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Genome sequence and analysis of *Thermobifida fusca*.

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Thermobifida fusca is a moderate thermophilic soil bacterium that belongs to actinobacteria. It is a major degrader of plant cell walls. Complete genome sequence showed that the *T. fusca* genome consists of a single circular chromosome of 3642249 bp with 85% of the genome sequence predicted to encode 3117 proteins and 65 RNA species. Genome analysis revealed the existence of 29 putative glycosyl hydrolases in addition to the 6 already identified cellulases. The glucosyl hydrolases include enzymes predicted to exhibit mainly dextran/starch and xylan degrading functions. At least two of the secreted cellulases have sequence signatures that indicate their secretion is mediated by the twin-arginine translocation system. Beside the twin-arginine translocation system, *T. fusca* possesses components of the *sec* system that allows proteins to cross the inner membrane and appears to lack other major secretion systems. *T. fusca* has the core phosphotransferase system components as other Actinobacteria but lacks PTS transporters. Genome comparisons reveal that 146 genes were laterally transferred to *T. fusca*. *T. fusca* has a small number (39) of unique genes.