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Fusarium is an ascomycete plant pathogen that causes crown and root rot of a broad spectrum of monocotyledonous and dicotyledonous plants ([@B1]). Crown and root rot (CRR) of rice is one of the most destructive diseases of cultivated rice (*Oryza sativa* L.) in tropical and sub-tropical regions of the world ([@B2]). Because CRR of rice is caused by phytopathogenic fungi in the genus *Fusarium* ([@B3]), a great deal of research has been conducted to elucidate CRR of rice. In this study, we report the draft genome sequence of a new *Fusarium* isolate (strain NRRL 37409) responsible for CRR of rice. The NRRL 37409 genome was sequenced on an Illumina HiSeq 2000 platform. After removal of adaptor sequences, trimmed reads were assembled using Velvet ([@B4]) with *k*-mer length set to 45 bp. The assembly contained 42 contigs larger than 2

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