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1   **Title: Methane Indicator Values for Peatlands: a comparison of species and functional**

2   **groups**

3   Running Title: *Peatland methane indicator values*

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2   **Type of Paper:** Primary Research Article

3

1   **Abstract (300)**

2   Previous studies have shown a correspondence between the abundance of particular plant

3   species and methane flux. Here we apply multivariate analyses, including a weighted

4   averaging approach, to assess the suitability of vegetation composition as a predictor of

5   methane flux. We developed a functional classification of the vegetation, in terms of a

6   number of plant traits expected to influence methane production and transport, and compared

7   this with a purely taxonomic classification at species-level and higher. We applied both

8   weighted averaging and indirect and direct ordination approaches to six sites in the UK, and

9   found good relationships between methane flux and vegetation composition (classified both

10   taxonomically and functionally). Plant species and functional groups also showed meaningful

11   responses to management and experimental treatments. In addition to the UK, we applied the

12   functional group classification across different geographical regions (Canada and

13   Netherlands) to assess the generality of the method. Again, the relationship appeared good at

14   the site level, suggesting some general applicability of the functional classification. The

15   method seems to have the potential for incorporation into large-scale (national) greenhouse

16   gas accounting programmes (in relation to peatland condition/management) using vegetation

17   mapping schemes. The results presented here strongly suggest that robust predictive models

18   can be derived using plant species data (for use in national-scale studies). For trans-national-

19   scale studies, where the taxonomic assemblage of vegetation differs widely between study

20   sites, a functional classification of plant species data provide an appropriate basis for

21   predictive models of methane flux.

1   **Introduction**

2   Methane (CH_4) is a potent greenhouse gas, and emissions from peatlands account for a large

3   proportion of the global total emissions, although, there is considerable uncertainty about

4   their magnitude (Billett *et al.*, 2010, Conrad, 2009, Petrescu *et al.*, 2010). Peatland CH_4

5   emissions may be expected to rise under warmer and wetter climate change predictions, and

6   in response to practices such as peatland restoration and re-wetting (Denman *et al.*, 2007,

7   Waddington & Day, 2007). It has been proposed that by changing peatland management,

8   both a reduction in greenhouse gas emissions and positive outcomes for biodiversity can be

9   achieved (Bain *et al.*, 2011). In addition, policy-makers require simple emission factors that

10   are responsive to the effects of land management activities in order to account for the net

11   emission of greenhouse gases but as yet, these are in the early stage of development

12   (Couwenberg *et al.*, 2011).

13   CH_4 fluxes are usually measured at small scales (often $<1m^2$) over a period of minutes using

14   chamber methods, and less frequently at larger scales ($<1 km^2$) by eddy covariance. There are

15   considerable difficulties in extrapolating these measurements to annual estimates at regional,

16   national, or global scales but the data are often used to parameterise CH_4 emission models

17   (Arah & Stephen, 1998, Smith *et al.*, 2007, Walter & Heimann, 2000, Zhang *et al.*, 2012).

18   Most commonly, a process-based model is used, which attempts to represent the responses of

19   methane production and oxidation to temperature, soil moisture, water table levels, anaerobic

20   state, pH, substrate concentrations, and other environmental factors deemed important (Arah

21   & Stephen, 1998, Smith *et al.*, 2007, Walter & Heimann, 2000). However, our

22   understanding of the responses of the different microbial taxa involved to environmental

23   variables is imperfect (Conrad, 2009). Furthermore, the correspondence between the

24   environmental variables measured in the field and those which actually drive CH_4 production

1   and oxidation is often not as good as would be desired. For example, Levy *et al.*, (2012)

2   found that environmental variables explained only 50 % of the variance in instantaneous CH_4

3   chamber flux measurements, although this was improved after temporal and spatial

4   averaging.

5   As an alternative or complementary approach, vegetation species composition provides a

6   long-term integrator of environmental conditions, and some studies have shown the potential

7   to use this to explain or predict CH_4 fluxes (Bubier *et al.*, 1995, Dias *et al.*, 2010). Bubier et

8   al., (1995) examined bryophytes as predictors of methane flux and found them to be good

9   surrogates for the degree of anaerobism/aerobism in two peatlands in Canada. In two

10   peatlands in the Netherlands, Dias et al., (2010) found that both vascular and non-vascular

11   species composition are good predictors of methane flux. The use of vegetation-based proxies

12   have been proposed as a basis for large-scale peatland greenhouse gas flux accounting by

13   Couwenberg et al., (2011). However, this approach requires testing on a much wider scale to

14   assess its applicability and generality. Because plant species data are widely available, if a

15   robust relationship could be established between CH_4 fluxes and vegetation, this may provide

16   an effective indicative tool for CH_4 fluxes to larger scales and for national-scale inventories.

17   Despite the demonstrated importance of plant species for CH_4 emissions, taxonomically

18   defined species may not be the best approach for reflecting CH_4 emissions. This is because a

19   natural species classification seeks to classify organisms in terms of their evolutionary

20   relationships rather than with respect to their influence on biogeochemical processes. In

21   addition, to make comparisons across regions a common framework is required. However,

22   species pools differ from region to region and hence a taxonomic classification may not be

23   the best basis as methane indicators. A solution to this problem might be to classify species

24   into functional groups; this approach has been applied several times in peatland systems (e.g.

1 Backstrand *et al.*, 2008, Baird *et al.*, 2009, Ward *et al.*, 2009). These would ideally reflect the

2 function-process-vegetation relationship and be sensitive enough to demonstrate responses to

3 changes in environmental conditions. However, defining a functional group in peatlands can

4 be problematic simply because quantitative trait data are absent for many peatland vascular

5 species and the majority of bryophytes. On the other hand, comparable qualitative attribute

6 data for both vascular plants and bryophytes have been collated for the UK (Hill *et al.*, 2007,

7 Hill *et al.*, 2004). This offers the possibility of defining an *a priori* set of plant attributes that

8 relate to CH_4 flux, such as the possession of aerenchyma (air channels that allow gaseous

9 exchange between the shoot and the root) or the association of methanotrophic bacteria with

10 *Sphagnum* species (Raghoebarsing *et al.*, 2005). In addition to the fact that plant species

11 respond to the same environmental factors that influence CH_4 emission, it also has been

12 shown that plants can have a direct effect on CH_4 production and emission (Aulakh *et al.*,

13 2001, Joabsson *et al.*, 1999, Shannon *et al.*, 1996).

14 Levy *et al.*, (2012) analysed nearly 5000 chamber measurements of CH_4 flux from 21 sites

15 across the UK. They found that less than half of the observed variability in instantaneous

16 fluxes could be explained by independent variables measured but where plant species

17 composition data were available, this provided the highest explanatory power. Here, we

18 extended the analysis of Levy et al., (2012) by adding further data from sites where plant

19 species composition has been determined. We applied a "weighted averaging" approach to a

20 range of sites in the UK, as well as continental Europe and Canada. To enable a degree of

21 generality across continents where the degree of species overlap is incomplete, species were

22 classified into functional groups. These are defined by a number of qualitative traits related to

23 species responses to environmental factors that also control CH_4 emission and to direct

24 effects of plant species on CH_4 emission. We compared the results based on this functional

1   classification with those based on the original species composition data using a purely

2   taxonomic classification.

3

1 **Materials and Methods**

2 *Site Descriptions*

3 The measurements analysed here were made at sites in Scotland, Wales and England in the

4 U.K. (Table 1). These peatland sites are all characterised by high water table levels and

5 acidic deep peat; further site specific details can be found in Table 1 and elsewhere (Billett *et*

6 *al.*, 2010, Carfrae *et al.*, 2007, Dinsmore *et al.*, 2009, Gray, 2006, Ward *et al.*, 2007). Two

7 sites have plots located in a designed experiment (Whim and Moor House: nitrogen; burning;

8 grazing) and the rest of the plots are located within sites on a range of different management

9 practices (remaining sites: drainage; grazing; burning).

10 *CH_4 flux measurements*

11 At each site CH_4 fluxes were measured using a similar measurement procedure. A cylindrical

12 PVC collar was inserted into the soil and left in place for a number of weeks or months. On

13 each sampling occasion, a lid was sealed on top, and left in place for up to 2 h, but more

14 commonly 30 min to 1 h. Samples were removed by syringe through a 3-way tap or rubber

15 septum, and analysed on a gas chromatograph, together with replicates of three or four

16 standard gases with known concentrations. For each sequence of gas samples from a

17 chamber, the flux (mol m^{-2} s^{-1}) was calculated as the rate of change in concentration (mol

18 mol^{-1}) with time (s), by linear regression; taking into account the density of air, chamber

19 volume, and surface area . At most of these sites, measurements were made approximately

20 monthly over one or more years, covering all seasons. Where there are important differences

21 in methodology (chamber size, gas sampling method etc.), these are detailed in Table 1 of

22 Levy *et al.,*(2012). Full details of the methods used can be found elsewhere (Billett *et al.*,

23 2010, Carfrae *et al.*, 2007, Dinsmore *et al.*, 2009, Gray, 2006, Ward *et al.*, 2007).

Peatland methane indicator values

1   *Vegetation Sampling*

2   At each site vegetation composition was assessed as percentage cover by species for vascular

3   plants, bryophytes, macro-lichens and bare peat from within each of the CH_4 chambers

4   except at Moor House. At Moor House vegetation was averaged from three randomly located

5   quadrats within each treatment plot; deriving a mean cover for each treatment. Cover was

6   assessed from the chambers located in Wales (Migneint) from photographs with species

7   identification confirmed from voucher specimens. All percent cover values were converted to

8   the ten point DOMIN scale (sensu Dahl and Hadač (1941) see Rodwell, 1991a) prior to

9   analyses.

10   *Functional Classification*

11   De Deyn et al., (2008) suggest a trait base approach to plant classification in relation to

12   carbon. However, in bryophyte dominated systems such as peatlands, quantitative plant trait

13   data are not yet widely available. We therefore use a systematic approach to define functional

14   groups from qualitative characteristics that we expect to have a relationship to CH_4 fluxes;

15   these attributes are defined in Table S1. Most of the attributes are taken directly from Hill et

16   al., (2004) for vascular species and Hill et al., (2007) for bryophytes, however, there were

17   some exceptions to this. For *Sphagnum* spp., life forms were derived to reflect a microhabitat

18   classification with the assumption that this has a close relationship to water table depth.

19   Vascular plants were classified as possessing aerenchyma from literature sources or this was

20   assumed in the absence of evidence but where strong habitat association exists i.e. those

21   known to inhabit inundated sites. We also include a literature derived nitrogen fixation

22   classification. Functional groups were classified such that groups of species that have the

23   same life form, woodiness, aerenchyma and N fixation, comprise the same functional group

24   (Table S2). The following serve as examples: *Myrica gale* is functionally coded "PnwAAct"

1   meaning it is a nanophanerophyte (Pn), woody (w) , possesses aerenchyma (A), and has an

2   actinorhizal nitrogen fixation relationship (Act); *Hylocomium splendens* and *Pleurozium*

3   *schreberi* are both coded "Weh" having a weft life form (We) and being herbaceous (h);

4   *Sphagnum capillifolium* and *S. fuscum* were coded "HumhCya" meaning hummock form

5   (Hum), herbaceous (h) and likely to harbour N fixing cyanobacteria (Cya). An additional

6   standalone type was also used for bare peat; ultimately the 135 different species recorded

7   from the UK, Canadian and Netherlands sites were arranged into 20 functional groups.

8   Abundance data were summed for each functional group.

9   *Data Analysis*

10   Vegetation data were first analysed by Detrended Correspondence Analysis (DCA) to

11   determine the correlation between the first axis and log mean CH_4 emissions, entered as a

12   passive variable; additionally site was also included as a passive variable. We then performed

13   a Canonical Correspondence Analysis (CCA) to determine the relationship between

14   species/functional groups and the experimental/management treatments. Due to the

15   differences in methodology between sites, site was included as a co-variable. As with DCA,

16   CH_4 emissions were included as a passive variable. Both these analyses were carried out

17   using Canoco 4.5 and Canodraw 4.1 software (ter Braak & Šmilauer, 2002).

18   Models to derive predictions of CH_4 flux were developed using weighted averaging (WA)

19   regression as in Bubier et al., (1995) and Dias et al., (2010). WA assumes a unimodal

20   response of species to a certain environmental variable. This means that species have their

21   maximum abundance at their optimum position along the environmental gradient. Although,

22   plants do not respond directly to CH_4 fluxes nor have an optimal CH_4 flux in any biological

23   sense, but the terms optimum and tolerance are retained for consistency with the literature on

24   gradient analysis. As our approach is analogous to Bubier et al., (1995) and Dias et al.,

1   (2010) we refer the reader to these publications, and in addition, ter Braak and Barendregt

2   (1986), Jongman *et al.,* (1987), Birks *et al.*, (1990) and ter Braak and Juggins (1993) for

3   specific details of the WA methodology. The WA species optima are calculated as an average

4   of the CH_4 flux weighted by species abundance and that these optima, together with species

5   abundance, are used to predict fluxes. To account for the prediction of extreme values we use

6   only the classical deshrinking procedure as inverse deshrinking gave very similar results (see

7   Birks *et al.*, 1990, Osborne, 1991, ter Braak & Barendregt, 1986, ter Braak & van Dam,

8   1989). The deshrinking procedure corrects the inherent bias toward the median of the

9   observed range, resulting from taking averages twice during WA reconstitution: once in WA

10   regression and once in WA calibration (see also Bubier *et al.*, 1995)

11   To explore the predictive ability of the WA technique a 70/30 spilt of the data was used to

12   perform cross-validation; for each WA model a completely random selection without

13   replacement of 30% of the vegetation stands were left out in turn for all possible

14   combinations. The WA function from the selected vegetation stands was then applied to the

15   omitted ones, giving for these plots a prediction and an error prediction.

16   Finally, our approach to functional group classification was applied to the datasets from

17   Bubier et al., (1995) and Dias et al., (2010). Here the species were grouped in the same way

18   as detailed above; functional classifications for each of the species included can be found in

19   the supporting material (Table S2). As neither Bubier et al., (1995) nor Dias et al., (2010)

20   give species abundance data, we used the published optima to derive a median value for each

21   functional group and taxonomic family for use in the WA calculations. We confine our

22   comparison to family and functional groups as there was as no abundance data for assessing

23   dominant species and as Bubier does not include any vascular species so it was not possible

24   to include aerenchymatous species. Nevertheless, by using the same approach with our larger

1   dataset from our sites, a comparative evaluation of the success of our functional classification

2   outwith the UK was made.

1   **Results**

2   The DCA analysis showed a negative correlation between axis one and CH_4 emission in both

3   species (-0.54) and functional group (-0.50). This indicates a strong relationship between the

4   variance in species or functional group and CH_4 emission. The variation explained by axes 1

5   and 2 for the species and function group data was 15.9% and 29.2% respectively. As

6   expected some species/functional groups/species are more correlated than others to CH_4

7   (Figure 1).

8   Monte Carlo permutations of the canonical correspondence analysis (CCA) of the species

9   data set showed that axis 1 (eigenvalue of axis 1 = 0.174,) and all axes (sum of all axes

10   canonical eigenvalues = 0.480) were significant ($p< 0.01$). The cumulative percentage

11   variance explained by all axes of the species data was 9.7% and of the species-environment

12   relation was 76.2%. Axis 1 and 2 were more strongly correlated with grazing treatments than

13   other treatments. A similar pattern was evident in the functional group dataset the canonical

14   correspondence analysis (CCA) showed that axis 1 (eigenvalue of axis 1 = 0.119,) and all

15   axes (sum of all axes canonical eigenvalues = 0.272) were significant ($p< 0.01$). The

16   cumulative percentage variance explained by all axes of the species data was 16.1% and of

17   the species-environment relation was 36.3%. Axis 1 and 2 were again more strongly

18   correlated with grazing treatments than other treatments. In both species and functional group

19   analyses CH_4 emissions were most highly correlated to axis 3 but the correlation was weak

20   (0.2 in both cases); the highest treatment correlation with axis 3 was a positive correlation to

21   burning (spp: 0.39; FG: 0.25) and negative to drainage (spp: -0.32; FG: -0.27).

22   Functional group appear to have a slightly narrower range of WA optima than species (Spp. –

23   0.5 to 1.6; FG - 0.9 to 1.4), in addition species also appear to have wider tolerance (Figure 2).

24   Species also have a propensity to be less widely distributed, for example, the highest WA

1   optima for species are associated with *Vaccinium oxycoccos* (1.6) and *Sphagnum*

2   *magellanicum* (1.6) and lowest WA optima with *Deschampsia flexuosa* (0.5) and *Festuca*

3   *ovina* (0.5); these species only appear in one site Whim, Forsinard and Auchencorth

4   respectively. In comparison the functional group members are likely to be more widespread

5   for instance *LawnhCya* occur in 2 sites, *bare peat* in 3 sites, *hch* in 2 sites and *tfh* in 5 sites.

6   The WA optima (Figure 2) for species and functional groups allowed reliable predictions of

7   CH_4 fluxes based on both cross validation (Table 2) and the complete dataset (Figure 3a-h).

8   Changing the spatial resolution from individual sites to sub site, treatment and plot levels

9   decreases the predictive power as shown by decreases in r square (adjusted) values (Figure

10 3). On the whole, functional groups appeared to be slightly better in linear predictive power (r

11 squared) than taxonomic classification, species/family. However, the root mean squared error

12 (RMSE) tended to be slightly higher for functional group than in species suggesting a better

13 1:1 relationship for taxonomic classification such as species (Table 2 and Figure 3a-h).

14 We found two published studies (Bubier *et al.*, 1995, Dias *et al.*, 2010) where there was plant

15 species data to allow our functional group classification to be applied and the original

16 correlation between species CH_4 WA predictions and observed CH_4 was good. The

17 predictions based on WA calculated for our functional group classification for these studies

18 showed good agreement with the published observed CH_4 fluxes (adj r^2 = 87.7). When WA

19 predictions are plotted for all sites including the additional published sites against the

20 observed values the r-squared (adjusted) is very high (0.87) and close to a 1:1 fit (WA CH_4 =

21 - 8.823 + 1.796 Observed CH_4) (Figure 4). However, when using the family classification the

22 correspondence between observed and predicted was poor (adj r^2 = 2.7).

1   **Discussion**

2   The low percentage of variance explained in the unconstrained ordination analyses here is

3   due to the presence of many zero values in the data, and is typical for such noisy data sets

4   representing long environmental gradients (*c.f.* Bubier, 1995). Nevertheless, significant

5   relationships were detected for both species and functional groups in the constrained analyses

6   in relation to land management practices and experimental treatments. Species tend to show a

7   better correlation with the explanatory variables than functional groups. However, both

8   classifications were significant. This serves to underline the evidence that practices such as

9   grazing, drainage, burning and nitrogen manipulation can have a strong influence on species

10   and thus functional group composition (e.g. Carfrae *et al.*, 2007, Cooper *et al.*, 2001, Grant *et*

11   *al.*, 1976, Gunnarsson, 2000, Hobbs, 1984, Kuhry, 1994, Marrs *et al.*, 2004, Rawes &

12   Hobbs, 1979, Stewart & Lance, 1991). The WA method appears to work well for explaining

13   variance in observed mean CH_4 using either taxonomic or functional classifications. Bubier

14   (1995) used the same technique and reported similarly high r^2 values using on bryophyte

15   composition data. Again using WA, Dias et al., (2010) also reported good relationships

16   though with slightly lower r^2 (0.47 - 0.67; derived from the published r values) for the fit

17   between vascular and non-vascular species WA predictions and observed CH_4 fluxes.

18   The increase in variance explained with increasing spatial scales from plot-

19   level/treatment/sub-site /site is in accordance with the findings of Levy et al., (2012). Possible

20   reasons for this were discussed at length in Levy et al., (2012) e.g. random measurement error

21   in the flux and/or independent variable data, cancelling out as more measurements are

22   averaged. However, one additional source of random measurement error here is the

23   unaccounted observer error in the plant abundance data, although, the use of the DOMIN

24   scale and including site as a co-variable in the ordination should compensate for this to some

1   extent.

2   Methane flux has frequently been related to abiotic variables such as temperature (Kettunen

3   *et al.*, 2000, Laine *et al.*, 2007, MacDonald *et al.*, 1998), and water table levels (Liblik *et al.*,

4   1997, MacDonald *et al.*, 1998) and this approach frequently forms the basis of process

5   models (e.g. Smith *et al.*, 2007). In an analysis of a large UK dataset, Levy et al., (2012)

6   found that when spatial and temporal variation were controlled, up to ~75 % of the variance

7   in CH_4 fluxes could be explained. Soil carbon, peat depth, soil moisture and pH together

8   provided the best sub-set of explanatory variables. However, for the three sites where plant

9   species composition data were available, this provided the highest explanatory power (Levy

10   *et al.*, 2012). Plant species composition is less routinely examined than environmental

11   variables such as water table levels or temperature but there is increasing evidence of their

12   power as an indicator of methane flux. In a UK bog (Greenup *et al.*, 2000) and in Germany

13   (Couwenberg *et al.*, 2011) good relationships were evident between aerenchymatous species

14   and CH_4 emission. In contrast we found weaker relationships with aerenchymatous species

15   than either all plant species or our functional groups. We suspect this is because

16   aerenchymatous species are only showing one functional response and there are likely to be

17   multi-functional responses that promote or decrease methane flux with regard to

18   anaerobic/aerobic decomposition processes. Strong correlations between the emission of CH_4

19   and bryophytes abundance were found in Canada (Bubier *et al.*, 1995) that were indicative of

20   long term water table levels and temperature regimes. In the Netherlands, good agreement

21   between plant species composition and methane flux were detected (Dias *et al.*, 2010) again

22   directly related to water table level. The data examined here add to this evidence and

23   indicates that both species and functional groups appear to be good predictors of methane

24   flux. Nevertheless, the previous analyses (Levy *et al.*, 2012) suggests that plants may not

25   always have simple relationships to long term water table level and temperature and that

1   other mechanisms may be responsible. That said, there still seems to be good potential for

2   either species or functional groups to be indicators of methane flux. Species and higher

3   taxonomic classifications tended to show a slightly better 1:1 relationship with predicted and

4   observed CH_4 emissions as indicated by lower RMSE values but higher r^2 were found for

5   functional groups. Nonetheless, if plant composition is to be used to predict or indicate

6   methane flux on wider spatial scales then it would seem that a functional group approach may

7   have a reasonable predictability and wider geographic applicability than species.

8   That the functional classification applied here is at least as good (in terms of r^2) as the

9   taxonomic classification is encouraging. It also suggests that the classification of functional

10   groups used here captures to some extent the function-process-vegetation relationship and is

11   somewhat sensitive to responses to disturbance. In addition, the functional group

12   classification gives generality to the method spanning multiple sites and regions, as

13   demonstrated by the application to the Canadian and Dutch data. As the total number of

14   species involved in larger scale studies can be quite large the use of functional groups

15   addresses the problem of some species being isolated to single sites or regions. By

16   aggregating species into functional groups this become less of a problem without the loss of

17   explanatory power.

18   To improve this approach it would be useful to evaluate whether the functional characteristics

19   used here are the most appropriate. Quantitative traits (see e.g. De Deyn *et al.*, 2008) with

20   more 'biogeochemical' characteristics may be a more appropriate for classifying functional

21   groups (e.g. foliar C/N ratio, annual growth rate, below and above ground biomass ratio,

22   rooting depth, quantitative assessment of labile substrate production for methanogenesis etc.)

23   and traits related to the response to environmental factors that also control CH_4 flux (such as

24   water table level and N availability). However, at present these cannot be defined for many

1 species across a range of taxa, particularly bryophytes, as pertinent data are lacking. Further

2 refinements to improving this approach need co-located datasets of both CH4 flux and

3 vegetation from broad geographical scales (different countries and continents). These data

4 would give a more comprehensive testing of the WA and functional group approaches

5 proposed here and assess its applicability on a global scale.

6 The obvious potential strength of a vegetation indicator approach is that by using species or

7 functional group abundance there is the potential for indicative fluxes to be mapped. For

8 example, from data commonly gathered for vegetation mapping programmes such as the

9 National Vegetation Classification or Countryside Survey (NVC; CS) in the UK (Rodwell,

10 1991b) or Corine Biotope mapping in Europe (Moss *et al.*, 1991) or national vegetation

11 classification in Northern America (Grossman *et al.*, 1998) one could potentially derive

12 methane flux indicator values for plant communities from species or functional group. In

13 addition, it may also be possible to assess the effects on methane flux indirectly through

14 examining vegetation change in relation to vegetation degradation or restoration activities.

15 This may however require the regional calibration of WA optima for species and functional

16 groups within regions. In terms of UK plant communities, it appears as though functional

17 group approach may perform slightly better than species in relation to community level

18 fluxes (see supplementary material Fig S1). The limiting factor is that the approach requires

19 the raw species abundance data, which is not always readily available, and a calibration of the

20 NVC communities using co-located flux data, which is also not routinely undertaken. We

21 would therefore encourage researchers to routinely incorporate vegetation measures into

22 studies of methane and other GHG's to allow more comprehensive analyses of the indicator

23 value of vegetation for GHG inventory.

24 The method also has the potential for incorporation into large-scale (national) greenhouse gas

Peatland methane indicator values

1   accounting programmes (in relation to peatland condition/management). Couwenberg et al.,

2   (2011) have suggested a method for the incorporation of vegetation data into GHG

3   inventories. However, much of their proposed model relies on 'expert judgement' and at

4   present we lack sufficient data for a critical evaluation of the use of expert judgement. Of

5   particular concern is the question of scaling up and the transmission of flux and vegetation

6   data from the small scale of chambers ($<1m^2$) to landscapes. We know of no studies where

7   this has been attempted, yet techniques for testing this are available such as eddy covariance

8   and co-located landscape scale vegetation survey.

9   De Deyn et al., (2008) call for a need to identify easily measurable, cost-effective,

10   aboveground traits that capture belowground carbon dynamics across different spatial and

11   temporal scales. Our results strongly suggest that predictive models for methane emissions

12   could be derived using both species (for use in national studies) and/or functional groups (for

13   use in both national and global studies) using abundance data alone. However, we suggest

14   that further study is required using co-located vegetation and methane flux measurements at a

15   range of spatial scales before the links between vegetation and GHG flux are more coherently

16   established.

1   **Acknowledgements**

4

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Peatland methane indicator values

1   **Supporting Information**

2   The supporting information includes two tables and one figure comprising the following:

3   Table S1: Attributes used in the classification of functional groups

4   Table S2: Species functional group classification from datasets used in this analysis

5   Figure S1: Predicted CH_4 flux using a weighted average of species and functional group
6   abundance against observed mean CH_4 flux (Log) for National Vegetation Communities for
7   the UK

1 Table 1: Details of site characteristics and experimental manipulations and/or management practices. *Modified here means that the vegetation is no
2 longer indicative of semi-natural bog and has been altered by practices such as drainage, and grazing.

3

Country	Site	Latitude	Longitude	Peatland Type	Altitude (m)	Annual rainfall (mm)	Sub Sites	Experimental treatments/Management practices	total number of plots
Scotland	Auchencorth	55.79 N	3.24 W	*Modified ombrotrophic blanket bog	260	1100	None	9 plots, site drained and sheep grazed	9
	Forsinard	58.37 N	3.97 W	Ombrotrophic blanket bog	180	1500	Nam Breac	5 deer grazed plots	5
							Sletil	5 semi-natural plots	5
							Maol Donn	5 semi-natural plots	5
							Leir	5 semi-natural plots	5
							Big House	3 burnt and 3 unburnt plots all open to sheep grazing	6
							Cross Lochs	12 plots of drain blocked, unblocked and 6 semi-natural controls	30
	Whim	55.76 N	3.27 W	Ombrotrophic raised bog	280	1100	None	Nitrogen manipulation experiment 4 plots each of NH3, NH4, NO3 additions and control	16
Wales	Migneint	52.99 N	3.80 W	Ombrotrophic blanket bog	480	2000	Migneint A	Blocked and open drains open to (light) sheep grazing	36
							Migneint C	Semi natural open to (light) sheep grazing	8
							Migneint D	Blocked and open drains open to (light) sheep grazing	36
England	Moor House	54.69 N	2.40 W	Ombrotrophic blanket bog	600	1900	Hard Hill	burning 10 year rotation with (light) sheep grazing plots and control plots	16

Peatland methane indicator values

1 Table 2: Results of cross-validation predictions for CH$_4$ emission from plant species
2 composition for five sites using weighted averaging from different classification levels,
3 taxonomic: family, species and dominant species, and functional: functional group and
4 aerenchymatous/*Sphagnum* spp. only. A 70/30 split was used as training and test sets.

| Scale	Classification Level	r^2 (adj)	RMSE
Site	Family	0.66	0.18
	Species	0.72	0.14
	Dominant Species	0.67	0.23
	Functional Group	0.81	0.23
	Aerenchymatous/Sphagnum	0.24	0.24
Sub-site	Family	0.44	0.23
	Species	0.52	0.20
	Dominant Species	0.00	0.26
	Functional Group	0.59	0.25
	Aerenchymatous/Sphagnum	0.12	0.26
Treatment	Family	0.13	0.33
	Species	0.25	0.28
	Dominant Species	0.01	0.31
	Functional Group	0.21	0.30
	Aerenchymatous/Sphagnum	0.06	0.31
Plot	Family	0.08	0.34
	Species	0.18	0.30
	Dominant Species	0.14	0.33
	Functional Group	0.23	0.34
	Aerenchymatous/Sphagnum	0.06	0.34

5

1 **Figure Legends**

2 Figure 1: DCA biplots of plant species (a) and functional group (b) composition. CH_4

3 flux and site centroids plotted as supplementary variables. Only species with weight

4 above 10% were included for clarity.

5 Figure 2: Methane flux weighted averaged optima and tolerances of plant species and

6 functional group derived from the complete data set.

7 Figure 3: Plots of WA-predicted CH_4 flux (nmol CH_4 m^{-2} s^{-1}) using species (a) and

8 functional group (b), versus observed values for the five main sites, sub-sites and

9 treatment plots based on all data. In all plots the black line represents a 1:1 fit. (i) Mean

10 plot level WA predictions for species, r^2 (adj) – 0.31, and functional group, r^2 (adj) –

11 0.24. (ii) Mean treatment level WA predictions for species, r^2 (adj) – 0.39, and

12 functional group, r^2 (adj) – 0.33. (iii) Mean sub-site level WA predictions for species, r^2

13 (adj) – 0.59 and functional group. r^2 (adj) – 0.80. (iv) Mean site level WA predictions

14 for species, r^2 (adj) - 0.91, and functional group, r^2 (adj) - 0.96.

15 Figure 4: Predicted CH_4 flux using a weighted average of functional group abundance

16 against observed median CH_4 flux data from Bubier et al. (1995) and Dias et al. (2010);

17 the UK sites analysed here are also included. The blue line indicates a 1:1 fit (r^2 (adj) -

18 0.87). N.B. This Figure has units in mg CH_4 m^{-2} d^{-1} (c.f. Figs 1-3 where units are nmol

19 CH_4 m^{-2} s^{-1}) for consistency with the data presented in Bubier *et al.,* (1995) and Dias *et*

20 *al.,* (2010).

Figure 1

(a)

(b)
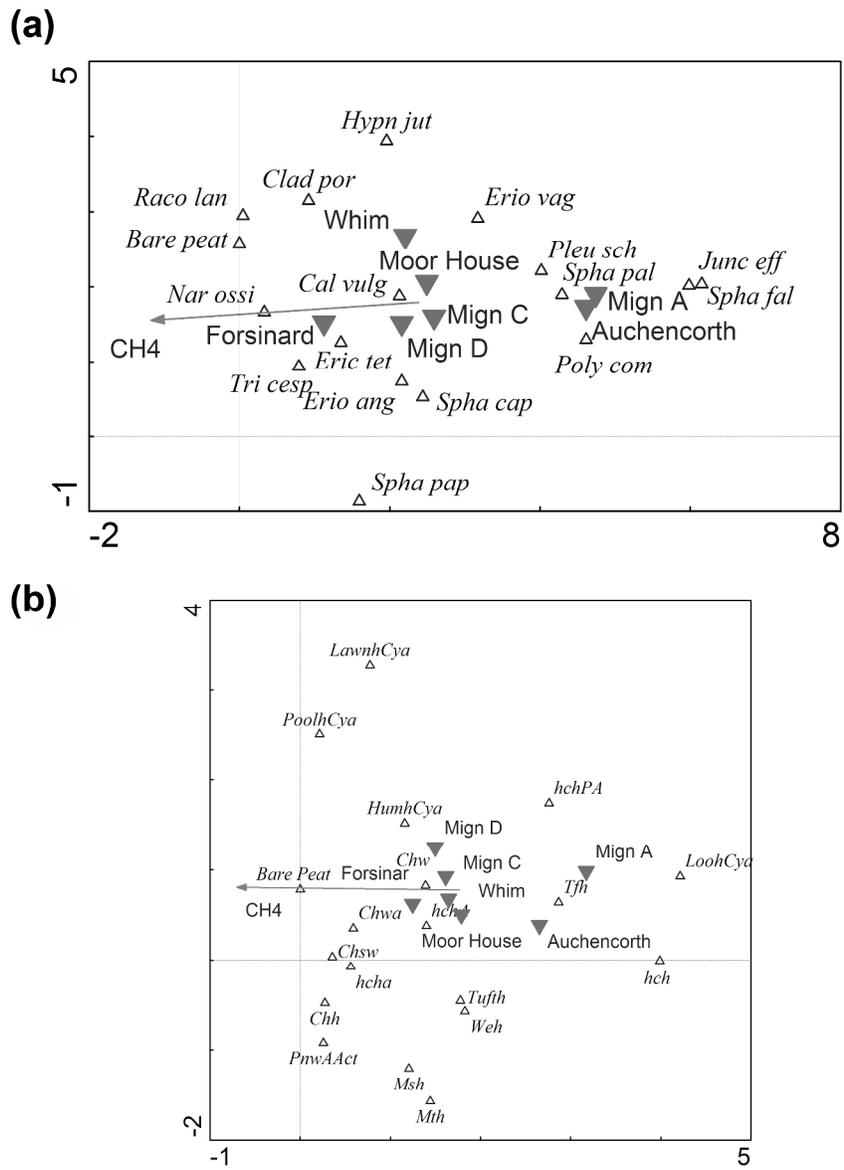
289x402mm (300 x 300 DPI)

$$\textbf{log } \textbf{CH}_4\textbf{(nmol m}^{-2}\textbf{ s}^{-1}\textbf{)}$$
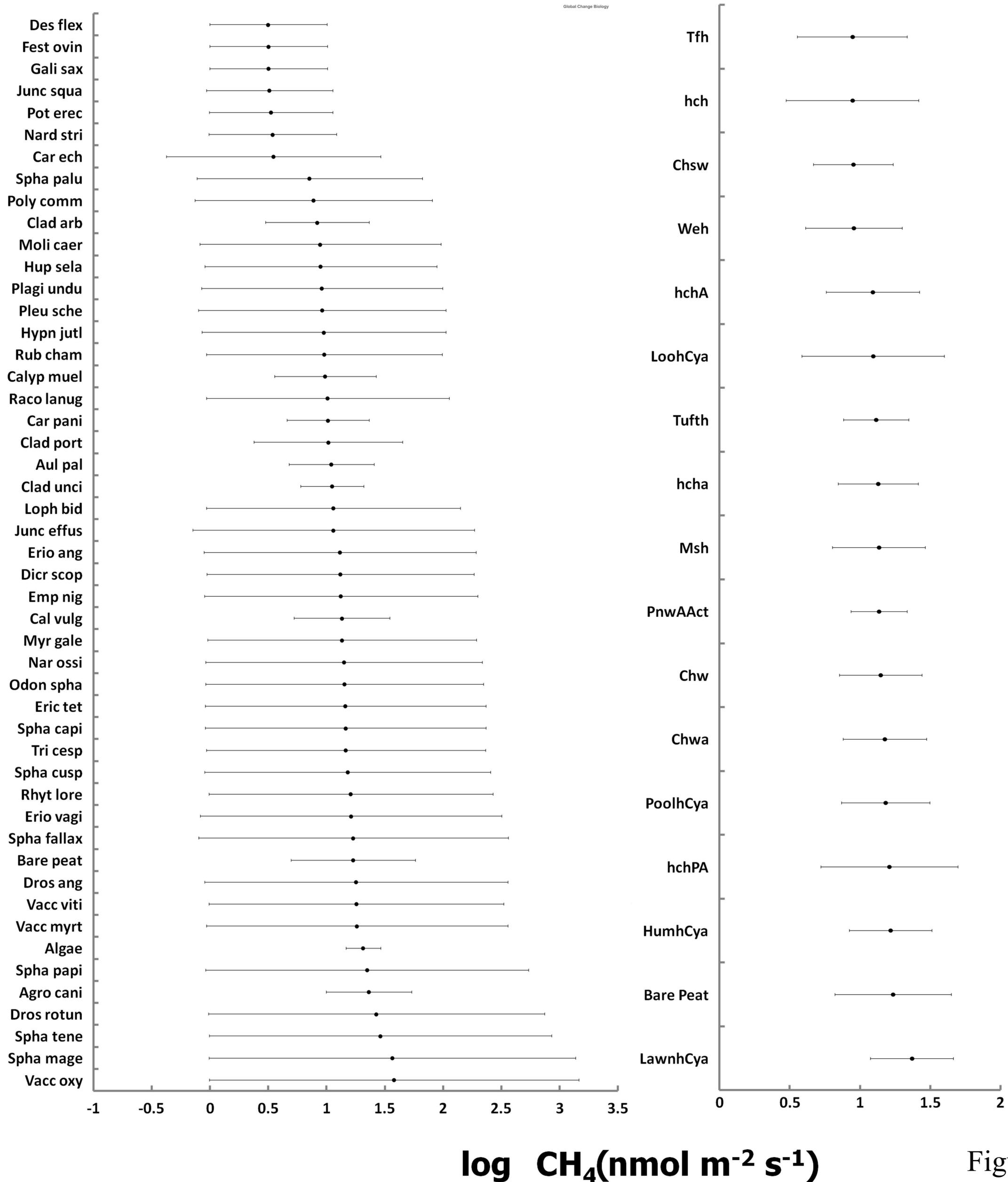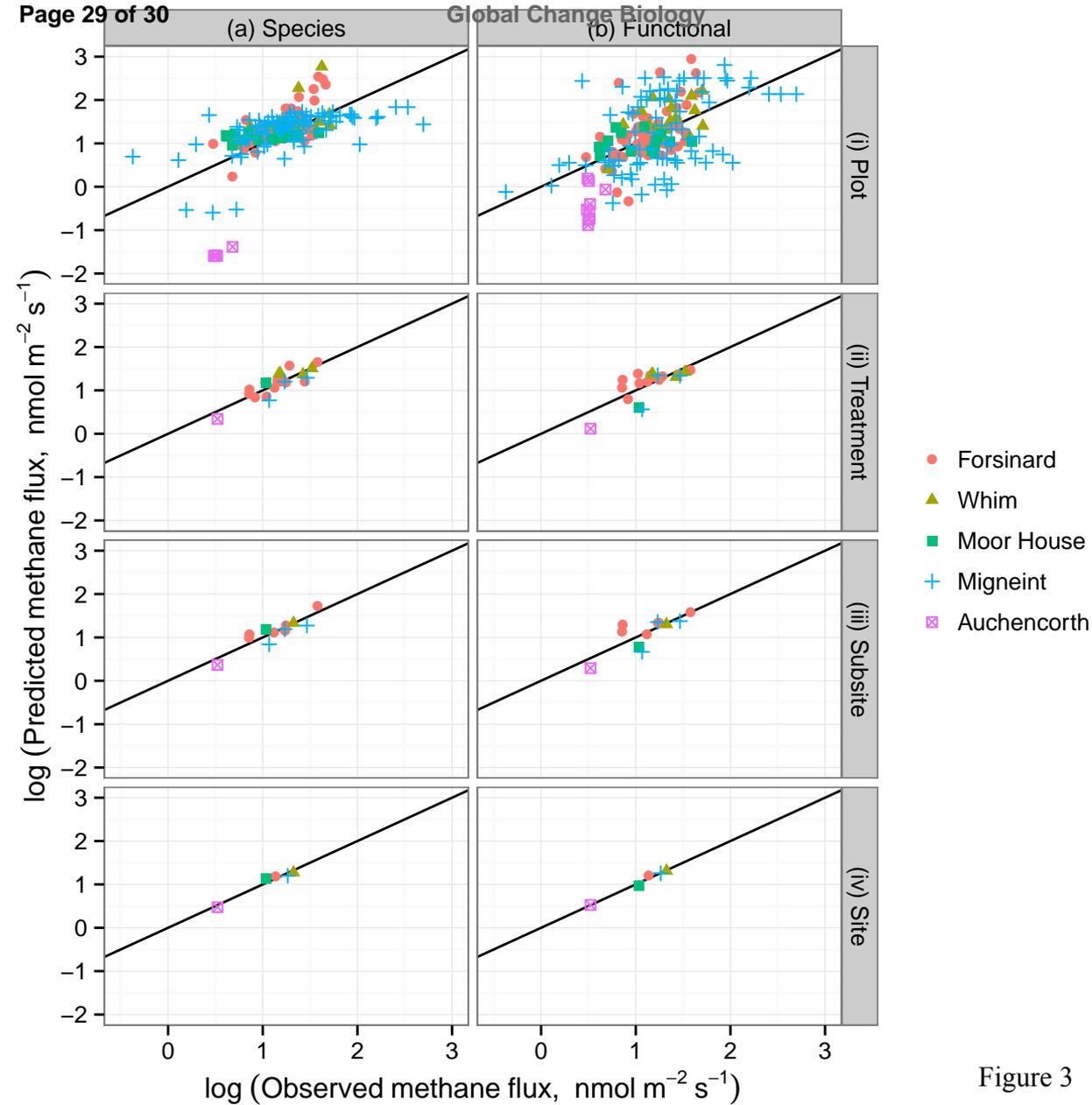
Figure 2

Figure 3

Figure 4
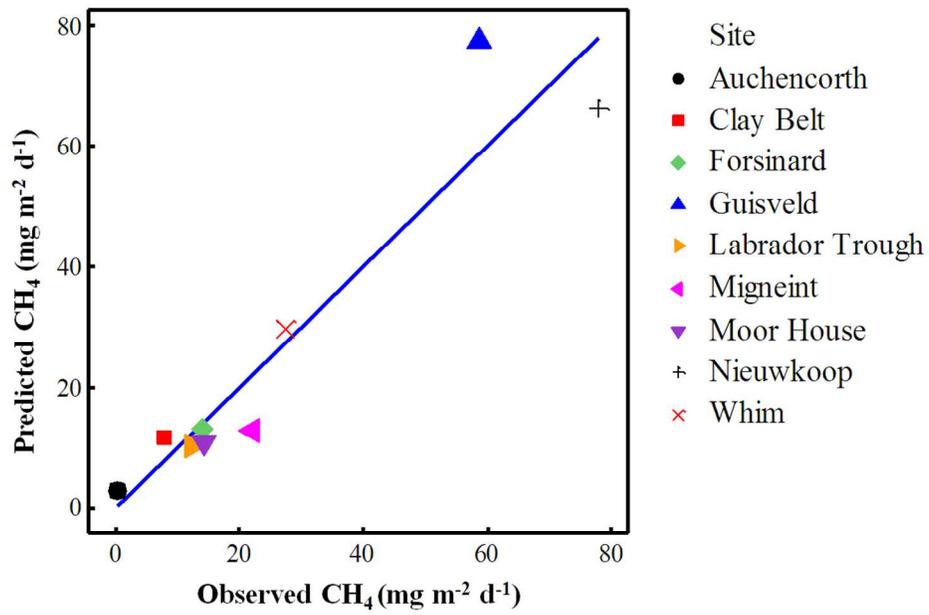
109x73mm (300 x 300 DPI)

Methane Indicator Values for Peatlands: a comparison of taxonomic species and functional groups

Supporting Information

Table S1: Attributes used in the classification of functional groups (from Hill *et al.*, 2007a, Hill *et al.*, 2004). **V** and **NV** superscripts relate to whether traits are associated with vascular or nonvascular plants. Species are attributed to functional groups according to which attributes they possess in relation to life form, woodiness, aerenchyma, N fixation, and an additional standalone type of bare peat. Note that not all life forms shown here were included in our functional groups but they are included for completeness.

Functional trait (relationship to CH$_4$ flux)	Code	Definition
Life Form (disturbance/decomposition/water table)	Ch	Chamaephyte [V]
	Gb	Bulbous geophyte [V]
	Gn	Non-bulbous geophyte (rhizome, corm or tuber) [V]
	hc	Hemicryptophyte [V]
	Hy	Perennial hydrophyte (perennial water plant) [V]
	Hz	Annual hydrophyte (aquatic therophyte) [V]
	Ph	Mega-, meso- and microphanerophyte [V]
	Pn	Nanophanerophyte [V]
	Th	Therophyte (annual land plant) [V]
	Holl	Plants (mainly Sphagnum and other) that are associated with Hollows [NV]
	Hum	Plants (mainly Sphagnum and other bryophytes) that are associated with Hummocks
	Lawn	Plants (mainly Sphagnum and other bryophytes) that are associated with Lawns or Mats [NV]
	Loo	Plants (mainly Sphagnum and other bryophytes) that are associated with Loose Hummocks [NV]
	Pool	Plants found mainly in Pools [NV]
	Ac	Aquatic colonial (formless loose colonies) [NV]
	At	Aquatic trailing (attached to substrate) [NV]
	Cu	Cushion (dome-shaped colonies) [NV]
	De	Dendroid (with stolons and erect shoots) [NV]
	Fa	Fan (branches in plane on vertical substrate) [NV]
	Le	Lemnoid (floating on the water) [NV]
	Mr	Mat, rough (creeping, lateral branches erect) [NV]
	Ms	Mat, smooth (creeping, branches lying flat) [NV]
	Mt	Mat, thalloid (creeping, thalli forming a layer) [NV]
	Sc	Solitary creeping (creeping solitary shoots) [NV]
	St	Solitary thalloid (rosette forming patch not mat) [NV]
	Tf	Turf (vertical stems with little or no branching) [NV]
	Thread	Thread (solitary thread-like creeping stems) [NV]
	Tp	Turf, protonemal (persistent protonema) [NV]
	Ts	Turf, scattered (scattered vertical shoots) [NV]
	Tuft	Tuft (loose cushions, not dome-shaped) [NV]
	We	Weft (intertwining branched layers) [NV]
Woodiness (decomposition substrate)	h	Herbaceous [V & NV]
	sw	Semi-woody [V]
	w	Woody [V]
Aerenchymatous (CH$_4$ emission)	A	Plants possessing aerechymatous tissue in the roots [V]
	PA	Plants possessing aerenchymatous tissue and have been shown to have increased methane emission or pressurised flow [V]
	a	Plants assumed to posses aerechymatous tissue in the roots [V]
N Fixation (CH$_4$ emission/root exudation)	Rhi	Rhizobia N fixing [V]
	Act	Actinorhizal N fixing [V]
	Cy	Known relationship with N fixing Cyanobacteria [NV]
Bare peat (decomposition)	Bare peat	No above ground vegetation present

Table S2: Species functional group classification from datasets used in this analysis.

Each study is coded as follows: 1-This study; 2 - Bubier et al. (1995); 3 - Dias et al.

(2010). Codes for Figure 1 are shown for this study only.

Plant Type	Species	Author	Functional Groups	Fig 1 code	Study
Vascular	*Agrostis canina*	L.	hch		1
	Agrostis stolonifera	L.	hch		3
	Alopecurus pratensis	L.	hcha		3
	Anthoxanthum odoratum	L.	hch		3
	Bellis perennis	L.	hch		3
	Calluna vulgaris	(L.) Hull	Chw	Cal vulg	1
	Caltha palustris	L.	hchA		3
	Cardamine pratensis	L.	hcha		3
	Carex acuta	L.	hchPA		3
	Carex cuprina	(I. Sándor ex Heuff.) Nendtv. ex A. Kern.	hchPA		3
	Carex echinata	Murray	hchPA		1
	Carex nigra	L.	hchPA		1
	Carex panicea	L.	hchPA		1+3
	Cerastium fontanum	Baumg.	hch		3
	Cirsium palustre	(L.) Scop.	hcha		3
	Deschampsia flexuosa	(L.) Trin.	hch		1
	Drosera anglica	Huds.	hcha		1
	Drosera rotundifolia	L.	hcha		1+3
	Dryopteris carthusiana	(Vill.) H.P. Fuchs	hchA		3
	Dryopteris cristata	(L.) A. Gray	hchA		3
	Eleocharis palustris	(L.) Roem. & Schult.	hchPA		3
	Empetrum nigrum	L.	Chw		1+3
	Erica tetralix	L.	Chwa	Eric tet	1+3
	Eriophorum angustifolium	Honck.	hchPA	Erio ang	1+3
	Eriophorum vaginatum	L.	hchA	Erio vag	1
	Festuca pratensis	Huds.	hcha		3
	Festuca rubra	L.	hch		3
	Festuca ovina	L.	hch		1
	Galium saxatile	L.	hch		1
	Galium palustre	L.	hcha		3
	Glechoma hederacea	L.	hch		3
	Glyceria fluitans	(L.) R. Br.	hcha		3
	Glyceria maxima	(Hartm.) Holmb.	hcha		3
	Holcus lanatus	L.	hch		3
	Huperzia selago	(L.) Bernh. ex Schrank & Mart.	Chsw		1
	Hydrocotyle vulgaris	L.	hchPA		3
	Juncus acutiflorus	Ehrh.	hchA		3
	Juncus effusus	L.	hchPA	Junc eff	3

Plant Type	Species	Author	Functional Groups	Fig 1 code	Study
Vascular	*Juncus squarrosus*	L.	hchA		1
	Leontodon autumnalis	L.	hch		3
	Lolium perenne	L.	hch		3
	Lonicera periclymenum	L.	hch		3
	Lotus uliginosus	Hoffman	hchA		3
	Molinia caerulea	(L.) Moench	hchA		1+3
	Myrica gale	L.	PnwAAct		1
	Nardus stricta	L.	hch		1
	Narthecium ossifragum	(L.) Huds.	hcha	Nar ossi	1
	Pedicularis palustris	L.	hchA		3
	Persicaria maculosa	Gray	hch		3
	Phragmites australis	(Cav.) Trin. ex Steud.	hchPA		3
	Plantago lanceolata	L.	hch		3
	Poa pratensis	L.	hcha		3
	Poa trivialis	L.	hcha		3
	Polygala serpyllifolia	Hose	Chh		1
	Potentilla anserina	L.	hch		3
	Potentilla erecta	(L.) Raeusch.	hch		1
	Ranunculus acris	L.	hch		3
	Ranunculus repens	L.	hch		3
	Rhinanthus angustifolius	C.C. Gmel.	hch		3
	Rubus chamaemorus	L.	hcha		1
	Rubus sp.	N/A	Pnw		3
	Rumex acetosa	L.	hch		3
	Taraxacum officinale	F.H. Wigg.	hch		3
	Trichophorum cespitosum	(L.) Hartm.	hchA	Tri cesp	1
	Trifolium repens	L.	hch		3
	Vaccinium myrtillus	L.	Chw		1
	Vaccinium oxycoccos	L.	Chwa		1
	Vaccinium vitis-idaea	L.	Chw		1+3
Non Vascular	Algae	N/A	Msh		1
	Aulacomnium palustre	(Hedw.) Schwägr.	Tfh		1+2
	Calliergon giganteum	(Schimp.) Kindb.	Tfh		2
	Calliergon stramineum	(Dicks. ex Brid.) Kindb.	Weh		2
	Calypogeia meylanii	H. Buch	Msh		2
	Calypogeia muelleriana	(Schiffner) K. Müller	Msh		1
	Campylium stellatum	(Hedw.) C.E.O. Jensen	Weh		2
	Campylopus atrovirens	De Not.	Tufth		1
	Cephalozia bicuspidata	(L.) Dumort.	Msh		1
	Cephalozia sp.	N/A	Msh		2
	Cinclidium stygium	Sw.	Tfh		2
	Cladonia arbuscula	(Wallr.) Hale & W.L.Culb.	Weh		1
	Cladonia bellidiflora	(Ach.) Schaerer	Tfh		1
	Cladonia chlorophaea	(Flörke *ex* Sommerf.) Sprengel	Tfh	Clad port	1

Plant Type	Species	Author	Functional Groups	Fig 1 code	Study
Non Vascular	*Cladonia portentosa*	(Dufour) Coem.	Weh		1
	Cladonia uncialis	(L.) Weber *ex* F.H.Wigg.	Weh		1
	Cladopodiella fluitans	(Nees) Jörg.	Weh		2
	Cratoneuron filicinum	(Hedw.) Spruce	Weh		2
	Dicranum polysetum	Sw.	Tufth		2
	Dicranum scoparium	Hedw.	Tufth		1
	Dicranum undulatum	Schrad. ex Brid.	Tufth		2
	Diplophyllum albicans	(L.) Dumort.	Msh		1
	Drepanocladus aduncus	(Hedw.) Warnst.	Weh		2
	Hypnum jutlandicum	Holmen & Warncke	Msh	Hypn jut	1
	Hylocomium splendens	(Hedw.) Schimp.	Msh		1
	Hypogymnia physodes	(L.) Nyl.	Mth		1
	Limprichtia revolvens	(Sw.) Loeske	Weh		2
	Loeskhypnum badium	(Hartm.) Paul	Weh		2
	Lophocolea bidentata	(L.) Dumort.	Weh		1
	Lophozia sp	N/A	Msh		2
	Meesia longiseta	Hedw.	Tfh		2
	Moerckia hibernica	(Hook.) Gottsche	Mth		2
	Mylia anomala	(Hook.) Gray	Msh		2
	Mylia taylorii	(Hook.) Gray	Tufth		1
	Odontoschisma sphagni	(Dicks.) Dumort.	Msh		1
	Oncophorus wahlenbergii	Brid.	Tfh		2
	Paludella squarrosa	(Hedw.) Brid.	Tfh		2
	Plagiomnium ellipticum	(Brid.) T.J. Kop.	Tfh		2
	Plagiothecium undulatum	(Hedw.) Schimp.	Msh		1
	Pleurozium schreberi	(Willd. ex Brid.) Mitt.	Weh	Pleu sch	1+2
	Pohlia nutans	(Hedw.) Lindb.	Tufth		2
	Polytrichum commune	Hedw.	Tfh	Poly com	1+3
	Polytrichum strictum	Menzies ex Brid.	Tfh		2
	Pseudoscleropodium purum	(Hedw.) M. Fleisch.	Weh		1
	Ptilidium ciliare	(L.) Hampe	Weh		1
	Ptilidium pulcherrimum	(Weber) Hampe	Weh		2
	Ptilium crista-castrensis	(Hedw.) De Not.	Weh		2
	Racomitrium lanuginosum	(Hedw.) Brid.	Tfh	Raco lan	1
	Rhytidiadelphus loreus	(Hedw.) Warnst.	Weh		1
	Rhytidiadelphus squarrosus	(Hedw.) Warnst.	Weh		1+3
	Sanionia uncinata	(Hedw.) Loeske	Weh		2
	Scapania sp.	N/A	Weh		2
	Scorpidium scorpioides	(Hedw.) Limpr.	Weh		2
	Sphagnum angustifolium	(Warnst.) C.E.O. Jensen	HumhCya		2
	Sphagnum annulatum	Warnst.	LawnhCya		2
	Sphagnum capillifolium	(Ehrh.) Hedw.	HumhCy	Spha cap	1+2
	Sphagnum centrale	C.E.O. Jensen	LoohCya		2
	Sphagnum compactum	Lam. & DC.	LoohCya		2

Plant Type	Species	Author	Functional Groups	Fig 1 code	Study
Non Vascular	*Sphagnum cuspidatum*	Ehrh. ex Hoffm.	PoolhCy		1
	Sphagnum fallax	H. Klinggr.	LoohCy	Spha fal	1+2+3
	Sphagnum flexuosum	Dozy & Molk.	LoohCya		2
	Sphagnum fuscum	(Schimp.) H. Klinggr.	HumhCya		2
	Sphagnum girgensohnii	Russow	LoohCya		1
	Sphagnum lindbergii	Schimp.	LoohCya		2
	Sphagnum magellanicum	Brid.	LawnhCy		1+2
	Sphagnum majus	(Russow) C.E.O. Jensen	LoohCya		2
	Sphagnum palustre	L.	LoohCya	Spha pal	3
	Sphagnum papillosum	Lindb.	LawnhCy	Spha pap	1
	Sphagnum platyphyllum	(Lindb.) Warnst.	LoohCya		2
	Sphagnum pulchrum	(Lindb.) Warnst.	LoohCya		2
	Sphagnum russowii	Warnst.	HumhCya		2
	Sphagnum subnitens	Russow & Warnst.	HumhCya		2
	Sphagnum tenellum	(Brid.) Brid.	LoohCy		1
	Sphagnum tenerum	Sull. & Lesq. ex Sull.	HumhCya		2
	Sphagnum warnstorfii	Roll	LoohCya		2
	Tomenthypnum falcifolium	Ren. ex Nich.	Tfh		2
	Tomenthypnum nitens	(Hedw.) Loeske	Tfh		2
	Warnstorfia exannulata	(Schimp.) Loeske	Weh		2
N/A	Bare Peat	N/A	Bare Peat	Bare peat	1

Figure S1: Predicted CH_4 flux using a weighted average of species and functional group abundance against observed mean CH_4 flux (Log) for National Vegetation Communities for the UK. Plots were classified according to the NVC community they best fitted by a weighted species match and then an NVC community mean for observed and WA flux estimates were calculated. The blue line indicates a 1:1 fit (species r^2 (adj) - 0.46; functional group r^2 (adj) - 0.85). Bare peat is a not an NVC community but indicates those plots where bare peat dominates and NVC community was ambiguous. NVC communities are: M1 - *Sphagnum auriculatum* bog pools; M2 - *Sphagnum cuspidatum/recurvum* bog pools; M6 - *Carex echinata, Sphagnum auriculatum /recurvum* mire; M15 - *Scirpus cespitosus, Erica tetralix* wet heath; M16 - *Erica tetralix, Sphagnum compactum* wet heath; M17 - *Scirpus cespitosus, Eriophorum vaginatum* mire; M18 - *Erica tetralix, Sphagnum papillosum* mire.