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## Transposition of autonomous and engineered *impala* transposons in *Fusarium oxysporum* and a related species

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Due to a technical error part C of Fig. 4 was omitted. The whole figure is printed below.

wt CCTATCCCAT ACTCT  
 niaD160 CCTATCCCAT**Acagt**..imp160..actg**TACTCT**

#### A *Fusarium oxysporum*

##### Fo5nia13 + imp160

n=5 CCTATCCCAT**TA**cag.....**TA**CTCT  
 n=1 CCTATCCC.....**TA**CTCT  
 n=1 CCTATCCCAT**TA**ca.....**TA**CTCT

##### Fo115nia50 + imp160

n=6 CCTATCCCAT**TA**cag.....**TA**CTCT  
 n=5 CCTATCCCAT.....ctg**TA**CTCT  
 n=4 CCTATCCCAT**TA**ca.....**TA**CTCT

##### Fo150nia9 + imp160::hph

n=6 CCTATCCCAT**TA**cag.....**TA**CTCT  
 n=1 CCTATCCCAT**TA**ca.....**TA**CTCT

##### Fo5nia13 + imp160::hph + impE, impC or impD

n=2 CCTATCCCAT**TA**cag.....**TA**CTCT  
 n=3 CCTATCCCAT.....ctg**TA**CTCT  
 n=1 CCTATCCCAT**TA**c.....**TA**CTCT

#### B *Fusarium moniliforme*

n=4 CCTATCCCAT**TA**cag.....**TA**CTCT  
 n=1 CCTATCCCA.....**TA**CTCT  
 n=1 CCTATCCCAT**TA**c.....**TA**CTCT

#### C Reinsertion sites

FO5 TGTCCATCT**TA**cag..imp..ctg**TA**TACGTGCG  
 FOL15 GTTGATAG**TA**cag..imp..ctg**TA**TATCTGGCA

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**Fig. 4A–C** Structure of *impala* excision sites in *F. oxysporum* revertants (**A**) and in *F. moniliforme* revertants (**B**). Sequences of the wild-type gene (wt) and the original insertion mutant (*niaD160*) are given at the top. n = number of revertants with the indicated sequence. **Bold capitals**: duplicated target site TA. **Bold lower cases**: *impala* ends. Nucleotide insertion, relative to the wild type, are *framed*. **C**. Sequences of two reinsertion sites. *impala* sequences are in italics and the duplicated target sites are in bold