowledge about the constraining factors as well as the designation of potential strategies to compensate or correct for such constraints.

Therefore, the purpose of the present study is to provide a critical review of the current state of knowledge with respect to the applicability of molecular proxies in soil science, specifically focusing on the factors constraining such applicability. Based on this we will identify areas for future research both with respect to the application of molecular proxies in soil science as well as the constraints thereof.

The vastness of the field of molecular proxies forced us to restrict the scope of the present study. With respect to the molecules to consider, a first restriction was to focus on those related to the earlier mentioned main areas of application of molecular proxies in soil science. A second restriction was to focus on the main classes of components as used by several researchers. Finally, in spite of their common application, we explicitly excluded lignin and phospholipid fatty acids (PLFA) as lignin was subject of another recent review article (Thevenot et al., 2010) and PLFAs are considered in such a large set of studies (c.f. Table 1) that they would require a separate review. Finally GDGTs were excluded because their application is predominantly in aquatic sediments rather than soils and they have been recently reviewed (Schouten et al., 2013). This leaves the component classes labeled in bold in Table 1 to be considered in the present study. Our study is relevant to the application of compound-specific isotope analysis inasmuch that such analysis is directly affected by variability and transformation of the underlying molecules. However, we did not explicitly consider sources and effects of variation of the stable $\delta^{13}C$ and $\delta^{2}H$ isotope signature of specific molecules themselves, this being a research area of its own and also subject of other recent reviews by Sachse et al. (2012) and Diefendorf and Freimuth (2017). Furthermore, when considering application and preservation of molecular proxies we restricted ourselves to topsoils (i.e. surface soil horizons = A horizons as defined by the FAO in the Guidelines for soil description (2006)) as archives.

2 Source related variability of molecular proxies

2.1 Definition

Source related variability of molecular proxies pertains to intra-species variation in the abundance of the molecules that are used as proxy. Such variability entails: i) variation in relative abundance of individual compounds that together constitute the proxy, e.g. of *n*-alkanes of different chain length in leaf waxes of a certain species; ii) variation in absolute abundance of the molecules used as proxy either between different specimens or between different parts of a single specimen. Depending on the research question, intra-species variability of molecular proxies may be desirable or not. For instance when preserved leaf wax lipids patterns are used to reconstruct past vegetation composition, the implicit assumption is that the intra-species variability in the source vegetation is small compared to the inter-species variability.

There are two main causes of intra-species variability in molecular proxies: internal variation related to genetics and/or ontogeny; and external variation related to the growing environment. Both are related in the sense that differences in response to environmental factors are also often genetically determined (Shepherd and Griffiths, 2006). Here we discuss both causes separately with a third paragraph devoted to studies where combined effects were examined. For a detailed description of the biomolecular mechanisms of wax genesis and all potential sources of change, the reader is referred to the review provided by Shepherd and Griffiths (2006).

2.2 Variation related to genetics and/or ontogeny

2.2.1 Wax lipids

Many studies have indicated that the clear genetic control of leaf wax genesis leads to a significant and meaningful difference in their composition (Shepherd et al., 1995; Shepherd and Griffiths, 2006). For instance, prompted by the early works in this area (e.g. Eglinton et al., 1962; Herbin and Robins, 1968; Herbin and Robins, 1969), Maffei performed an extensive evaluation of the *n*-alkane patterns in several hundreds of plant species belonging to the Poaceae, Apiaceae, Brassicaceae, Fabaceae, Cactaceae, Pinaceae, Lamiaceae, Boraginaceae, Verbenaceae, Solanaceae and Scrophulariaceae (Maffei, 1994; Maffei, 1996a; Maffei, 1996b; Maffei et al., 1997; Maffei et al., 2004). These studies were replenished by those on Styracaceae (Li et al., 2013), Moraceae (Sonibare et al., 2005), and Clusiaceae (Medina et al., 2004; Medina et al., 2006). Further, Dove et al. (1996) described the alkane diversity among a grassland plant community, which enables tracing of the diet of grazing animals due to the different alkane compositions of the plants. Recently, Mueller-Niggemann and Schwark (2015) were able to differentiate rice from alternating crop plants based on their *n*-alkane patterns. The results support the chemotaxonomic discriminatory power of *n*-alkane patterns at family, sub-family and tribal level, which has been further examined by Diefendorf et al. (2017). Examining plant *n*-alkane and *n*-alcohol distribution of 37 C_4 grasses, Rommerskirchen et al. (2006) also found chemotaxonomic differentiation was possible at the sub-family level. Mongrand et al. (2001) examined the fatty acid composition of the leaves of over 137 species of gymnosperms belonging to 14 families and collected from different locations in France. They found a taxonomically meaningful clustering into four main groups, with the highest discriminatory power in the Pinaceae at the genus level (Mongrand et al., 2001). Additionally, Wiesenberg and Schwark (2006) determined differences in the fatty acid composition between temperate C_3- and C_4-crops. Within the same *Brassica* species of kale and swede Shepherd et al. (1995) observed a difference in chain length distribution of wax lipids between two genotypes of the same species, indicative of genetic control through variation in the enzyme system. Also for the isoprenoids, a genetically driven discriminatory power related to (groups of) plant species is attributed (Ohsaki et al., 1999; Jansen et al., 2007).

The chemotaxonomic potential of wax lipids as just described has been exploited to reconstruct past vegetation history from wax lipids preserved in soil archives (e.g. Bull et al., 1999; Zech et al., 2009; Jansen et al., 2013). Such reconstructions often focus on the use of shifts in ratios of certain dominant higher chain length *n*-alkanes, fatty acids and *n*-alcohols representative of a shift in dominant vegetation over time (Jansen et al., 2010; Gocke et al., 2016; Wiesenberg et al., 2015). In few instances also the entire suite of higher chain length *n*-alkanes and *n*-alcohols (Jansen et al., 2013) or *n*-alkanes and fatty acids have been used (Wiesenberg et al., 2015).

However, in addition to other issues such as discussed in the other sections of this review paper, an important issue when exploiting the chemotaxonomic potential of leaf wax lipids is the phenotypic plasticity of the genetic variability in leaf wax lipid patterns found and the implications thereof for the stability of the patterns observed. Maffei et al. (2004) concluded that phenotypic plasticity may overcome genetic variability, particularly when plant developmental stages are considered along with abiotic and biotic stress conditions. Several plant physiological studies have focussed on wax lipid composition related to plant life stage, and report different results. Avato et al. (1984) found that where the relative contribution of *n*-fatty acids, *n*-alcohols and *n*-alkanes differed between *Sorghum* seedlings and mature leaves, the chain-length distribution within a component class remained the same for the *n*-alkanes and *n*-alcohols. Giese (1975) observed a difference in homologue dominance of *n*-alkanes between leaves of seedlings and mature barley plants. Also Herbin and Robins (1969), Dyson and Herbin (1970), Baker and Hunt (1981), and Zhang et al. (2004) identified increasing chain length dominance of leaf wax alkanes with increasing leaf age. However, averaging of sampling over leaves of different age, position etc. within a stand of trees did allow for distinction from other stands, indicating that inter-species variation was larger than intra-species variation (Dyson and Herbin, 1970). Baker and Hunt (1981) observed differences between adaxial and abaxial parts of leaves for some of the plant species. Also Tulloch (1973) observed a variation of leaf waxes of several *Triticum* species with age. In particular the whole plant *n*-alkane predominance shifted from C_{31} at 24 days after germination to C_{29} at 100 days after germination (Tulloch, 1973). Furthermore, Wiesenberg et al. (2004; 2012) and Wiesenberg and Schwark (2006) observed changes in *n*-alkane and *n*-fatty acid compositions of a variety of temperate crop species with plant age. Other publications reported seasonal variations in the *n*-alkane composition for variety of pasture and crop plants by Dove et al. (1996), Hellgren and Sandelius (2001), Moseley (1983), Shelvey and Koziol (1986) and various trees especially by Gülz and collaborators (Prasad and Gülz, 1990; Gülz et al., 1991; Gülz and Muller, 1992; Gülz and Boor, 1992). Variations in the alkane composition could be observed during the growing season among all investigated plants, but general trends of increasing or decreasing chain length and *n*-alkane contents have not consistently been determined. The *n*-alcohol predominance also varied but to a much smaller extent, not affecting the predominance of a specific *n*-alcohol (Tulloch, 1973). Esters gradually showed an increase in esters of trans 2,3-unsaturated C_{23} and C_{24} acids with plant age (Tulloch, 1973). The variation was related to the development of the plant, in particular that of flag leafs and sheets between 55 and 66 days (Tulloch, 1973).

In contrast to the previous, Li et al. (1997) studied the influence of ontogeny on leaf wax lipids (*n*-alkanes, *n*-aldehydes, *n*-alcohols, esters, β-diketones, flavonoids and triterpenoids) in several *Eucalyptus* species of the subgenus *Symphyomyrtus* on Tasmania, and found no significant effect of ontogeny on leaf wax composition, which they found to clearly and consistently differ between species (Li et al., 1997). Also Eglinton et al. (1962) observed that the *n*-alkane composition of leaf waxes of 74 species of Crassulaceae from the Canary Islands showed no appreciable variation with respect to leaf position, age, size or specimen. Further, Bush and McInerney (2013) found no influence of canopy position or sampling time on the *n*-alkane patterns of mature leaves from 24 tree species.

2.2.2 Cutin and suberin monomers

Cutin and suberin monomers are mainly used as proxies to distinguish leaf from root input in soils (Schreiber et al., 1999; Bull et al., 2000; Mendez-Millan et al., 2011) or as proxy for related phenomena such as the degree of bioturbation in the topsoil (Nierop and Verstraten, 2004). Therefore, the possible (onto)genetic effects on cutin and suberin composition are a concern if they were to alter the composition of the polyesters to such an extent that the separation between cutin and suberin is compromised.

Some general observations in literature are that long-chain even numbered C_{20}-C_{30} ω-hydroxy fatty acids and α,ω-alkanedioic acids mainly originate from suberin, whereas shorter chained C_{16} and C_{18} ω-hydroxy fatty acids mainly derive from cutin (Schreiber et al., 1999; Otto et al., 2005; Mendez-Millan et al., 2011). However, several publications challenge the universal applicability of such general observations, indicating instead that genetic variability results in many exceptions to such general rules. For instance, Hamer et al. (2012) found that $\omega C_{22:0}$, $\omega C_{24:0}$ and $\omega C_{26:0}$ hydroxy fatty acids were not exclusively associated to roots, but also occurred in the shoots of several species. In addition, $\omega C_{16:0}$ and $\omega C_{18:0}$ fatty acids were not exclusive to the leaves, but also occurred in the roots of several species.

2.3 Variation related to environmental factors

2.3.1 Effects of temperature

Increased solar radiation levels are generally reported to lead to higher absolute amounts of waxes produced (Sanchez et al., 2001; Shepherd and Griffiths, 2006). In addition, the composition of the various component classes of wax lipids, i.e. the relative contribution of *n*-fatty acids, *n*-alkanes, *n*-alcohols etc., has been reported to change. A shift towards lower chain lengths within different component classes was sometimes found (Shepherd and Griffiths, 2006). Thus, a positive correlation of long-chain odd *n*-alkanes with temperature was observed (Maffei et al., 1993; Zhang et al., 2004). Also, the abundance of membrane fatty acids with 16 and 18 carbons can change as a result of temperature (Maffei et al., 1993; Williams et al., 1995; Matteucci et al., 2011). Often, under heat stress the relative abundance of $C_{16:0}$ fatty acid was found to increase and vice versa the abundance of polyunsaturated $C_{18:3}$ fatty acid to decrease (Larkindale and Huang, 2004; Bakht et al., 2006). Furthermore, effects of temperature were observed for mono- and sesquiterpenes, with compounds like limonene and myrcene having a close correlation with temperature, whereas others like 1,8-cineol were not affected by temperature (Maffei et al., 1993). As a cause, a different sensitivity of individual steps in the genesis of the wax lipid components is assumed (Shepherd and Griffiths, 2006). However, results were found to vary between different species and genotypes, indicating a species or genotype related sensitivity to changes in irradiation (Shepherd and Griffiths, 2006), whereas cold- or heat-acclimated plants respond differently than those that are not acclimated (Larkindale and Huang, 2004). Thus, a dependency of temperature and lipid metabolism is widely observed, but especially in plants other factors such as humidity or greenhouse gas composition might coincide with a larger effect on the overall lipid composition.

In addition to the effect of temperature on lipid synthesis, temperature can also influence lipids after production specifically as a result of fire. This topic is addressed in section 4.2.

2.3.2 Effects of humidity

With respect to the effects of water stress and/or high humidity, in their review Shepherd and Griffith (2006) reported mixed results, with respect to absolute amounts as well as chain length distribution. Bondada et al. (1996) reported an increase in absolute amounts of epicuticular wax production by 69% in the leaves of cotton (*Gossypium hirsutum*) under water stress, which was confirmed by Hamrouni et al. (2001), Koch et al. (2006), Kim et al.

(2007), and Bettaieb et al. (2010) for neutral lipids of other plant species. However, Kim et al. (2007) found that water stress had only a minor effects on chain length distribution. The relative contribution of different component classes to the wax composition remained unchanged except for *Brassica oleracea* var. *gongylodes* at the highest relative humidity, which showed an increased contribution of ketones and primary alcohols and a reduction of secondary alcohols and aldehydes (Koch et al., 2006). Recently, Srivastava et al. (2017) determined that sustainable effects of drought on plant lipid composition are commonly missing with few exceptions for perennial plants. Thus, several months after exposure to drought the lipid biosynthesis and composition of leaves is resilient. The existing data shows that general effects of drought on plant lipid composition are difficult to draw.

2.3.3 Effects of increased CO_2

Changes in greenhouse gases such as CO_2 have also been discussed to influence the lipid biosynthesis and thus the lipid composition of plants. Short-term exposure of several hours to elevated CO_2 concentrations e.g. during $^{13}CO_2$ or $^{14}CO_2$ labelling experiments has no or little effect on the lipid composition, especially if sampling occurs several days after labelling (Wiesenberg et al., 2009). In contrast a long-term rise in atmospheric CO_2 concentration has been investigated in laboratory or free air carbon dioxide enrichment (FACE) experiments (Ainsworth and Long, 2005). Although numerous such experiments have been maintained in the meantime, implication of investigations of lipid composition is limited. Greenhouse experiments showed that elevated CO_2 concentration affects the relative composition of saturated and unsaturated fatty acids in wheat plants (Williams et al., 1994; Williams et al., 1995; Williams et al., 1998). However, rising nitrogen fertilization and rising temperature can lead to competing trends so that with elevated temperature and nitrogen fertilization (Williams et al., 1995; Griepentrog et al., 2016). Although specific abundances of individual long-chain alkanes and alcohols changed under elevated CO_2 concentration, the overall lipid composition expressed as ACL and CPI did not change (Huang et al., 1999). Nevertheless, concentration changes like an increase in *n*-alkane and *n*-alcohol abundances and a decrease in *n*-fatty acid abundance was determined under rising CO_2 concentration, whereas nitrogen fertilization led to a decrease in the effect (Huang et al., 1999), which was confirmed by Wiesenberg et al. (2008a) for *n*-alkanes, *n*-fatty acids and *n*-alcohols. In some forest FACE and open top chamber experiments, the effect of elevated CO_2 on plant lipid concentration were not identified (Feng et al., 2010; Griepentrog et al., 2015), but the $^{13}CO_2$ labelling associated with the CO_2 enrichment was used for tracing turnover of lipids in soils as introduced by Wiesenberg et al. (2008b) for lipids.

2.4 Other or combined genetic, ontogenetic and/or environmental effects

Many studies considered the effects of e.g. geographical location on wax amounts and/or composition without differentiating between individual genetic or environmental causes. Again the exact parameters investigated vary greatly between studies, as do the conclusions drawn. Cowlishaw et al. (1983) examined the *n*-alkane, *n*-alcohol, *n*-aldehydes and ester composition of composite samples of four species of the Poaceae *Chionochloa*, one of which was sampled at three different environmental locations to investigate environmental effects. They found distinct chain length patterns that allowed for chemotaxonomic identification, where variation between the three sampling sites did not alter dominant chain length patterns for any of the component classes (Cowlishaw et al., 1983). Similar observations were made by Herbin and Sharma (1969) for ω-hydroxy fatty acid composition of *Pinus* species from Asia, Europe, North-America, Central America and the Caribbean. Kreyling et al. (2012) described differences in the *n*-fatty acid and *n*-alkane composition of the same plant species originating from different regions across Europe with different climatic conditions most likely due to biosynthetic adaptation to the specific conditions. Piervittori et al. (1996) found that the distribution of C_{25}, C_{27}, C_{29} and C_{31} *n*-alkanes in the lichen *Xanthoria parietina* varied significantly between two different Piedmont valleys in Italy, and within those with altitude, reflecting a combined influence of elevation, water availability, radiation and temperature. For plaggen ecosystems Kirkels et al. (2013) also observed a significant variability in reported ratios of the dominant *n*-alkanes with chain lengths C_{27}, C_{29}, C_{31}, C_{33} most likely attributable to the causes examined here. However, in spite of this they found meaningful clustering of the three different plant groups grasses, shrubs and trees indicating that the variability did not obliterate the power of distinction (Kirkels et al., 2013). In a larger study based on 2093 observations from 86 sources of plant material, Bush and McInerney (2013) concluded that the general observation that C_{27} and C_{29} *n*-alkanes are dominant markers for woody vegetation and C_{31} for graminoids does not rigorously hold true. At the same time C_{23} and C_{25} *n*-alkanes do seem to be robust indicators of *Sphagnum* (Bush and McInerney, 2013) as already observed by Baas et al. (2000) and Pancost et al. (2002). Bush and McInery (2013) indicated that the lack of rigour of the mentioned proxies is likely caused by environmental conditions as indicated by a shift in patterns across African savannah and rainforest environments.

The distinction between African savannah and rainforest environments in general and C_3 versus C_4 vegetation in particular have been the subject of more detailed research. Vogts et al. (2009) studied the leaves and sometimes whole plants of 24 African rain forest and 45 savannah species. They found that as a result of environmental influence, including temperature and aridity, chain length distributions of the *n*-alkanes and *n*-alcohols of some species shifted to different chain length predominance. The environmental influences overshadowed a taxonomic distinction at the order, family or sub-family level (Vogts et al., 2009). Patterns in grasses were more consistent and thus less dependent on environmental factors (Vogts et al., 2009). As a result, in spite of the environmental variability observed, Vogts et al. (2009) found that by averaging lipid patterns within a given environment a clear distinction between rain forest and savannah plants can be made, with a dominance of C_{29} *n*-alkane representative of the average rain forest plant signal and a dominance of C_{31} *n*-alkane of the savannah plants and C_4 savannah grasses. For the *n*-alcohols, C_{28} dominated on average for savannah plants, C_{30} for rain forest plants and C_{32} for C_4 savannah grasses (Vogts et al., 2009).

Rommerskirchen et al. (2006) observed a generally higher content of C_{31} and C_{33} *n*-alkanes and therefore higher ACL value in African C_4 grasses with respect to C_3 grasses from the same area as a result of the genetic adaptation of C_4 grasses to warm, arid habitats. In addition, *n*-fatty acid patterns have also been shown to vary with C_3 and C_4 metabolism, with C_3 crops having relatively large proportions of C_{24} *n*-fatty acid in leaves, stem and roots as compared to C_{22} and C_{26} *n*-fatty acids in C_4 crops (Wiesenberg and Schwark, 2006).

2.5 Conclusions and implications regarding source related variability

Already Herbin and Robins (1969) concluded that there is a basic genetic control on the composition of the wax components, including the alkanes, of plant leaves. However, variable factors associated with age and environment can be superimposed upon the specific pattern in some cases, while in others the genetically controlled pattern appears to be stable and unaffected by external influences (Herbin and Robins, 1969). Now, 48 years later, a much more extensive database has been accrued, albeit with a large emphasis on leaf wax lipids in general and *n*-alkanes in particular. Nevertheless, the results are still equivocal. On the one hand, there is ample evidence that genetically driven variability of leaf wax lipid composition in principle leads to chemotaxonomically meaningful clustering that can form the basis of the application of leaf wax lipids as molecular proxies. On the other hand, it is clear that both ontogeny and environmental factors can have a significant and sometimes dominant influence on lipid composition like e.g. chain length distribution. Matters are complicated by the fact that much data with respect to the effects of environmental stress originates from studies where plants were studied for a limited period of time (typically one growing season), where extreme conditions were artificially imposed. In contrast, the lipid signal from soil or sediment archives as used in reconstructions typically represents a mixture of input of decades or longer from plants in various life stages of perennial plants, the induced diversity of plants by frequent changes of annual plants in managed ecosystems and the average of natural fluctuations in stress conditions during that time period.

In general from what is known to date, the conclusion seems justified that on the one hand because of genetic and environmental influences there are no unique compounds nor ‘golden ratios’ of different chain lengths of compounds that can always be linked to certain plants under all circumstances. On the other hand, there are many situations where the influence of genetic and environmental effects are small enough that they do not prevent the use of plant lipids as molecular proxies. The currently available data does not allow for objective, quantitative rules to be formulated in this respect. From the plant wax components, the *n*-alkanes are the dominant class studied. In addition, research attention has focussed to a lesser extent on *n*-alcohols and *n*-fatty acids. The other wax components such as isoprenoids and ester bound lipids received hardly any research attention to date with respect to source related variability in the context of their use as molecular proxies. Yet even for the *n*-alkane patterns in leaf waxes, only a tiny portion of dominant plant species on the planet have been examined in detail for the effects of genetics and environment on their amounts and patterns. It is clear that much more research is needed in this respect.

Based on the current insights it seems prudent to explicitly take the possibility of genetically and environmentally driven variability of lipid patterns into account when considering the use of lipids as molecular proxies. For instance by considering plant species from the same climatic zone as where the reconstruction takes place, and by mixing plant material from different life stages to obtain the average molecular fingerprint to look for.

3 Input pathway related variability of molecular proxies

3.1 Definition

Here we discuss differences in the amount and composition of molecules used as proxies, which is possible due to different input pathways of such molecules to the soil. A schematic representation of the different input routes of molecular proxies into the soil is provided in Fig. 1. The emphasis lies on potential effects for their use as molecular proxies. For a general description of the different molecular origins of organic matter in soil, the reader is referred to a dedicated review on this topic by Kögel-Knabner (2002).

3.2 Leaf versus root input

Conservative estimates calculate roots to represent 33% of global annual net primary productivity (Jackson et al., 1997), whereas more recent studies highlight that the contribution of root-derived organic matter in soils can account for >70% of total plant-derived carbon (Rasse et al., 2005). As a result, roots form a considerable input of organic matter in soils and are proposed to improve carbon storage in soils (Kell, 2012). In addition, root input occurs to considerable depth in soils, ranging from an average depth of 0.5 m in tundra biomes to 15.0 m in tropical grassland/savannah (Canadell et al., 1996). But also in the temperate zone under certain circumstances such as the presence of nutrient rich fossil A horizons at depth, deep rooting can be very significant (Gocke et al., 2015). However, on average the majority of root biomass appears to be incorporated in the top 0.3 m of the soil in most biomes, i.e. in the topsoil (Jackson et al., 1996). The ratio of root/shoot biomass input is also very variable across biomes, ranging from an average of 0.10 in cropland to 4.5 in deserts (Jackson et al., 1996). Table 2 represents an overview of the average maximum rooting depth, root biomass input in the first 0.3 m of the soil and root/shoot biomass input for different biomes (see also Fig. 1).

Therefore, if the molecules to be used as proxy are present in both leaves and roots of plants, the possibility of root input is a factor that has to be considered depending also on the purpose of the proxy. In the case of cutin and suberin monomers root input does not cause interference as discerning root from leaf input is the specific purpose of this molecular proxy (Mendez-Millan et al., 2011). However, this may be different for the wax lipids, i.e. *n*-alkanes, *n*-alcohols, *n*-fatty acids and isoprenoids, that have been found to occur in leaves as well as roots of species at varying concentrations (Jansen et al., 2007; Huang et al., 2011).

Particularly when such wax derived lipids are applied as molecular proxies for vegetation cover in soil, root input can be an issue for two reasons: i) roots may contain a different wax lipid composition than leaves qualitatively and quantitatively, thereby clouding the leaf signal (Jansen et al., 2006; Martelanc et al., 2007); ii) young root input at depth may disrupt the chronology of a reconstruction in time by overprinting the originally present signal (Lavrieux et al., 2012; Gocke et al., 2014).

The main discussion with respect to the influence of root input in wax lipid based environmental reconstructions from soils therefore revolves around assessing the relative importance of root versus aboveground biomass input. Since plant wax lipids reside on the outer parts of leaves and roots, relative surface area and bioproductivity are important. On a global scale root surface area is almost always calculated to be higher than leaf surface area, more than an order of magnitude so in grasslands (Jackson et al., 1997). However, in many cases the absolute amount of lipids present per mass unit of root material is an order of magnitude or more lower than on leaf material (Marseille et al., 1999; Zech et al., 2011). In addition, also with respect to the degree in which wax lipid chain length patterns vary between the leaves and roots of plant species, there appears to be quite some variability. In general, the observed differences between roots and leaves of the same species are reported to be of the same order of magnitude as the differences between leaves of different species (e.g. Jansen et al., 2006; Kirkels et al., 2013; Gocke et al., 2014).

The concurrent influence of such various quantitative and qualitative factors makes the impact of root input a complex issue that still is subject of scientific debate (Wiesenberg and Gocke, 2013). Given that different factors will have a highly variable influence in different situations, no general conclusion can be drawn. In some situations, the influence of roots as input pathway of extractable lipids to be used as molecular proxy may be limited (Quenea et al., 2006). In others, root input may be dominant (Van Mourik and Jansen, 2013). In addition, the relative degree of influence may vary greatly with depth leading to the concurrent presence of leaf lipid dominated and root lipid dominated zones at different depths in the same profile (Angst et al., 2016).

3.3 Microbial input

In general, microbial biomass can be a significant source of soil organic matter, with up to 40% transformed to non-living soil organic matter, but is turned over much faster than plant residues (Miltner et al., 2012). Focussing specifically on lipids, isotopic studies show that

90% of fatty acids of microbial origin are turned over rapidly after cell death, whereas the majority of biomass derived residual bulk C was stabilized in the non-living soil organic matter pool (Kindler et al., 2009). In spite of the potentially shorter residence time, a concurrent faster production makes that microorganism derived molecules are a factor to consider when applying molecular proxies in soils except when such proxies are used to study microbial input.

For wax lipids generally *n*-alkanes, *n*-alcohols and *n*-fatty acids with longer chain lengths ($>C_{20}$) and a distinct odd-over-even (*n*-alkanes) or even-over-odd (*n*-alcohols and *n*-fatty acids) chain length predominance are considered to be higher plant derived, whereas shorter chain length homologues are considered to be predominantly of microbial origin (Eglinton et al., 1962; Dinel et al., 1990). Moreover, with the exception of an abundance of C_{16} and C_{18} *n*-alcohol and *n*-fatty acid, such microbial lipids are described to lack a specific chain length predominance (Stevenson, 1994; Lichtfouse et al., 1995). However, several researchers challenge the observation that higher chain length lipids in soils are exclusively of higher plant origin. Microorganisms have been shown capable of synthesizing higher chain length straight-chain lipids, albeit usually to a limited extent (Ladygina et al., 2006; Nguyen Tu et al., 2011). Jambu et al. (1978) indicated that while chain lengths $>C_{20}$ in soils are predominantly plant derived, particularly in acidic soils fungi may contribute such lipids as well. Furthermore, Marseille et al. (1999) observed an abundance of C_{25} and C_{27} *n*-alkanes that they also attribute to *in-situ* production by fungi. This was confirmed for an agricultural soil by Quenea et al. (2006), who observed old forest and fungi derived odd long-chain alkanes based on compound-specific isotope analysis and lipid distribution patterns. Possible pathways of *in-situ* genesis of *n*-alkanes in soils are reduction of *n*-alkenes and *n*-alcohols, decarboxylation of bacterial *n*-fatty acids as well as degradation of biopolymers containing aliphatic side chains (Lichtfouse et al., 1998). Nevertheless, based on the large number of studies where typical higher plant derived patterns of lipids are reported and used in soils (Table 1), including indicative ACL and CPI values, microbial input of longer chain length straight-chain lipids generally does not seem to be a major factor compared to direct plant derived input in the topsoil (Jansen and Nierop, 2009; Bai et al., 2009). In contrast, for steroids and triterpenoids such as camposterol, stigmasterol and lupeol, microbial input in soils can be considerable (Naafs et al., 2004). As another example, arbuscular mycorrhizal fungi derived β-sitosterol is by far the most abundant sterol identified in soils (Grandmougin-Ferjani et al., 1999).

With respect to cutin and suberin monomers, *in-situ* genesis in soils through microbial transformation of other precursor molecules can be an issue. For instance, oxidation of free fatty acids could be a source of *ω*-hydroxy fatty acids, whereas microbial β-oxidation of unsaturated fatty acids and/or mid-chain hydroxy fatty acids may be a source of *α,ω*-alkanedioic acids, thus clouding the cutin/suberin signal (Naafs et al., 2004)

3.4 Airborne input

In addition to *in-situ* production and incorporation of soil lipids, airborne input must be considered. The distance of airborne transport of larger constituents such as leaves can be expected to be limited. However, smaller physical forms containing lipids, such as aerosols and dust particles, can travel substantial distances (Conte and Weber, 2002) thus causing input of alien molecules that may influence the local signal. This is of special importance where airborne sediments with low content of organic matter are investigated as in these environments already low inputs of foreign organic matter can significantly influence the molecular proxies. Liu et al. (2007) showed that the $\delta^{13}C$ signature of sediment organic carbon in loess deposits of the western Chinese Loess Plateau corresponds to that of dust sources instead of the local vegetation. While in a study of marine sediment cores along the Southwest African continental margin, Rommerskirchen et al. (2003) revealed that aerosol derived input of higher chain-length *n*-alkanes and *n*-alcohols provides a significant signal, the $\delta^{13}C$ signal of which corresponded well with continental C3/C4 plant distribution and fossil pollen input when prevailing wind patterns were taken into account. However, in this case, in contrast to vegetated soils, there was no *in-situ* input from higher plant vegetation.

Aerosol studies above plant canopies revealed a certain relationship of the plant wax composition of the present plants, but significant differences from the biomass were observed for *n*-alkanols and *n*-alkanes (Conte et al., 2003). While the wax molecular composition was not directly linked between biomass and aerosol, especially the compound-specific isotope composition ($\delta^{13}C$) revealed a closer link of both. For Bermuda aerosols it could be shown that the aerosol compound-specific isotope composition of *n*-alcohols and *n*-acids reflects the plant wax compound-specific isotope composition as well as the course of the bioproductivity during the different seasons of the years (Conte and Weber, 2002).

In a study of PM_{10} aerosols collected during a winter season in Baoij, China, Xie et al. (2009) found concentrations of C_{21}-C_{33} *n*-alkanes in the 10-600 ng/m^3 range as a result of intensive coal burning in the region. In a two year study of PM_{10} and $PM_{2.5}$ aerosols in urban sites in

Nanjing, Wang et al. (2006) observed C_{21}-C_{33} *n*-alkanes present in the 10-100 ng/m^3 range. Concentrations of C_{21}-C_{35} *n*-alkanes in PM_{10} aerosols in urban sites in Beijing sampled in all seasons were even lower (Zhou et al., 2009). In this study also *n*-fatty acids and hopanes were considered, but were found in small concentrations that, together with the *n*-alkanes, constituted ca. 3% of the total organic matter in the aerosols (Zhou et al., 2009). In all studies, the straight chain lipid patterns lacked the odd-over-even chain length predominance typical of higher plants (Wang et al., 2006; Xie et al., 2009; Zhou et al., 2009). Nevertheless, in a large survey a clear odd-over-even chain length predominance was found in spite of such potentially intense aerosol derived input (Rao et al., 2011). This indicates that even in areas under large aerosol deposition, as in the case of intensive anthropogenic pollution associated with fossil fuel burning, the effect of aerosol deposition on *n*-alkane patterns in the soil is limited as a result of the large *in-situ* input via roots and leaves of the local vegetation.

3.5 Conclusions and implications regarding input pathway related variability

The diversity of input pathways offers both opportunities and limitations for the use of molecular proxies. Opportunities arise when different sources can be elucidated using molecular proxies. Examples are the differences in molecular composition of leaf and root waxes as used to differentiate between their respective influences, or when aerosol associated lipids are used for source apportionment of terrestrial plant input in terrestrial or marine sediments. This can help budgeting organic matter input of different sources and thus improve (paleo-)environmental interpretations and reconstructions. Limitations are posed when input through multiple pathways clouds the linkage of a (set of) molecule(s) to a certain source for which it is to serve as proxy. For instance when linking a suite of straight-chain lipids to a particular group of plants at a certain site. When looking at the application of molecular proxies in soils, in particular the assessment of the influence of root derived input is a challenge that is not always acknowledged. The significance of root derived organic matter in soils and terrestrial sediments has been neglected for decades and has only been recently highlighted (Rasse et al., 2005; Rumpel and Kögel-Knabner, 2011). More research attention is needed to pinpoint how large possible interferences are and how the potential can be to compensate for them, e.g. through modelling approaches. For instance, the VERHIB model was designed to unravel the mixed *n*-alkane, *n*-alcohol and/or *n*-fatty acid signal observed in soils into the most likely combination of plant groups responsible for the original lipid input, treating leaves and roots explicitly as separate entities (Jansen et al., 2010). This might form a starting point to disentangle leave and root derived lipid input.

Although the aerosol studies so far provide useful information that plant wax components are transported via aerosols to remote places, other factors like degradation during transport and integration of regional vegetation patterns may hamper direct source-to-sink relationship of airborne molecular markers. Nevertheless the overall impact of aerosol borne molecules on molecular proxy based reconstructions seems to be limited whenever the total abundance in the soil is high.

4 Transformations and turnover in soil

Transformations and turnover of soil organic matter are an important study area in their own right (Kögel-Knabner, 2002; Von Lützow et al., 2008). Important in the context of the application of molecular proxies is the recent paradigm shift to the attribution of external factors as drivers of soil organic matter turnover rates as opposed to inherent recalcitrance related to molecular structure (Schmidt et al., 2011; Lehmann and Kleber, 2015). Coupled to this are indications that microbial recycling of organic matter upon entering the soil decouples the molecules from their biological sources (Miltner et al., 2012; Gleixner, 2013). Here, we focus on the effects of (differences in) transformations/degradation of molecules in soils for their use as molecular proxies. This includes transformations during the stages of senescence or litter and covers attempts to estimate successive degradation processes of organic matter occurring after burial until stages of long-term preservation (see also Fig. 1). Transformation processes can also include processes that affect the detectability of a molecule used as proxy, for instance a transformation from the extractable to the non-extractable lipid fraction as a result of chemical alterations or interactions with the mineral phase (e.g. Almendros et al., 2001). A special case is the influence of fire on SOM, including molecular proxies, as reviewed by González-Pérez et al. (2004).

All of the attempts dealing with incorporation and preservation of organic matter deal with different assumptions and entail different problems in terms of uncertainties. Thus, in dependency of the environmental conditions, assumptions that are relevant for incorporation and burial of organic matter play a major role, as should the different aspects of degradation and preservation. However, currently much uncertainty exists regarding the influences of individual environmental and genetic factors concerning degradation and preservation.

Therefore, the following paragraphs only provide the first insights tackling these issues, which need further attention in future research projects.

Molecular transformations and variations thereof of molecular proxies mostly offer complicate application of molecular proxies. However, in some instances they may also offer opportunities. For instance, *n*-alkanes can be degraded to *n*-methyl ketones through β-oxidation (Chaffee et al., 1986; Amblès et al., 1993), which can be used to assess and trace *n*-alkane degradation in soils (Jansen and Nierop, 2009). Similarly, the presence of certain *seco*-acids formed through A-ring opening of 3-oxytriterpenoids under anaerobic conditions, may be used as proxy for the occurrence of such anaerobic episodes (Jaffe et al., 1996), e.g. under stagnant water conditions.

4.1 Differences related to incorporation pathway

The incorporation pathway (Fig. 1) may influence subsequent turnover of molecular proxies. This includes (differences in) degradation during senescence and/or litter degradation stages, e.g. due to different input shapes (like root vs. leaf) offer a different degree of physical protection. It also includes alterations induced by fire prior to or upon incorporation of organic matter into the soil.

In a study of *Gingko biloba* leaf wax lipids during the senescence and litter stages, Nguyen Tu et al. (2003) found limited degradation that did not affect the dominant chain lengths of alkyl molecular proxies. When comparing different classes of wax lipids they found the *n*-alkanes to be the most resistant to degradation, followed by the *n*-fatty acids and then the *n*-alcohols (Nguyen Tu et al., 2003). Also, more in general, in a study of grassland and forest soils, Otto and Simpson (2005) determined that characteristic patterns of wax lipids and isoprenoids were preserved throughout the stages between fresh plant material and soil organic matter. They also determined preferential enrichment of suberin with respect to cutin monomers in particular in one of the grassland soils (Simpson et al., 2008). This indicated for example the fact that the former is embedded in woody tissue while the latter is exposed on leaf surfaces (Simpson et al., 2008) (see also 4.3.3).

When looking at bulk organic matter in soils, Rasse et al. (2005) estimated that the main residence time of root derived organic matter is on average 2.4 times that of shoot derived organic matter. When comparing cutin and suberin monomers, Andreetta et al. (2013) described selective preservation of leaf derived monomers in the more acidic and dryer soil, while in the more fertile soil root derived monomers were preferentially preserved. They attributed the former to inhibited microbial degradation due to drought and acidity, and the latter to protection within aggregates. In another study still small differences in degradation of the same *n*-alkanes that derived from different plants were found, with a slower degradation of *n*-alkanes derived from more woody roots (Nierop and Jansen, 2009), although lipids were generally well preserved. Killops and Frewin (1994) reported that persistency of plant cuticles protected their composite isoprenoids from degradation in mangrove sediments. Similar preservation in soils is also perceivable.

More in general, Mambelli et al. (2011) observed root litter, including biomarkers, to be selectively preserved with respect to needle litter, which was confirmed by Mendez-Millan et al. (2010) for maize and wheat roots versus shoots. Using isotopic signatures, Mendez-Millan et al. (2011) were able to quantify and subsequently compensate for such differences in turnover rate. This further emphasizes the significance of root derived organic matter for turnover determinations as already discussed by Wiesenberg et al. (2004). In other words, the relative abundance of roots and the uncertainties in terms of root related overprint in the rhizosphere and rhizosphere extension entail large uncertainties and strong differences between different plant species and environmental settings, especially at a molecular level. Further research is required to enable extrapolations to or across ecosystem scales.

With respect to the effects of fire, burning of litter or biomass can release additional extractable lipids (González-Pérez et al., 2004). In addition, fire has been reported to alter the chain length distribution of *n*-alkanes and *n*-fatty acids, shifting it towards shorter chain lengths (González-Pérez et al., 2004; Wiesenberg et al., 2009; Knicker et al., 2013). Also the composition of terpenoids can be influenced, resulting in preferential degradation of those with the lowest thermal stability (González-Pérez et al., 2004). All such processes potentially adversely affect the application of molecular proxies to an extent that depends on the frequency and intensity of fires. At the same time, fire events may also offer opportunities. For instance thermal alteration of animal fats in fireplaces may produce specific *n*-alkane/*n*-alkene doublets preserved in the soil, the presence of which can be used to reconstruct human fire usage in an archaeological context (Lejay et al., 2016).

4.2 Differences between different soil compartments

When soils are used as archives of molecular proxies, mostly bulk samples are used and replication per horizon or stratigraphic layer is often limited or absent. However, several studies indicate that preservation of molecules used as proxies can differ between different soil compartments (Flessa et al., 2008; Clemente et al., 2011; Griepentrog et al., 2014). Depending on the research question this may pose a problem, for instance it might obscure chronology when molecules are used as proxies to reconstruct changes over time.

Already Lichtfouse et al. (1998) showed that straight-chain lipids can become encapsulated in larger organic macromolecules, thus being protected against degradation. In addition, physical protection in (micropores of) aggregates and/or through association with clay minerals have been identified as important pathways for stabilization of soil organic matter in general, including molecules used as molecular proxies (Tonneijck et al., 2010). Using bulk and compound-specific $\delta^{13}C$ analysis, Cayet and Lichtfouse (2001) showed that plant-derived *n*-alkanes in a soil under maize cultivation varied in average age per particle size fraction, with the C_{31} *n*-alkane from the 200-2000μm fraction being significantly younger than that from the 50-200μm and 0-50μm fractions. A general trend of preferential preservation in smaller size fractions, in particular the clay fraction, is also reported in other studies. For instance, Quenea et al. (2004) and Flessa et al. (2008) observed longer turnover rates of soil organic matter in smaller size fractions. Clemente et al. (2011) studied the preservation of long chain aliphatic compounds in three soils with similar clay mineralogy but different carbon contents and standing vegetation. Irrespective of these differences, they too found the aliphatic compounds to be preferentially preserved in the silt and clay fractions, and again linked this to strong interactions with the present clay minerals. In a recent study, Griepentrog et al. (2015, 2016) confirmed the higher residence time of organic matter in small sized density fractions when compared to macro-aggregates as a result of interaction with the mineral phase. This implies an improved preservation of organic matter associated with higher density and thus mineral association when compared to organic matter associated to lower density. However, physical fractionation techniques such as particle and density fractionation have a potential of creating analytical artifacts, especially when molecular proxies are investigated. In addition, occlusion or strong adsorption in the smallest mineral fractions might hamper extraction and analysis of the proxy in question.

Furthermore, the effects of size or density fractions of soil on preservation of organic matter, including molecular proxies, are not uniform. For instance, Höfle et al. (2013) found size and density fraction related organic matter stabilization to be much less pronounced in the active upper layer than in the deeper soil horizons. This points to selective preservation of organic matter in the deeper soil because of more extensive aggregation and organo-mineral association. In a study of volcanic ash soils, Stewart et al. (2011) did not find differences in preservation of bulk soil organic matter in general or lipids in particular between different size fractions. They attributed this lack of differentiation to the presence of a large proportion of the soil organic matter that was not associated with mineral components as these were already saturated with previously incorporated soil organic matter (Stewart et al., 2011).

In general a combination of physical protection and sorptive preservation seems to be responsible for the observed differences (or lack thereof) in preservation of organic molecules in soils between different size or density fractions. This is corroborated amongst others by a study by Guggenberger et al. (1995), where they observed differences in the preservation of soil organic matter derived from tropical pastures compared to the preceding native savannah vegetation. They attributed this effect to a difference in interactions with the mineral phase, leading to physical protection of soil organic matter and molecular proxies contained therein. Similarly, differences in turnover rates of ca. one order of magnitude between forest and grass derived molecules after land use change have been observed as a result of saturation of the adsorption sites on the mineral phase (Hamer et al., 2012).

In addition to heterogeneity in the effects of interactions with the mineral phase on preservation of molecular proxies, analytical artifacts cannot be completely excluded when physical and chemical fractionation techniques are applied to separate particle size or density fractions. To date systematic investigations addressing these issues are lacking, which hampers the drawing of general conclusions with respect to processes that are relevant e.g. under different climates and for different soil mineralogical composition.

4.3 Selective preservation within or between classes of molecules

Turnover rates of molecular proxies do not only vary between different compartments, but may also vary within the same compartment; between and even within different (classes of) molecules (Dinel et al., 1990; Bull et al., 2000; Amelung et al., 2008). For instance, Feng and Simpson (2007) found preferential enrichment of straight-chain lipids as well as cutin and suberin monomers with increasing depth with respect to bulk soil organic matter. In contrast, in a study of grain-maize and silage-maize cropped soils Wiesenberg et al. (2004) found turnover times in the sequence bulk soil organic matter > *n*-alkanes > *n*-fatty acids, with rate differences that varied substantially between the two cultivations. The differences could be related to the different biomass input on the one hand and large amount of lignite dust and the low biomass input on the other hand, thus hampering degradation at this site. The faster turnover of fatty acids than alkanes as also confirmed by Wiesenberg et al. (2008a) and Griepentrog et al. (2015; 2016). In contrast, it may also offer opportunities to apply such differences between molecular classes and their response to external factors to trace transformations and input of organic matter in soils (Feng and Simpson, 2007).

An important issue with respect to the application of straight-chain lipids as molecular proxies is also preferential degradation of certain chain lengths within a certain class of molecules, as molecular ratios of various (higher) chain lengths are often used as proxies for certain vegetation types (see paragraph 2). This issue is addressed in the following paragraphs.

4.3.1 Straight-chain lipids

Already Moucawi et al. (1981) reported decreasing degradation rates with larger chain-length for *n*-alkanes in soils, which was confirmed by Lichtfouse et al. (1998) who determined a higher resistance of long straight-chain lipids in soil compared to their shorter chain counterparts. However, such preferential degradation was found in agricultural and acidic soils and in the absence of $Fe(OH)_3$ (Moucawi et al., 1981; Lichtfouse et al., 1998). Similar results were found for other lipid classes as well (Moucawi et al., 1981). More recently, several authors also indicate that such preferential degradation can occur in other soils (Jansen and Nierop, 2009; Cui Jingwei et al., 2010). However, the extent of the effect questions the suitability of the compounds in question as molecular proxies. For instance, Jansen and Nierop (2009) found the overall effect of preferential degradation on higher plant derived *n*-alkane patterns in soils to be small and not of influence for their use as vegetation proxy. Similarly, Lei et al. (2010a, 2010b) determined that in spite of strong evidence of microbial degradation, relative abundance of long-chain *n*-alkanes could still be used to distinguish coniferous from broadleaf tree input in soils.

Within the group of straight-chain lipids, overall degradation rates of subclasses have been found to vary depending on soil physicochemical properties. For instance, *n*-alkanes have been reported to be better preserved in alkaline soils, whereas *n*-fatty acids accumulate in more acidic soils (Simpson et al., 2008).

4.3.2 Isoprenoids

Isoprenoids are reported to have varying turnover rates both under oxic and anoxic conditions in soils (Jaffe et al., 1996; Amelung et al., 2008). Generally, sterols, diterpenes and pentacyclic triterpenes are reported to be turned over rapidly as compared to straight-chain lipids in grassland as well as forest soils, hindering their application as molecular proxies for their sources (Bull et al., 2000; Naafs et al., 2004; Jansen et al., 2007). However, Otto and Simpson (2005) observed the exact opposite trend, indicating a strong environmental control on the relative transformation rate of different classes of components. In an incubation study of derived triterpenols, Koch et al. (2005) highlighted marked differences between degradation rates of individual triterpenols, leading to a sharp relative increase in the proportion of taraxerol with respect to the other triterpenols.

In addition, Δ^5 sterols are transferred both aerobically and anaerobically to 5α- and 5β-stanols (De Leeuw and Baas, 1986), which are reported to persist much longer in soils than their precursors (Bull et al., 2000). Simpson et al. (2008) suggest to use the ratio of precursor sterols to their stanol and stanone degradation products as measure for their degree of degradation.

4.3.3 Cutin and suberin monomers

Bull et al (2000) observed different degradation rates for different components within the classes of free and ester bound lipids, depending on soil chemical and physical composition. However, Otto and Simpson (2006) found degradation of cutin and suberin to take place without preference for specific constituents. In general, Quenea et al. (2004) described cutin and suberin to be more resistant to degradation than free lipids residing in the same particle size fraction.

In a study of hydrolysable lipids using compound-specific ^{13}C analysis, Feng et al. (2010) described mean turnover times for cutin and suberin derived ester-bound lipids of 32-34 years. While slower than for bulk soil organic matter in this system, it was much shorter than anticipated, leading them to conclude that a large portion of cutin and suberin derived compounds reside in the non-hydrolysable fraction (Feng et al., 2010).

As mentioned earlier (section 4.1), Simpson et al. (2008) observed preferential enrichment of suberin monomers with respect to cutin monomers, which was confirmed by Mendez-Millan et al. (2010). In addition to the physical location of suberin versus cutin as potential cause, Simpson et al. (2008) suggested a higher resistance of suberin to degradation than cutin owing to a larger content of phenolic units in the former. Mendez-Millan et al. (2010) argued that microbial degradation, potentially influenced by the access to degradation sites are other factors influencing the slower turnover of suberin vs. cutin monomers. Regardless of the mechanism, the general difference in root vs. aboveground biomass derived suberin and cutinin monomers and their individual turnover would clearly influence the application of the cutin/suberin monomer ratio as proxy for leaf vs. root input.

4.4 Conclusions and implications regarding differences in transformations and turnover of molecular proxies in soils

Although available data is limited, it is clear that degradation of organic matter at a molecular level in terrestrial archives such as soils, paleosols and sediments can significantly influence the applicability of molecular proxies. As a result it seems useful to explore the possibility for a correction to improve the determination of paleovegetation and vegetation shifts and other paleoenvironmental information like paleotemperature and pH. The number of published approaches to compensate for the influence of degradation on paleoenvironmental reconstructions is still small. Zech et al. (2009) provided a simple two endmember model approach to improve paleovegetation reconstruction based on molecular ratios of different long-chain *n*-alkanes (C_{27}-C_{33}). Assuming that forest vegetation is dominated by *n*-C_{27} alkane and grass vegetation by *n*-C_{31} and *n*-C_{33} alkanes, high relative contributions of the respective homologues of the assumed source vegetation are used as end-members. At the same time the source vegetation is typically characterized by high odd-over-even predominance of long-chain *n*-alkanes. On the other hand, soils reveal a low odd-over-even predominance and abovementioned molecular ratios with smaller differences between the different vegetation types. In theory, the degradation continuum from plant leaves to soils of the respective vegetation type thus enable the identification of the degradation intensity of an unknown sample, if the sample is mainly influenced by a single vegetation. If the unknown sample does not plot on the degradation continuum, but between the different lines of different vegetation types, the relative contribution of grass vs. tree derived vegetation might be estimated and also corrected for the vegetation.

A slightly different approach was established by Buggle et al. (2010) who also used long-chain *n*-alkane ratios and the odd-over-even predominance of alkanes for their correction. While Zech et al. (2009) used correlations and then graphical-based reconstructions, Buggle et al. (2010) used a calculation based approach. The degradation in the continuum from recent soils is taken as an analogy and the slope of the regression line is multiplied with the odd-over-even predominance and the addition of the intercept of a long-chain *n*-alkane ratio in the crossplot of the ratio with the odd-over-even predominance. By moving the regression line to an ancient sample set, the end of the regression line yields the former topsoil value of the molecular ratio and odd-over-even predominance. Variation in the corrected long-chain *n*-alkane ratio enable the assessment of fluctuations in palaeovegetation.

Both mentioned approaches rely on the general differentiation of grass vs. forest vegetation based on long-chain *n*-alkane composition. As mentioned above such clear distinction of vegetation types exclusively based on compounds deriving from one compound fraction such as alkanes might be hampered by various factors such as variability within and between plant species, thus leading to similar composition of e.g. alkane from coniferous trees and grass plants (Maffei, 1996b; Maffei et al., 2004). Thus, such simple approaches might be appropriate only in very well defined settings, where independent records such as pollen data confirm the composition of specific plant assemblages determined by molecular proxies.

The expansion of approaches like the ones mentioned here to a broader range of molecular proxies is required to receive more complete pictures and to acknowledge the different turnover and degradation of different substance classes. However, the availability of datasets on plant and soil chemical composition for substance classes other than the *n*-alkanes are quite limited, hindering such expanding approaches. Thus, further surveys are required for other molecular proxies than *n*-alkanes for a high diversity of plants and soils from different climates. Afterwards, combined studies of more than one substance class enable improved paleoenvironmental reconstructions, whereas cross-checking with other non-molecular proxies, e.g. fossil pollen data, might be essential, especially if the paleorecord is targeted. Also the extrapolation of such approaches to different environmental and climatic settings might be limited as the effects of temperature, moisture, oxygen availability and others influence the degradation of organic matter as discussed above. Consequently, proper modelling approaches are required to assess not only palaeoenvironmental changes, but also to acknowledge and identify degradation of organic matter at a molecular scale.

5 General conclusions

In this review we considered the three most important constraining factors for the application of molecular proxies in soil science: i) variability in the molecular composition of plant derived organic matter as a result of genetic or life stage variations or external environmental factors; ii) variability in (relative contribution of) input pathways into the soil; and iii) transformation and/or (selective) degradation of (some of) the molecules once present in the soil. From the various studies done within and outside of soil science over the last decades the following general picture emerges. All constraining factors considered can have a significant influence on the applicability of molecular proxies in soil science. The degree of influence of the constraining factors strongly depends on the type of molecular proxy as well as the environmental context in which it is applied. In addition, the research question to be addressed by application of the molecular proxy has a strong influence. A factor that poses a constraining factor in one study might offer an opportunity in another. For instance fire induced alteration of biomass may release lipids to the soil that potentially confound their chemotaxonomic application, but may offer opportunities for reconstruction of the occurrence of human induced fire in an archaeological context. Recently, the first modelling approaches to potentially compensate for some of the constraining factors, specifically variability in input pathways and degradation of molecular proxies once in the soil, have started to emerge. Based on the previous we strongly recommend that the potential constraining factors are always explicitly considered whenever studies are planned in which molecular proxies in soils play a role. This review may serve as starting point for gathering the necessary information to decide, which constraining factors may play a role and how they can be addressed best. At the same time, it became clear from available literature that much information about the mentioned constraining factors is still lacking. In particular for molecular classes other than *n*-alkanes, systematic information is often very scarce. We therefore strongly appeal to the soil scientific community to address this knowledge gap. Also for this our review may serve as a starting point with future applicability in soil science and furthermore in paleopedology.

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Tables

Table 1: Compounds frequently used as molecular proxies in soils

Compound (the ones considerd in this review indicated in **bold**)	Most commonly used as proxy for:	Examples of recent publications[a]:	Number of articles published until 2017 *(publications 2007-2016)*[b]
Molecules of plant origin			
***n*-alkanes, *n*-alcohols (*n*-alkanol), *n*-fatty acids (*n*-alkanoic acid)**	(groups of) plant species	(Zhang et al., 2006; Zeng et al., 2011; Jansen et al., 2013; Gocke et al., 2013)	alkane: 1588 *(1025)* alcohol: 1972 *(1123)*; alkanol: 18 *(11)* *n*-fatty acids: 43 *(27)*; *n*-alkanoic acid: 67 *(41)*
***n*-methyl ketones**	degradation/transformation of soil organic matter	(Bai et al., 2006; Jansen and Nierop, 2009; Lei, B. et al., 2010)	methyl ketone 104 *(50)*
plant sterols and pentacyclic triterpenoids	(groups of) plant species	(Volkman, 2005; Jansen et al., 2007; Lavrieux et al., 2011)	plant sterol: 1682 *(590)* pentacyclic triterpenoid: 25 *(10)*
lignin monomers	coniferous species vs. broadleaf species vs. grasses and organic matter transformation	(Nierop et al., 2006; Heim and Schmidt, 2007; Thevenot et al., 2010; Simpson and Simpson,	lignin monomer: 115 *(74)*

		2012; Moingt et al., 2016)	
cutin and suberin monomers	root vs. aboveground biomass input	(Mendez-Millan et al., 2011; Hamer et al., 2012)	cutin monomer: 25 *(17)* suberin monomer: 32 *(18)*
Molecules of animal or bacterial origin			
Manure compounds such as coprostanol, 5β-stigmastanol, sitosterol and their epimers	Human impact, animal husbandry	(D'Anjou et al., 2012; Birk et al., 2012; Prost et al., 2017)	coprostanol: 35 *(17)* stigmastanol: 12 *(7)* sitosterol: 70 *(47)*
glycerol dialkyl glycerol tetraethers (GDGT)	mean ambient air temperature, paleo-elevation and soil pH	(Luo et al., 2011; Weijers et al., 2011; Peterse et al., 2012; Ernst et al., 2013; De Jonge et al., 2014)	GDGT: 148 *(144)*
phospholipid fatty acids (PLFA)	microbial biomass	(Kramer and Gleixner, 2006; Kindler et al., 2009; Ngosong et al., 2012; Malik et al., 2013)	Phospholipid fatty acid: 2157 *(1628)* PLFA: 1525 *(1140)*
Compound-specific stable isotope signal of one or more of the above[c]			

$\delta^{13}C$	C_3 vs. C_4 plants and tracing carbon transformations e.g. by free air CO_2 enrichment (FACE)	(Feng et al., 2010; Mendez-Millan et al., 2012)	^{13}C: 13 *(11)*
$\delta^{15}N$	(past) land management	(Bol et al., 2005; Griepentrog et al., 2014)	^{15}N: 2 *(2)*
$\delta^{2}H$ (deuterium)	precipitation and paleo-elevation	(Peterse et al., 2009; Bai et al., 2011; Luo et al., 2011; Sachse et al., 2012; Hermann et al., 2017)	^{2}H: 6 *(4)* deuterium: 9 *(7)*
$\Delta^{14}C$ (radiocarbon)	Age and contamination determination	Marschner et al., 2008; Mendez-Millan et al., 2014	^{14}C: 3 *(1)* radiocarbon: 35 *(30)*

[a] Published from 2005 until 2017.

[b] According to ISI Web of Science, checked for ‘soil’ and ‘target compound’ in the topic of articles on 27th February 2017 included in all available databases.

[c] ’Compound-specific’ and the respective isotope (i.e. ^{13}C, ^{15}N, ^{2}H, and ^{14}C respectively) were used as separate keywords in addition to ‘soil’.

Table 2: average maximum rooting depth, biomass/depth distribution and root/shoot ratios in different biomes (Canadell et al., 1996; Jackson et al., 1996)

Biome:	Average maximum rooting depth [m]:	Average percentage of roots in the top 0.3 m:	Average root/shoot ratio:
Boreal forest	2.0±0.3	83	0.32
Cropland	2.1±0.2	70	0.10
Desert	9.5±2.4	53	4.5
Sclerophyllous shrubland and forest	5.2±0.8	67	1.2
Temperate coniferous forest	3.9±0.4	52	0.18
Temperate deciduous forest	2.9±0.2	65	0.23
Temperate grassland	2.6±0.2	83	3.7
Tropical deciduous forest	3.7±0.5	70	0.34
Tropical evergreen forest	7.3±2.8	69	0.19
Tropical grassland/savannah	15.0±5.4	57	0.70
Tundra	0.5±0.1	93	6.6

Figures

Figure 1

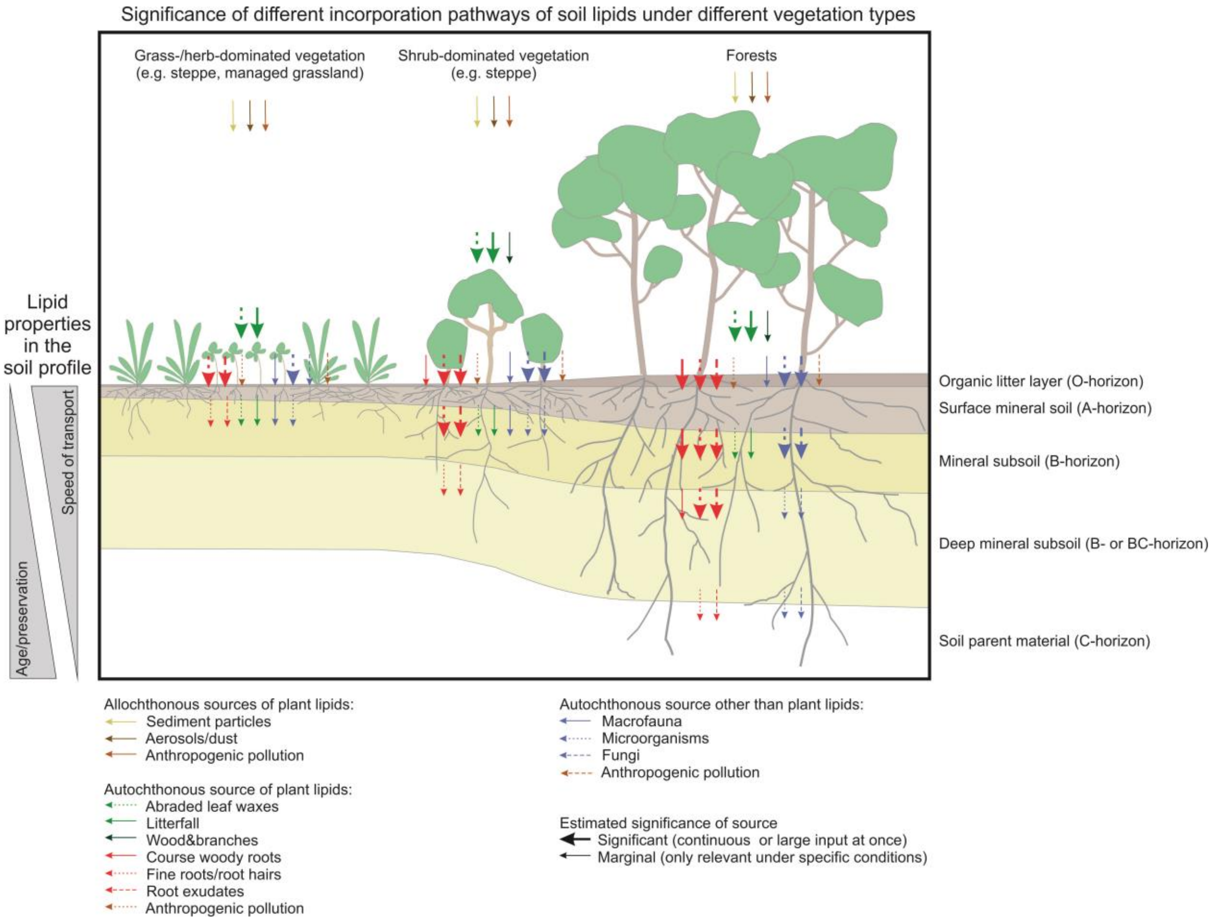

Figure caption

Conceptual overview of different incorporation pathways of lipids in soils originating from different biological sources and anthropogenic contamination. The different sources are indicated by distinct colors and lines of the arrows. The line thickness is an estimated significance of individual sources, without providing quantitative measure for different sources. Autochthonous sources are further distinguished by their significance in different soil depths or soil horizons, respectively. Further, the transport and age/probability of preservation as general properties of lipids are given at the left side of the figure.