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Tiivistelmä Referat Abstract			
<p>The <i>Aspergillus niger</i> aggregate consists of asexually reproducing strains. The strains are incompatible with each other. However they are highly variable on the basis of morphological, ribosomal and mitochondrial RFLP data. The research question was to detect possible recombination, which would explain the high variability of the strains.</p> <p>There are two transposons in the <i>A. niger</i> aggregate. Transposons <i>Ant1</i> and <i>Tan1</i>. <i>Tan1</i> has also transposable element <i>Vader</i>, which is capable of transposing with a help of transposase of <i>Tan1</i>, at the end of its coding region. <i>Vader</i> itself is noncoding. These transposons were used to detect the possible recombination. The research question for these transposons was; do the transposons exist in the studied strains and is there horizontal transfer of the transposons.</p> <p>There were 25 strains from the <i>A. niger</i> aggregate from different origins. These strains were analysed already on the basis of ribosomal and mitochondrial RFLPs and a three different genomic gene data. The research was done by using PCR amplification, sequence analysis and southern hybridisation. The southern hybridisation failed. Also the results, in the case of <i>Tan1/Vader</i>, were not very informative. <i>Ant1</i> sequences were successfully PCR amplified and sequenced. Seven acquired sequences were analysed. They were aligned with the published <i>Ant1</i> sequence and the phylogenetic tree of the <i>Ant1</i> sequences was compared to the phylogenetic tree of a <i>pgalI</i> gene. In the alignment differences between basepair composition of the sequences were detected. A comparison between the phylogenetic trees of <i>Ant1</i> and <i>pgalII</i> indicated a strong difference in the structure of the phylogenetic trees.</p> <p>The result strongly suggests; there is horizontal transfer of <i>Ant1</i> transposons in the <i>A. niger</i> aggregate. Differences in the alignment showed that the structure of <i>Ant1</i> is not conserved. Changes in, most likely, functioning sequences were detected. Some of the changes were silent and some changed the coded amino acid sequence. The phylogenetic tree comparison revealed identical <i>Ant1</i> sequences located far from each other in the <i>pgalI</i> gene phylogenetic tree. A vertical transfer of transposon combined with a drift could have explained the patchy distribution of <i>Ant1</i>, but only if the <i>Ant1</i> transposon would have been conservative. However, horizontal transfer of the <i>Ant1</i> transposon is the most probable explanation on the basis of the collected data.</p> <p>The final conclusion of horizontal transfer can be drawn only if additional information about the copy number can be obtained through southern blotting. If transposons can exist only in low copy numbers in one strain, the vertical transfer theory becomes more questionable than it already is.</p>			
Avainsanat Nyckelord Keywords			
transposons, transposable elements, <i>Ant1</i> , <i>Tan1</i> , <i>Vader</i> , incompatibility, horizontal transfer, <i>ASPERGILLUS NIGER</i>			
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