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We tracked the spread and progress of *Phytophthora ramorum* infections in southern Oregon forests from 2001 through 2008. Using microsatellite markers we identified 75 novel multilocus genotypes (MGs) with 10 to 35 MGs found in each year. While the majority of MGs were present in very low numbers (< 1%) one MG was dominant in all years representing 35 to 65% of isolates. Although microsatellites are neutral markers and different genotypes are not by their nature related to fitness, the presence of one dominant type led us to investigate if the most common MG is more fit. We examined relative fitness of the most and least common MGs occurring in all years. We used *P. ramorum* isolates from 2001 to 2007 representing the full geographic range. We set up a genotype by environment interaction (G X E) experiment. We assayed 40 isolates representing eight genotypes under five temperatures on nutrient rich and nutrient poor media. We measured colony growth rate, chlamydospore production, and morphology. We found very little difference among genotypes. Variation among individuals within temperature and media type was quite high. Colony morphology was highly variable even within clones under identical conditions. A similar experiment, on tanoak tissue, is currently underway.