

ABSTRACT

In the African and Asian tropics, termites of the subfamily Macrotermitinae play a major role in the decomposition of dead plant material. Their ecological success lies in the obligate mutualism of the termites with fungi of the genus *Termitomyces*. Before the advent of molecular studies, the interaction with these fungi was poorly understood. Here, we combined available ITS sequence data from West, Central, and South Africa with data of 39 new samples from East Africa to achieve the most comprehensive view of the diversity and host specificity of *Termitomyces* symbionts across Africa to date. A high amount of sequence divergence in the ITS sequences was found; 11 different *Termitomyces* lineages in East Africa and >30 lineages across Africa were identified, and the expected diversity is estimated to be about 41 lineages. The fungal lineages belong to four major clades, each almost exclusively associated with one termite host genus. Analysis of molecular variance revealed that 40% of the ITS sequence variation occurred between host genera, indicating close co-evolution at this level. However, within host genera, fungal lineages and haplotypes were frequently shared among host species and sampling localities, except for fungal symbionts of *Odontotermes*. Horizontal transmission of fungal symbionts may facilitate the transfer of haplotypes and species among hosts. However, at present, we have little understanding of the maintenance of specificity at the genus level. Possible explanations range from substrate specificity of fungi to an active selection of fungi by termites.