RECIPE meeting in Scheyern, microbial ecology group minutes

Points that were discussed:

FITR and sugar data
Fatima & Rebekka will work together on these. Data will be expressed both in reference to dry weight and to volume.

Environmental variables
Edward will compile environmental data for all samples. Please send the data!
We should be able to compile the following: water table, C/N totals, SON/SOC, soil pH (probably incomplete but see below), botanical composition, vegetation structure (we need to compare how this was determined in each country first)
Some material remains on which some analyses could be done, e.g. <1g left from FTIR in Scotland, but not for all, could be used for pH.

Numerical analyses
We will end up with very large data sets. How should we analyse this?
Question of site-specific vs stage-specific "species"
We should focus on similarities (there may be less than differences)
A preliminary analysis of all data should allow to identifying those variables that explain significantly the largest part of the variance. Then based on the first results, we could look at subsets of the data in more detail (e.g. sites or stages).
Edward will work with Rebekka on the data (Canoco etc.)

TRFLP
A open question here: does a program exist that allows to chose the best possible enzyme for TRFLP?
Rebekka will search for this.

Dating of the age of the old peat (i.e. not the date of the onset of regeneration, the age of the old peat representing the cutover surface).
Fatima will find out what prices she can get vis CNRS for ^{14}C dates (n.b. conventional, not AMS).
^{210}Pb dating will be performed at Chaux-d'Abel by Philippe Steinmann.
Could this also be done at other sites?
Rebekka will check whether Calluna remains can be used for dendrochronological determinations.

WPI surface samples
Question from Daniel Gilbert: should we analyse the spring samples?

> Useful for micro-organisms (whole community, inverted microscopy).
> … But we don't have the manpower to do this plus WPII (plus the extra experiment where sphagnum mosses were placed on peat of different ages).

Proposed priority order:

1. Finish fall samples (done by now?)

2. Count samples from extra experiment in FR (3 cores x 3 levels=peat ages x 2 sampling = 18 samples, 9 if only 1 sampling is counted.
3. Spring samples from SCO + one of the Jura sites (FR or CH)
4. Spring samples from the second Jura site.

WPII sampling

Proposed analysis strategy

<u>For fungi, CLPP, microbial biomass, C tot & N tot (Orléans), soluble C & N (Rennes)</u>
All sites (4), all treatments (4 ; 5 in Fin), all DWT (3), sampling depths (0-5 cm, 12.5-17.5 cm, 32.5-37.5 cm) –
EM: n.b. we discussed about 2 depth to be analyzed, but three sampled. It is unclear to my what strategy we finally adopted. Neither am I (RA) – I think this was left open at the time, to be decided on the basis of preliminary data from groups who have the capacity to analyse everything.

<u>For Amino-acids + sugars (hopefully), PLFA:</u>
2 sites (144 samples)

<u>For microbial turnover, C mineralization rate, C turnover:</u>
All sites, but 1 depth (144 samples).

<u>Microbial communities, testate amoebae, DNA fingerprinting for Euglyphida:</u>
All sites, but only Sphagnum mosses (= 36 samples, 9 of which in priority for microbial communities, FISH – bacteria.
E.M. n.b. which site will this be?

<u>Analyses that will NOT be done for WPII:</u>
FTIR
Rotifers, or perhaps at a later stage
Photonic microscopy
Cry or SEM

In all cases we start with 144 and do more if possible.

E.M. n.b. Which sites?
In Scotland Sphagnum was replaced and Eriophorum is dead in the highest water table experiments (it was ok in the other two WT).
Should the priority be for FR and FIN?

Compiled by E. Mitchell,
additions/corrections by: RA