Getting Inspiration from Malt Whisky

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Introduction

Miniature inverted-repeat transposable elements (MITEs) are a family of small mobile genetic elements. They are thought to be deletion-derivatives of DNA transposons, incapable of transposition unless the ancestral DNA transposon is also present in the genome to provide the enzymes needed for mobility. MITEs were discovered in 1992 in maize by Susan Wessler and Thomas Bureau, but are now being identified in many different organisms.

Looking for new MITEs

By using a combination of bioinformatics tools and molecular genetic techniques five new families of MITEs have been identified in barley.

Stretches of DNA sequence were isolated that showed some of the characteristics of MITEs i.e. short length (<800bp), terminal inverted-repeats, and target site duplication (fig 1). From nearly a thousand candidates I then looked for related groups sharing significant sequence homology between the possible MITEs, since one of the characteristics is high copy number.

Primers were designed that would amplify individual loci in 48 different barley accessions to determine any insertional polymorphism (fig 2) which would indicate mobility or transposition. Five of the candidate MITEs fulfilled all these criteria. To analyse these five new families I have amplified many members of each new MITE family, sub-cloned and sequenced them, and aligned them using Clustalw (fig3). For one of these families it has become apparent that there are long and short versions of the element (fig 4).

Fig 1 Typical MITE Structure

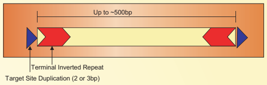


Fig 2 Islay Novel MITE

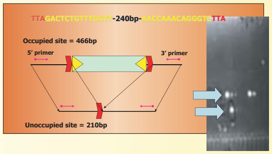
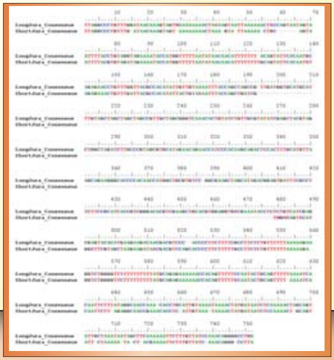


Fig 3

Fig 4



Naming new MITEs

In finding five new MITE families there is a certain responsibility associated with naming them. There has been a trend to have some fun with the naming of new MITEs e.g. *Vege* and *Mar* - MITEs in *Drosophila*; *Tourist* and *Stowaway* - MITEs found within genes or other MITEs in maize; *Snap*, *Crackle* and *Pop* - MITEs found in rice; *Bigfoot* - a MITE with a large footprint in *Medicago*. After much deliberation I decided to name my MITE families after Scottish Island malt whiskies. So far, I have *Talisker*, *Jura*, *Arran*, *Ardbeg*, and *Islay* but there is plenty of scope for many more discoveries. This naming system ties together the Scottish Crop Research Centre, the University of Dundee, the source plant - barley, and the feeling of movement within a landscape or transposition within the genome.

Future project aims

1) Copy number - use probe designed from consensus sequence against BAC library
2) Polymorphism level - determine evolutionary phylogeny of elements and their hosts by analysis of polymorphism
3) Genomic location preference - by sequencing flanking regions and identifying these
4) Potential for molecular markers - use the results of the above experiments to identify loci which will be useful as molecular markers

Further Reading

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