

# Supplementary Materials: Identification of Pathogenic *Fusarium* spp. Causing Maize Ear Rot and Potential Mycotoxin Production in China

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AF212436.1_Fusar	TCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	42
AF212444.1_Fusar	TCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	42
AJ543588.1_Fusar	TCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	42
FG-010	GGACAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	62
FG-015	GACAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	61
FG-017	GTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	40
FG-019	CAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	59
FG-020	AAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	58
FG-029	AAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	58
FG-030	AAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	58
FG-039	AGGACAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	63
FG-043	GAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	56
FG-044	AGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	57
FG-057	CAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	59
FG-078	CAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	59
FG-080	AAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	58
FG-082	AGGACAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	63
FG-086	AAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	58
FG-087	AGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	57
FG-092	AAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	58
FG-094	AGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	57
FG-096	AGGACAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	63
FG-098	AAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	58
FG-100	AAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	58
FG-102	CAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	59
FG-103	CAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	59
FG-104	TCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	36
FG-106	AGGACAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	63
FG-107	GGACAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	62
FG-128	AGTCCGACCCTG	12
FG-129	GGACAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	62
FG-130	AAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	58
FG-135	CAAGACTCACCTTAACGTCGTCGTCATCGGCCACGTGCGACTCTGGCAAGTCCGACCCTG	59

AF212436.1_Fusar	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAACGTTG	104
AF212444.1_Fusar	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	105
AJ543588.1_Fusar	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	104
FG-010	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	125
FG-015	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAACGTTG	123
FG-017	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAACGTTG	102
FG-019	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAACGTTG	121
FG-020	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAACGTTG	120
FG-029	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	120
FG-030	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	120
FG-039	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	125
FG-043	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	118
FG-044	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	119
FG-057	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	122
FG-078	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	121
FG-080	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	120
FG-082	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	125
FG-086	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	120
FG-087	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	119
FG-092	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	121
FG-094	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	120
FG-096	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	125
FG-098	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	120
FG-100	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAACGTTG	120
FG-102	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAACGTTG	121
FG-103	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	121
FG-104	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAACGTTG	98
FG-106	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAACGTTG	125
FG-107	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAACGTTG	124
FG-128	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAACGTTG	74
FG-129	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAACGTTG	124
FG-130	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAACGTTG	120
FG-135	TCAGTACCACCGCATCCCAACCCGCGCCGACACTTGGCGGGGCTAGTTTCAAATTTCCAATGTTG	121







AF212436.1_Fusar	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTG	644
AF212444.1_Fusar	TACTAACATGGCTCTCAGACGCTCCCGGTCACCGTG	644
AJ543588.1_Fusar	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTG	644
FG-010	TACTAACATGGCTCTCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGA	682
FG-015	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATG	680
FG-017	TACTAAC	613
FG-019	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGAT	680
FG-020	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGA	678
FG-029	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGAT	678
FG-030	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGAT	678
FG-039	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGAT	684
FG-043	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGA	675
FG-044	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGAT	677
FG-057	TACTAACATGGCTCTCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATG	678
FG-078	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGA	678
FG-080	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGAT	678
FG-082	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGAT	683
FG-086	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGA	678
FG-087	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGAT	677
FG-092	TACTAACATGGCTCTCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATG	677
FG-094	TACTAACATGGCTCTCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGA	677
FG-096	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGA	682
FG-098	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGA	677
FG-100	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGAT	679
FG-102	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGA	679
FG-103	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGAT	680
FG-104	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGA	656
FG-106	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGAT	684
FG-107	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGATC	684
FG-128	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGATCACTGGTA	641
FG-129	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGA	682
FG-130	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACA	675
FG-135	TACTAACATGGCTATCAGACGCTCCCGGTCACCGTGATTTTCATCAAGAACATGATC	681
AF212436.1_Fusar		
AF212444.1_Fusar		
AJ543588.1_Fusar		
FG-010		
FG-015		
FG-017		
FG-019		
FG-020		
FG-029		
FG-030		
FG-039		
FG-043		
FG-044		
FG-057		
FG-078		
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FG-082		
FG-086		
FG-087		
FG-092		
FG-094		
FG-096		
FG-098		
FG-100		
FG-102		
FG-103		
FG-104		
FG-106		
FG-107		
FG-128	CT	643
FG-129		
FG-130		
FG-135		

Figure S1: The alignments of *TEF-1α* gene sequences of FGSC isolates and standard reference strains. Blue color means the consensus of sequences.