Hur spår av arvsmassan kan ge insikt i miljöns tillstånd

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En serie på tre baser etter hverandre utgjør et kodon.

Et kodon er som et «ord» i «setningen» som uttrykker et gen.

Sukkerfosfatstreng

Nitrogenbase
Microbial cells
Skin cells
other tissue
Free DNA
saliva and buccal cells
Water temperature (°C)

Prob of observation

Log Odds Ratio eDNA vs trad.

Eiler et al. Nat Sci Rep 2018
Figure 1. Overview and detailed map of the Danube river catchment showing all sampling sites during the Joint Danube Survey 2; red dots indicate sampling points in the midstream of the Danube River; blue dots represent sampling points in tributaries before merging in the main river. Country abbreviations and large cities are written in black. The map was created using Quantum GIS (Quantum GIS Development Team, 2011).

Enterococci \[\log(\text{MPN}+1/100\text{ ml})\]

E. coli \[\log(\text{MPN}+1/100\text{ ml})\]

Longitudinal development of Enterococci and E. coli was investigated in 23 sites along the Danube River (USA; Staley et al., 1999; Zwart et al., 2002; Cottrell et al., 2005; Winter et al., 2008; Mueller-Spitz et al., 2011). The dominance of Cyanobacteria in the Amazon river (Ghai et al., 2009; Newton et al., 2010; Read et al., 2011; Liu et al., 2012) and the River Thames (UK; Read et al., 2002; Cottrell et al., 2005; Winter et al., 2008; Mueller-Spitz et al., 2011) indicates that the bacterial communities in rivers (Crump et al., 2004; Sommerwerk et al., 2010) were also confirmed in three recent high-throughput sequencing studies on the Upper Mississippi River (USA; Staley et al., 2013), the Yenisei River (RUS; Zvereva et al., 2014) and the River Thames (UK; Read et al., 2002; Cottrell et al., 2005; Winter et al., 2008; Mueller-Spitz et al., 2011). In particular, bacteria affiliated with the phyla Verrucomicrobia and Actinobacteria were found to dominate the bacterial communities from that of other freshwater lineages acI of the phylum Proteobacteria (particularly Bacteroidetes, Actinobacteria and Proteobacteria) were found to dominate the bacterioplankton in riverine ecosystems or the variability of its diversity along entire river networks.

Based on our results, we propose that the bacterioplankton communities in the midstream of such a large river develop slowly and particle-associated bacterioplankton communities are more specific to a catchment area of 801 000 km² (Fig. 1). The Danube River is 2780 km in length and drains a catchment area of 801 000 km², and the tributaries were sampled and the right river side (small squares). Colours depict the faecal pollution levels according to the river kilometer. Country abbreviations and large cities are written in black. The map was created using Quantum GIS (Quantum GIS Development Team, 2011).

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Eurasian perch (*Perca fluviatilis*) microbiome

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