Candida tropicalis is a clinically relevant yeast that causes candidemia in humans with a high mortality rate. The yeast primarily infects immunocompromised patients and causes outbreaks in health care facilities. A short tandem repeat (STR) typing scheme for C. tropicalis was applied to a collection of 217 clinical and environmental isolates from South America, predominantly from Brazil, and included nine fluconazole-resistant isolates. Application of the STR typing resulted in the identification of 153 genotypes. Typing demonstrated 11 clusters containing more than two isolates. In one cluster of six, we found three fluconazole-resistant isolates, while there were another five closely related fluconazole-resistant isolates. ERG11 mutation screening was performed on all 9 resistant isolates. The closely related resistant isolates all contained Y132F in combination with the novel Y237H/N mutation. The remaining resistant isolate did not exhibit mutations in ERG11 suggesting a different resistance mechanism. Altogether, we applied a novel STR genotyping for C. tropicalis and showed several in-hospital clusters suggesting cross-transmission.

Figure 1.