Identification of metabolically active microbial communities in sediments by two independent RNA-based *in vivo* labeling techniques

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**Methods & Results**

**Experimental approach SIP versus DIG-labeling**

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<th>Sediment incubations</th>
<th>RNA extraction</th>
<th>Separation of labeled and unlabeled RNA</th>
<th>Transcription of RNA into cDNA by RT-PCR</th>
<th>Analysis of active microbial community by targeting the 16S rRNA</th>
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**Community structure of metabolically active microorganisms**

- DGGE analysis of *de novo* synthesized RNA indicated high similarities between banding patterns of both approaches (Fig. 4)
- Distinct bacterial communities were identified for the oxic and anoxic layers
- Unlabeled RNA targets showed inactive background community

**Labeling efficiency of the DIG method**

- Up to 15% of the total RNA was labeled by the DIG method
- Increasing numbers of 16S rRNA targets indicated high activity
- Higher increase of targets in anoxic than in oxic incubations

**Conclusions**

- DIG-labeling was shown to be an appropriate method for the identification of metabolically active bacteria in sediments
- Advantages of the DIG method over SIP:
  - Short incubation times
  - Universal incorporation of the label into RNA independent from the investigated substrate

**Outlook**

- Detailed data analysis of active microbial community with pyrosequencing
- Application of the DIG method with various substrates and sedimentary settings