

Supplemental Data

Drosophila MUS312 and the Vertebrate Ortholog

BTBD12 Interact with DNA Structure-Specific

Endonucleases in DNA Repair and Recombination

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Figure S1. MUS312 is less conserved than MEI-9 or ERCC1.

This schematic illustrates conservation of amino acid sequence of *Drosophila melanogaster* MEI-9, ERCC1 and MUS312. Each bar represents the orthologous protein in two other *Drosophila* species, two more divergent arthropods (malaria mosquito and flour beetle), humans, and *S. cerevisiae*. Colored boxes indicate regions for which a significant match is found by BLASTP, using default parameters. Color indicates the percentage of residues in each region that score as similar or identical to the orthologous *Drosophila melanogaster* protein. Conservation is expected to be high for the C-terminal half of MEI-9, which contains the nuclease domain. ERCC1, however, is non-catalytic. Note that MUS312 is poorly conserved even in Arthropods. No regions of similarity are detected between MUS312 and Slx4.

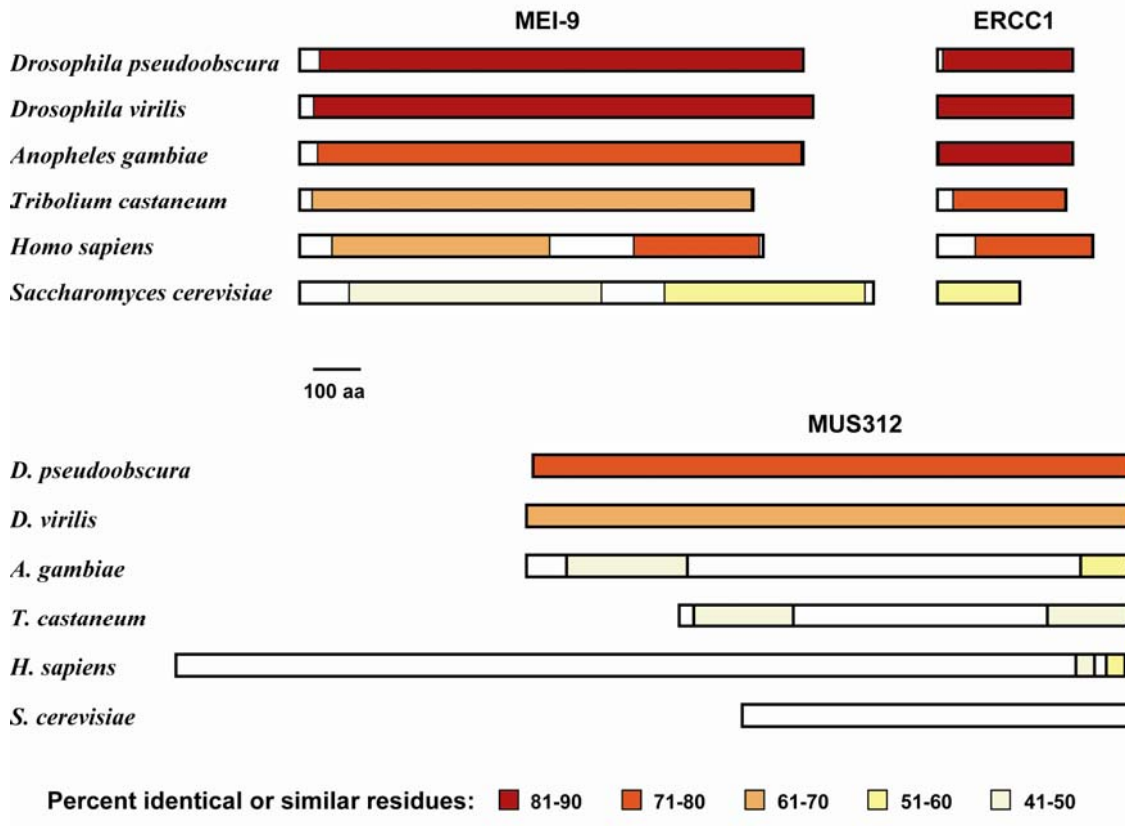


Figure S2. Conserved regions in MUS312, BTBD12, and BSP1.

(A) The BTB domain of BTBD12 from *Homo sapiens* (Hs), *Gallus gallus* (Gg) and *Xenopus laevis* (Xl) are aligned to similar regions in MUS312 from *Drosophila melanogaster* (Dm), *Drosophila erecta* (De), and *Drosophila grimshawi* (Dg) and BSP1 from *Cryptococcus neoformans* var. *neoformans* (Cnvn), *Cryptococcus neoformans* var. *gattii* (Cnvg), and *Cryptococcus gattii* (Cg).

(B) EVIL motifs are aligned from BTBD12 of *Homo sapiens* (Hs), *Mus musculus* (Mm), *Rattus norvegicus* (Rn), *Gallus gallus* (Gg), *Xenopus laevis* (Xl), MUS312 of *Drosophila melanogaster* (Dm), and BSP1 of *Cryptococcus gattii* (Cg).

A)

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HsBTBD12 : NNPHLSDVQFQTDG-GEVLYAH-KFVLYARCELLIQYV-----NNEGFSAVEDGVLTQR----- : 737
GqBTBD12 : NNPHLSDVQFQVDS-GEVLYAH-MFVLYARCEQAIQAV-----HSEGFVLEEDGNAQIRR----- : 624
XlBTBD12 : NNPHLSDAQLQTDG-GEVLSVH-MFVLYTRCELLVEAV-----HSEGFVWNEASTGRVRR----- :
DmMUS312 : QQPSTSNFLRNEQIFAEVTAQHCMADNFS--ADDIEMALAL-----SKSEF-----EKHGRLRLHDDDD-- : 159
DeMUS312 : QQPNTSNFLRNEQIFAEVTAQHCMADNFS--DDIEMALAL-----SKSEC-----EKQGRLRLHDDDD-- : 159
DqMUS312 : QQPSTSDFLRNEQLFAEVTAQHCIADNFS--NDIEMALAL-----SKSEA-----EKYGLRRLLEDTTQEE : 160
CnvnBSP1 : MPPRLSTRVSTSSSSSDEPVYLDCTPSFAPAEFRKPDASLPKATNSSNHESRSKA----- : 55
CnvgBSP1 : MPPRLSTPVSTSSSSSDEPVYLDCTPSFASAE LRRRDASLPKAMNSSNHESRSKA----- : 55
CgBSP1 : MPPRLSTRVSTSSS-DEPVNLDCRPSFCPPAIRRRNASTSSAKKPSNLKSRSEI----- : 54

HsBTBD12 : --VLLGDVSTEAARTFL-----HYLY-TADTG-----LPPGLSSELSSL--AARE-GVSELVHLCEQ : 788
GqBTBD12 : --VLLSDVTGEAARAFL-----RYLY-AADAD-----IPAEVVPQVGAL--AARE-GVRELMAKCEN : 675
XlBTBD12 : --LLNDVSAEAALCFE-----RFLY-SASIT-----IPMRCLTHVCEL--AARE-GVSSLIEICEH :
DmMUS312 : --AVV-DLLDDEE-KSTERIRHKL-QKYGFRTAAKEDYKSL--AVLPVVASKGRRGKWANKFTSLTLRNPVQVQ : 227
DeMUS312 : --AVV-DLLDDEE-QSTDRIRRKL-QKYGFRTAAKEDYKSL--AVLPVVAAGRRGKWANKFTALTLRNPVQVQ : 227
DqMUS312 : QEEVV-DLLDAQDDQSTENVRRKL-QKYGFRTAAKADYNMLTFASLP--GGKRGKRCWKANKETPLTLRNPVEQL : 231
CnvnBSP1 : --LVISDN-DDDEPEFIGPVLGNLAKYRFKEVSNLV--AEGKLSRPIKEMSRPSSKSNAKRKSVDVSEKPGAVSA : 125
CnvgBSP1 : --LVISDD-DDDEPEFIDSVWEGLAKYRFKEVSNV--AAGKLSRPTKEVSRPSSKSSAKRKSVDVSEKRSNAISA : 125
CgBSP1 : --VVISD--DDDEPEFIGPALGGLAKYWEKEIS-LP--AGGLSWETNEVSGQSYKSSAKRNSVDVSEKRDITISA : 122

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B)

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HsBTBD12 : EEDEVILLLLSD-EEL 1161
MmBTBD12 : KEDEVILLLLSD-EEL 966
RnBTBD12 : KEDEVILLLLSD-EEW 972
GqBTBD12 : KKGDVIVL-SSD-DEM 1069
XlBTBD12 : QEPGVILILSSD-EET
DrBTBD12 : KQVELIVL--SD-DSN 969
DmMUS312 : DENDAILL--SD-EEI 705
CgBSP1 : AQRE-VLVPASDSEE 396

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