FUNGI OF THE BULL ISLAND SALTMARSH SYSTEM: CULTURAL AND MOLECULAR DIVERSITY

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ABSTRACT

Fungi are one of the main biodegradatory groups in saltmarsh ecosystems. Their importance lies in their ability to break down and utilise recalcitrant biomolecules, such as lignocellulose, from substrates such as higher plants and algae which are the main primary producers of saltmarsh ecosystems. The following study was undertaken to systematically determine the diversity and distribution of fungi on a European temperate salt marsh.

The salt marsh studied was situated at the north lagoon of Bull Island, Co. Dublin. This marsh is divided into three vegetational zones, termed the upper, middle and lower marshes. Each zone possesses a characteristic flora, and is influenced to a different extent by tidal inundation. The lower marsh (mud flats) typically supports *Salicornia* spp., together with *Spartina anglica* and is most affected by tidal inundation and low soil redox potentials. On the middle marsh *Puccinellia maritima, Halimione portulacoides, Limonium* spp., *Spartina anglica,* and *Salicornia* spp. dominate, with grasses and *Juncus* spp becoming more frequent on the upper marsh. The marsh also becomes progressively drier, being flooded more infrequently by the tide.

Fungal diversity was studied using two approaches. A more conventional approach involved isolation and culturing fungi from a range of substrates taken across the salt marsh at different times. Pieces of plant tissue were systematically collected from Bull Island, surface sterilised and placed on agar plates to stimulate fungal growth. Fungi were isolated as pure cultures prior to identification on the basis of their sporulating structures. Ninety-four morphologically different strains were isolated from across the saltmarsh, of which 58 could be positively identified.

Conventional diversity approaches do not give information about the non-culturable component of fungal diversity. To give a more complete view of fungal diversity at Bull Island, a molecular approach was employed, using the 18S rRNA genes as fungal biomarkers. Using PCR, a population of amplicons can be generated which have specificity to fungal members of the saltmarsh community. Fungal DNA was successfully extracted and PCR-amplified from saltmarsh plant substrates. Two methods were used

to analyse and separate mixed amplicon populations; denaturing gradient gel electrophoresis, and terminal restriction fragment length analysis. Both methods gave a fungal community fingerprint of a range of individual substrates harvested from the marsh.