Background

*Fusarium oxysporum* is a ubiquitous fungus which spread worldwide. Some strains of the species are soilborne plant pathogens, invade the roots of plants and colonize in xylem to cause the wilt symptoms. In the plant pathogenic strains of the species, there are also hundreds of host-specific forms, each of which is designated forma specialis (f. sp.). Although *F. oxysporum* has a life-cycle with only asexual vegetative reproduction through mycelial growth and conidial production, the fungus possesses mating type genes (*MAT1*-1-1 and *MAT1*-2-1) necessary for sexual reproduction. Then I assumed that *F. oxysporum* originally had sexual reproduction in its life-cycle, but the sexual reproduction is suppressed.

Post-transcriptional regulation including RNA silencing is considered to be important in control secondary metabolism, sexual reproduction, and pathogenicity in fungi. RNA silencing was firstly reported in the antiviral mechanisms in plants to protect them from RNA viruses. General role of RNA silencing is the regulation of gene expression by the recognition of specific sequence. RNA silencing pathways have been actively studied in fungal plant pathogens.

Methods

This study was conducted to confirm that RNA silencing such as, MSUD (meiotic silencing by unpaired DNA) and Quelling, is involved in asexuality, vegetative growth and pathogenicity in
Fol.

For the purpose, first, I identified the genes which are predicted to be involved in RNA silencing in Fol by probing the genome database. I found that Fol has a RecQ helicase (FoRecQ), an SAD-3 (FoSAD-3), three RdRPs (FoQDE-1, FoSAD-1, FoRRP-3), a Dcl1 (FoDcl1), a Dcl2 (FoDcl2), and five argonaute genes (four QDE-s, FoQDE-2, FoQDE-2-2, FoQDE-2-3, FoQDE-2-4; a SMS-2, FoSMS-2) by the BLAST search using the amino acid sequence of N. crassa RNA silencing related proteins as queries, respectively. Second, targeted gene deletion was conducted in Fol 4287 (MAT1-1) to analyze the function of each gene. Each deletion mutant was evaluated for colony growth speed, formation of conidia and bud cells, germination rate of bud cells, formation of aerial mycelium, and virulence to tomato (cv. Momotaro).

Analysis

FoQDE-2 gene deletion mutants presented reduced pathogenicity to tomato, and FoQDE-2 was suggested to be involved in pathogenicity to tomato. FoRecQ, FoSMS-2 and FoDcl1 gene deletion mutants showed increased aerial hyphae compared to the wild-type, and suggested that FoRecQ, FoSMS-2 and FoDcl1 are involved in vegetative growth. No mutant presented sexual reproduction by the outcross with Fol Chiz-1 (MAT1-2).

Conclusions

These results indicated that RNA silencing is involved in pathogenicity and vegetative growth in Fol.