

ORIGINAL ARTICLE

## **Field survey of Fusarium stem rot of lisianthus (*Eustoma grandiflorum*) cultivated in Okinawa, Japan**

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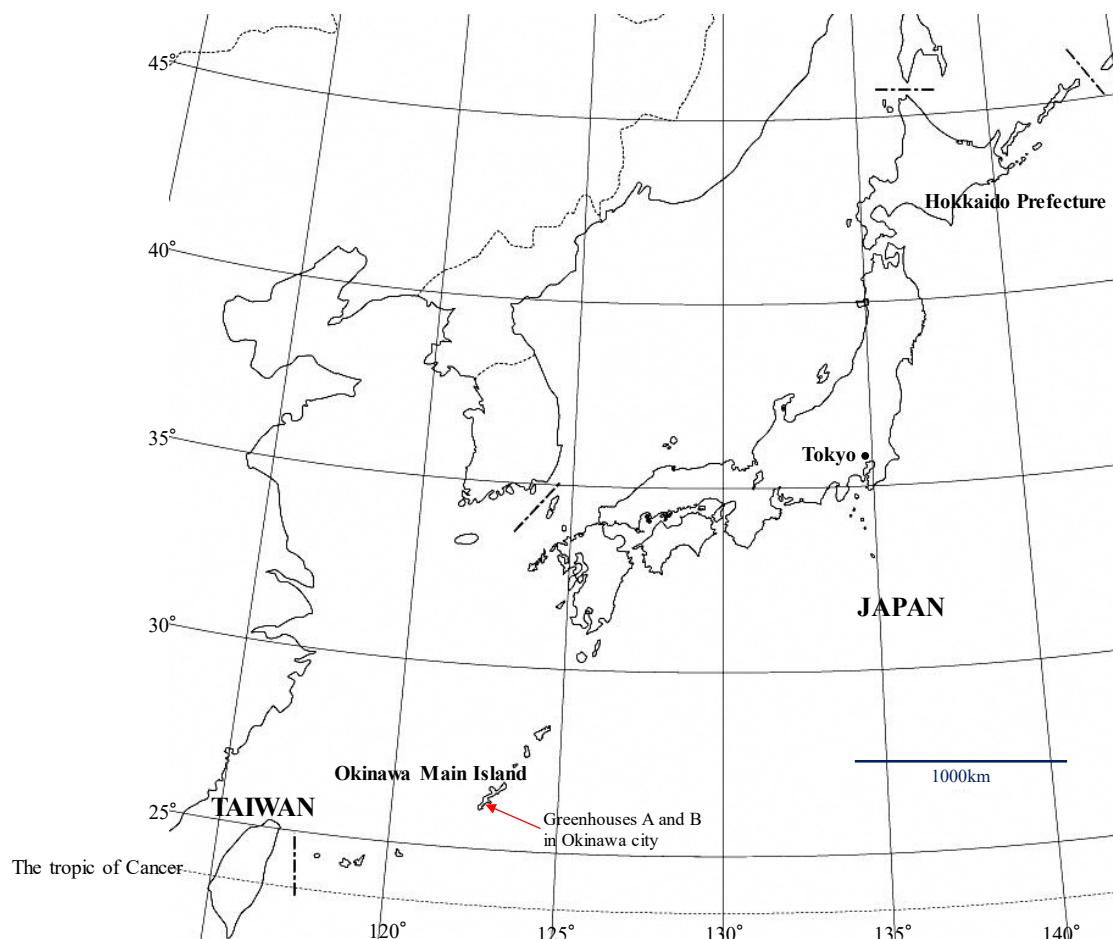
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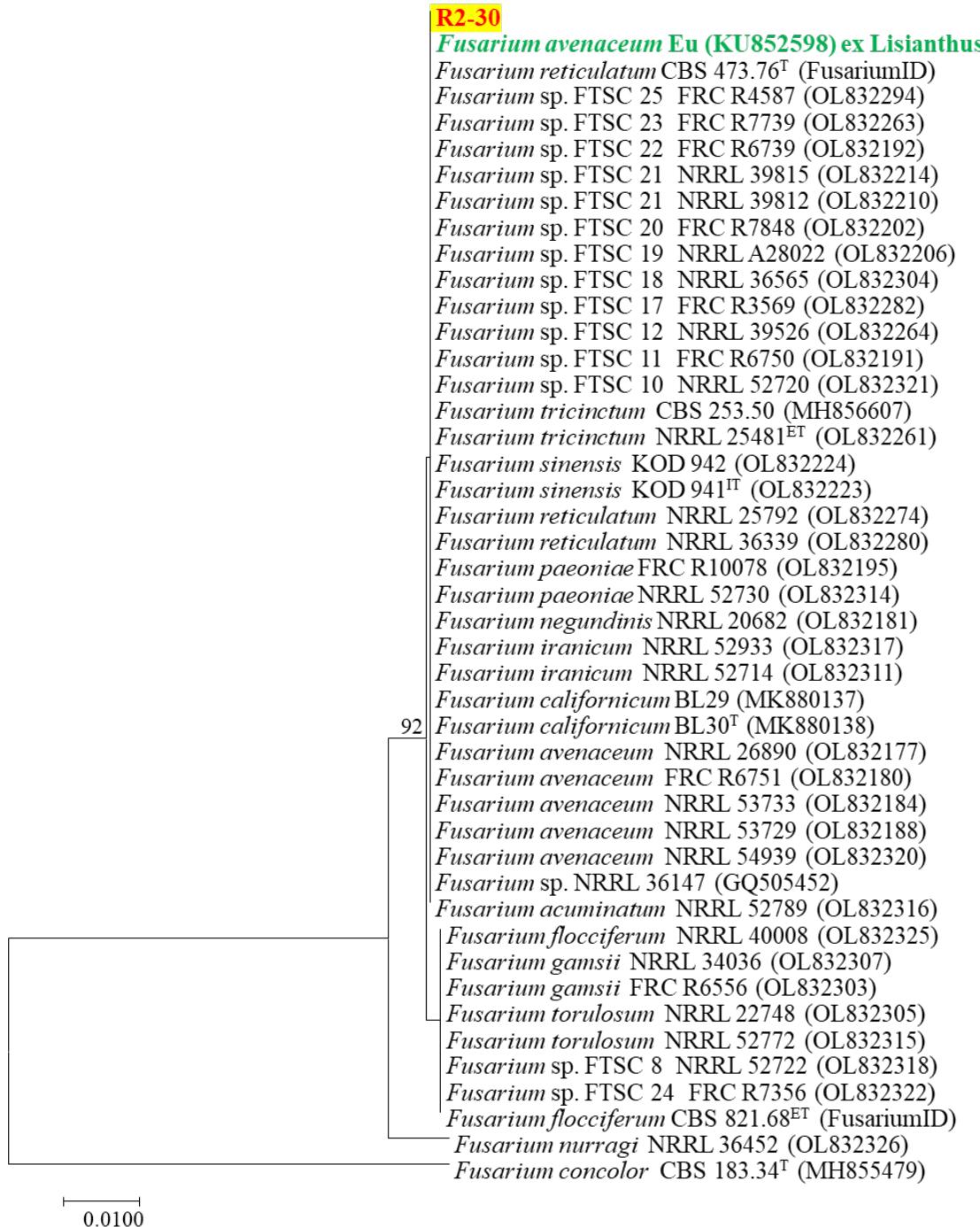
### **SUPPLEMENTARY MATERIAL**

The authors are fully responsible for both the content and the formal aspects of the supplementary material. No editorial adjustments were made.

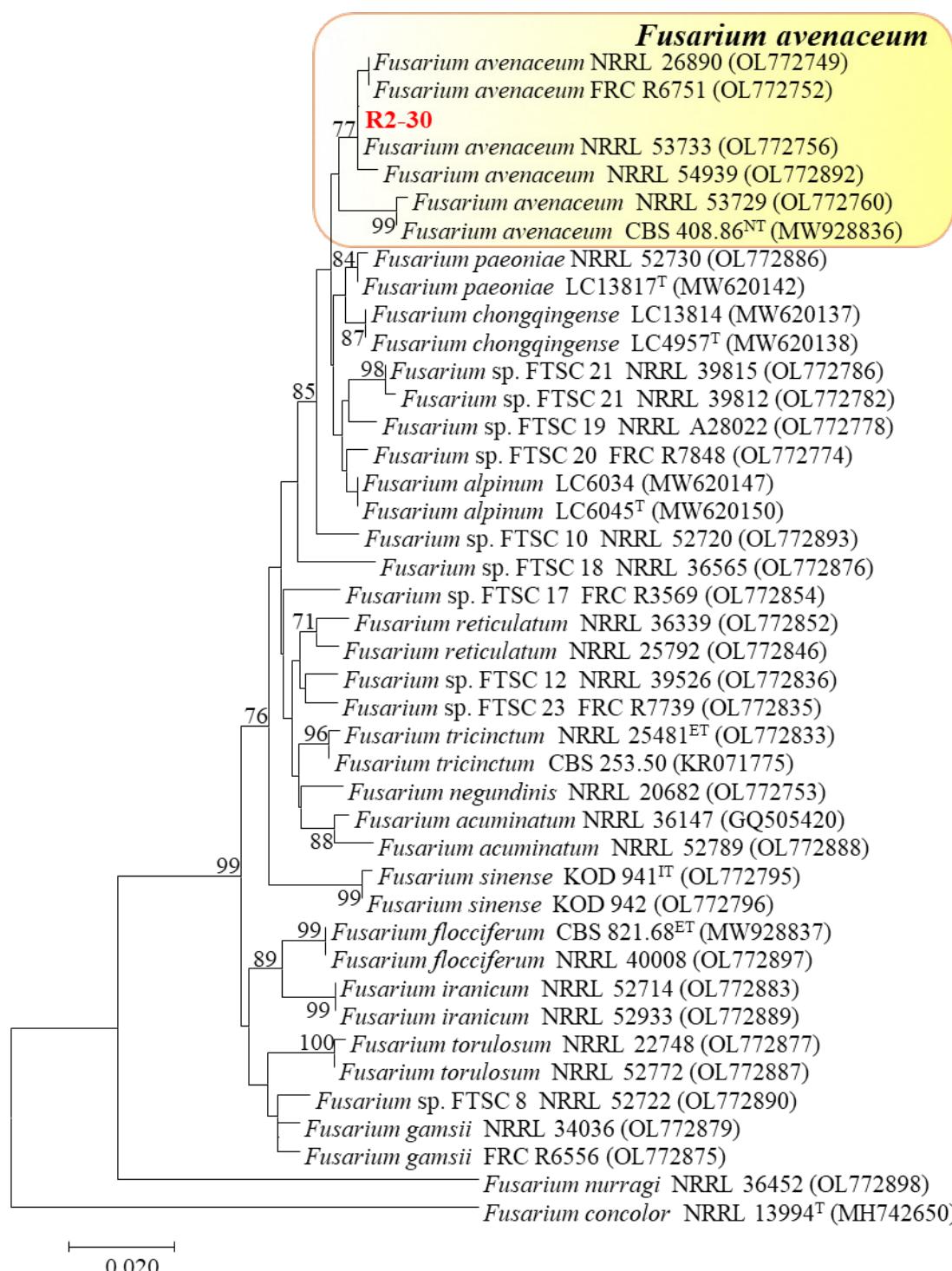
**Supplementary Table 1.** PCR Primers information of PCR amplification of the four loci

Locus	Primers	Sequence of primer (5'→3')	Direction	References
ITS	ITS5	GGAAGTAAAAGTCGTAACAAG	forward	White et al. (1990)
	ITS4	TCCCTCGCTTATTGATATGC	reverse	
	NL4 <sup>a</sup>	GGTCCGTGTTCAAGACGG	reverse	O'Donnell (1993)
<i>tef1</i>	EF1	ATGGGTAAGGARGACAAGAC	forward	O'Donnell et al. (1998)
	EF2	GGARGTACCAAGTSATCATGTT	reverse	
<i>rpb1</i>	Fa	CAYAARGARTCYATGATGGGC	forward	
	R8	CAATGAGACCTTCTGACCAGC	reverse	
	F7	CRACACAGAAGAGTTGAAGG	forward	
	R9	TCARGCCCATGCGAGAGTTGTC	reverse	O'Donnell et al. (2010)
	F6 <sup>a</sup>	CTGCTGGTGGTATCATTACG	forward	
	F8 <sup>a</sup>	TTCTTCCACGCCATGGCTGGTC	forward	
	G2R <sup>a</sup>	GTCATYTGDGTGCDGGYTCDC	reverse	
	Amp3f	GAYTACATCTCAAYCGTCAGCC	forward	Senatore et al. (2021)
	Amp3r	GTTCTGGGAHGAACACACRGCG	reverse	
<i>rpb2</i>	RPB2-5f2	GGGGWGAYCAGAAGAAAGGC	forward	Reeb et al. (2004)
	fRPB2-7cr	CCCATRGCTTGTTTRCCCAT	reverse	
	fRPB2-7cf	ATGGGYAARCAAGCYATGGG	forward	Liu et al. (1999)
	RPB2-11ar	GCRTGGATCTRTCRTCSACC	reverse	

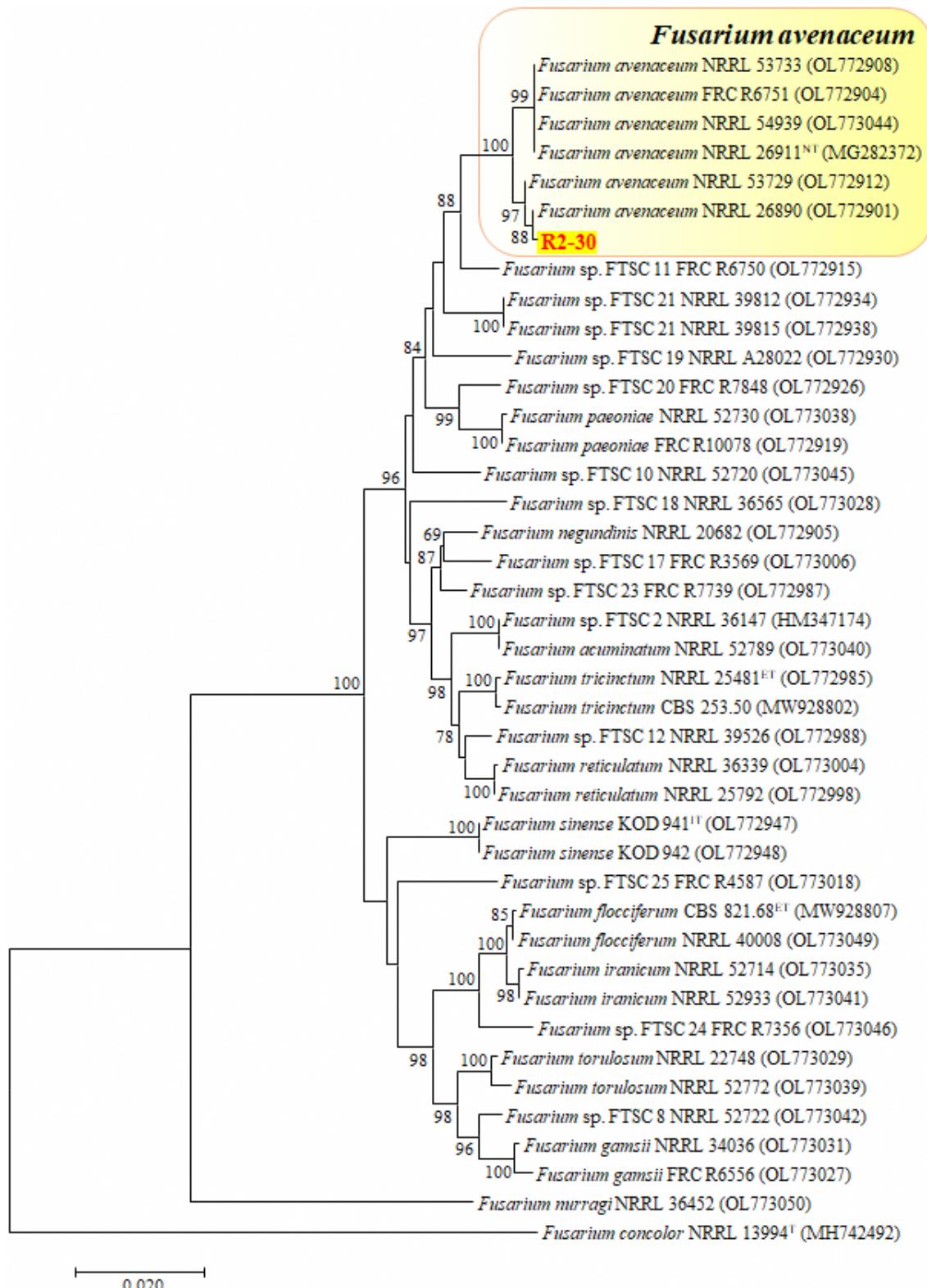
<sup>a</sup>used only for sequencing reactions**Supplementary Figure 1.** Map of Okinawa, indicating the localizations of the greenhouses



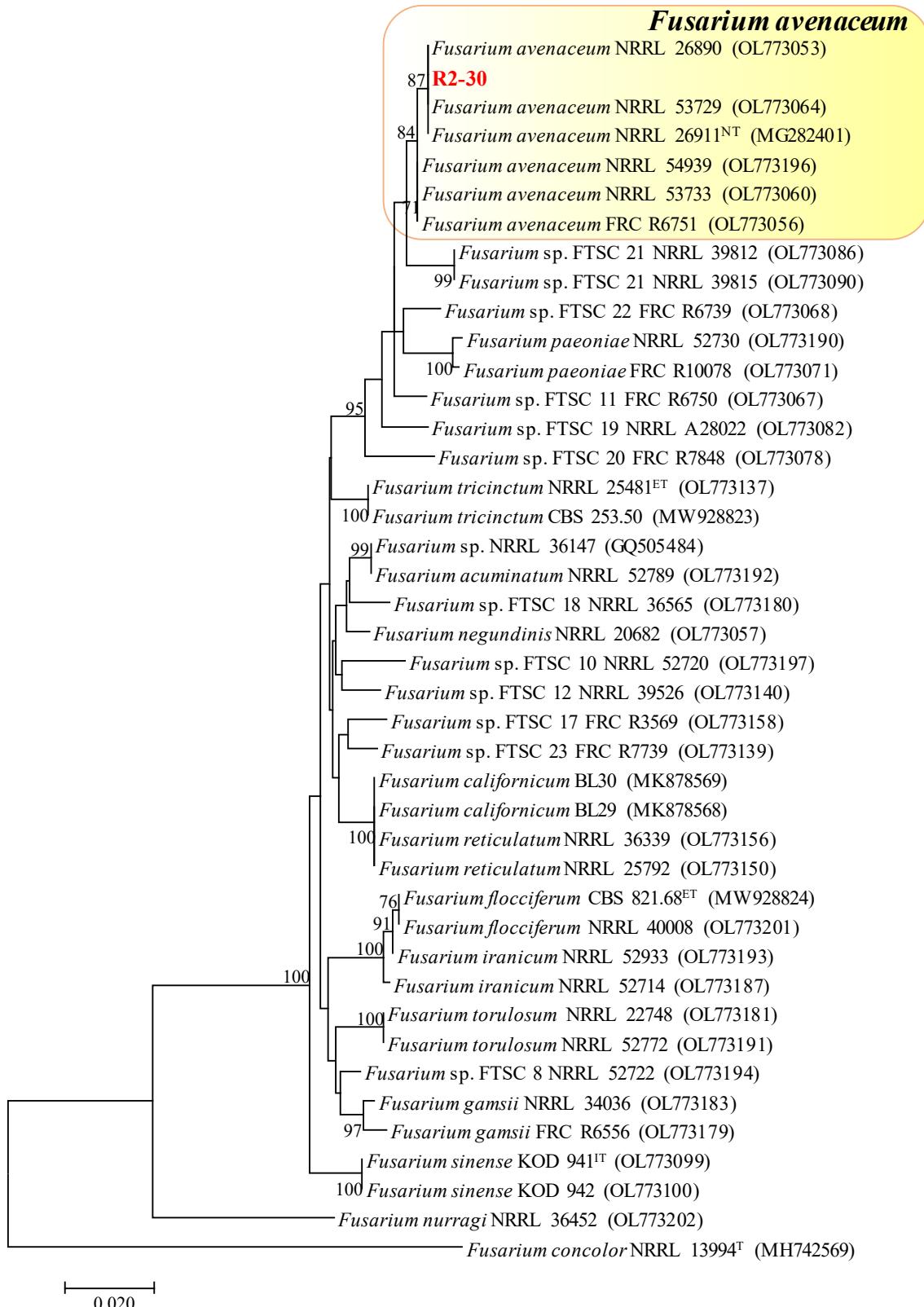
**Supplementary Figure 2.** Neighbor-Joining (NJ) phylogeny inferred from ITS sequences of R2-30, one strain from lisianthus, and species of *Fusarium tricinctum* species complex. Numbers on the nodes are NJ Bootstrap values above 70%



**Supplementary Figure 3.** Neighbor-Joining (NJ) phylogeny inferred from *tef1* sequences of R2-30 and species of *Fusarium tricinctum* species complex. Numbers on the nodes are NJ Bootstrap values above 70%



**Supplementary Figure 4.** Neighbor-Joining (NJ) phylogeny inferred from *rpb1* sequences of R2-30 and species of *Fusarium tricinctum* species complex. Numbers on the nodes are NJ Bootstrap values above 70%



**Supplementary Figure 5.** Neighbor-Joining (NJ) phylogeny inferred from *rpb2* sequences of R2-30 and species of *Fusarium tricinctum* species complex. Numbers on the nodes are NJ Bootstrap values above 70%