Figure 3: Blast result analysis of transposable elements (TE5P and TE3P) flanking the *Wolbachia* gene region in chromosome 3R. A) TEP5 B) TEP6.

A: Blast TEP5 comparison with *C. elegans* transposon

```
==> GI|17565388|REF|NP_503526.1| PREDICTED CDS, REVERSE TRANSCRIPTASE
            FAMILY MEMBER (5C378) (Handa and Guidotti, 1996)
          Length = 417

 Score =  109 bits (272), Expect = 1e-024
 Identities = 86/327 (26%), Positives = 151/327 (46%), Gaps = 22/327 (6%)
 Frame = +1

Query: 37   TKGLRQGDGLACLLFNLALERAIRD-SRVETTGT-----------IFYKSTQILACADDI 180
            TKG+RQGD ++  LF+  LE   R  S +E  G            +  K+   L  ADDI
Sbjct: 96   TKGVRQGDPISPNLFSACLEHVFRKLSCIEFKGEAEDYNTIPGMRVNGKNLTNLRFADDI 155

Query: 181  DIIGLRLSYVAEAYQGIEQEAESLGLQINEAKSKLMVATSAGLPINNQNLRRRDVQIGER 360
             +I    +  ++  Q + Q+   +GL+IN  K+K++          N+      V  G
Sbjct: 156  VLIANHPNTASKMLQELVQKCSEVGLEINTGKTKVL---------RNRFADPSKVYFGNP 206

Query: 361  T----FEVVPQFTYLGSKVSNDNSMEAELRARMLAANRSFYSLKKQFTSKNLLRRTKLGL 528
            +     + V ++ YLG +++  N++  E+  R  AA  +F  +K   T     ++ +  L
Sbjct: 207  SSTTQLDDVDEYIYLGRQINAQNNLMPEIHRRRRAAWAAFNGIKNT-TDSITDKKIRANL 265

Query: 529  YSTYIVPVLTYASETWTLFKSDKTLLAAFERKMLRRILGPVCVEGQWRSRYNDELYEMYG 708
            + + ++P LTY SE WT  K+    +      + RR++G    + + R  + +++ +M
Sbjct: 266  FDSIVLPALTYGSEAWTFTKALSERVRITHASLERRLVGITLTQQRERDLHREDIRKMSL 325

Query: 709  DLTVVQRIKLARLRWAGHVVRMETDDPARKVFLGRPQGQRRR-GRPKLRWQDGVE----- 870
                +  +K  +L WAGHV R +       +   RP G +R  GRP +RW D +
Sbjct: 326  VRDPLNFVKKRKLGWAGHVARRKDGRWTTLMTEWRPYGWKRPVGRPPMRWTDSLRKEITT 385

Query: 871  ASAINAGITDWQTKARDRERFRTLLKQ 951
              A    IT W T A+DR+ +  ++++
Sbjct: 386  RDADGEVITPWSTIAKDRKEWLAVIRR 412
```

3B: Blast TEP3 comparison with TF2 Transposable element of *S. pombae*

```
==> GI|19075455|REF|NP_587955.1| TF2 TYPE TRANSPOSABLE ELEMENT
            (Tatusov et al., 2003)
          Length = 1333

 Score =  194 bits (494), Expect = 4e-050
 Identities = 149/556 (26%), Positives = 269/556 (48%), Gaps = 29/556 (5%)
 Frame = +1

Query: 16   EAFETLREKLTQSPILAIFDPKKETELHCDASSFGFGAVLLQKQEDNKLHPVAYFSKTTS 195
            +A E +++ L   P+L  FD  K+  L  DAS    GAVL QK +D+K +PV Y+S   S
Sbjct: 684  QAIENIKQCLVSPPVLRHFDFSKKILLETDASDVAVGAVLSQKHDDDKYYPVGYYSAKMS 743

Query: 196  KEEAKLHSYELETLSVIYALKRFHVYVHGL--PLKIFTDCNSLVETLKNRN--ASAKIAR 363
            K +      + E L++I +LK +  Y+     P KI TD  +L+  + N +   + ++AR
Sbjct: 744  KAQLNYSVSDKEMLAIIKSLKHWRHYLESTIEPFKILTDHRNLIGRITNESEPENKRLAR 803

Query: 364  WSLFLENYDYTIHYRSGTSMAHVDALSR----TEAVGAIS-DLDLDFQLQIAQSQD---- 516
            W LFL+++++ I+YR G++    DALSR    TE +   S D  ++F  QI+ + D
Sbjct: 804  WQLFLQDFNFEINYRPGSANHIADALSRIVDETEPIPKDSEDNSINFVNQISITDDFKNQ 863

Query: 517  ---------PLINTLRQKLEAGSVQGFILQDGLVYRQSSTNHLQLYVPREMVDNIIRHNH 669
                      L+N L  + +    +   L+DGL+   +S + + L    ++   II+  H
Sbjct: 864  VVTEYTNDTKLLNLLNNE-DKRVEENIQLKDGLLI--NSKDQILLPNDTQLTRTIIKKYH 920

Query: 670  E--KIGHLAISKTCQTISQHYWFPHMKPRVENFIKNCLKCIVYSAPPRTNNRNMYSIPKT 843
            E  K+ H  I      I + + +  ++ +++ +++NC  C +  +        +  IP +
Sbjct: 921  EEGKLIHPGIELLTNIILRRFTWKGIRKQIQEYVQNCHTCQINKSRNHKPYGPLQPIPPS 980
```

```
Query: 844  PVPFDTLHIDHLGPLPNITSRKKYILVVIDAFTKFTKLYATATTNTNEVCEAL--TQYMS 1017
             P+++L +D +  LP  +S    + VV+D F+K   L     + T E    +   + ++
Sbjct: 981  ERPWESLSMDFITALPE-SSGYNALFVVVDRFSKMAILVPCTKSITAEQTARMFDQRVIA 1039

Query: 1018 YYSRPKRIISDRATCFTSTAFKEFVDSNDITHVLNATGSPQANGQVERVNRVLRPILSKL 1197
            Y+  PK II+D    FTS  +K+F    +     +    PQ +GQ ER N+ +  +L  +
Sbjct: 1040 YFGNPKEIIADNDHIFTSQTWKDFAHKYNFVMKFSLPYRPQTDGQTERTNQTVEKLLRCV 1099

Query: 1198 CNSSDHSDWSSHLRSAEHALNNTVHSSTNFLPSILLFGIEQRGQILDELHEFLNDKHVTT 1377
            C S+  + W  H+   + + NN +HS+T   P  ++         L EL  F +DK
Sbjct: 1100 C-STHPNTWVDHISLVQQSYNNAIHSATQMTPFEIVHRYSPALSPL-ELPSF-SDKTDEN 1156

Query: 1378 NRDLNLLRSEALSNIEYSQYRNEQYVANRTKPAPSFSEGDLVAIKYTDS--TNANEKLVC 1551
            +++   +      ++  +  + ++Y   + +    F  GDLV +K T +   + + KL
Sbjct: 1157 SQETIQVFQTVKEHLNTNNIKMKKYFDMKIQEIEEFQPGDLVMVKRTKTGFLHKSNKLAP 1216

Query: 1552 KFRGP-YIVHKVLPHD 1596
             F GP Y++ K  P++
Sbjct: 1217 SFAGPFYVLQKSGPNN 1232
```