

Using dPCR and eDNA to delineate the spawning period of three commercially important fish species

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Form of presentation: Oral

Abstract:

Introduction:

*Catching fish during their spawning season can be detrimental for the fish population. Nowadays, the spawning is delineated based on landing data, using discrete data points in time and space. However, the ease of environmental DNA (eDNA) collection may allow for an improved delineation of the spawning period and area. This study investigates whether eDNA quantification with dPCR can delineate the spawning period of plaice (*Pleuronectes platessa*), sole (*Solea solea*) and whiting (*Merlangius merlangus*). We hypothesized that eDNA concentrations will increase when the fish release gametes into the water column.*

Materials and Methods:

Water samples were collected monthly across nine coastal locations in the BPNS from 2021 - 2023. Sterivex filters were used to collect eDNA, and an exogenous internal positive control (IPC) was added during eDNA extraction. All measurements with IPC-concentrations below 0.5 copies/ μ l were excluded. Moreover, if the number of copies of the sample was below the limit of detection, it was reduced to 0 copies/ μ l.

Results:

For sole, with known spawning grounds in the shallow coastal waters of the BPNS, elevated eDNA-concentrations were detected within the predicted spawning period. For plaice and whiting, which prefer deeper waters for spawning, no link was detected between the elevated eDNA concentration and the predicted spawning period. However, for whiting the elevated eDNA concentration detected in autumn could be linked to high abundances of adults observed in beam trawl surveys.

Conclusion:

The use of eDNA to delineate the spawning period of fish has potential but further research is needed to strengthen the conclusions.

Word count: 247 words (max. 250)

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