Digital dermatitis (DD) is one of the main causes of lameness in dairy cattle worldwide, and it is frequently reported in high-yielding, free stall dairy herds from regions with a temperate climate. However, DD is also observed with high prevalence in grazing cattle with a low milk yield in tropical regions. To clarify whether these differences have an impact on the etiology of the disease, we studied DD lesions from all year round grazing cattle of mixed breed in Brazil using high-throughput 16S rRNA gene sequencing and fluorescent in situ hybridization. The study included samples from 66 skin lesions and 5 healthy skins collected from five farms. Both techniques showed Treponema spp. to be the most abundant bacteria, present in all but one of the samples with minimal epidermal alterations. We identified eleven different Treponema strains belonging to the six major phylotypes of Treponema which have all previously been identified in DD lesions. Furthermore, we identify Dichelobacter nodosus in DD lesions by gene sequencing and also by fluorescent in situ hybridization in almost half of biopsy specimens in areas with mild epithelial damage and together with Treponema. The present data support the hypothesis that Treponema constitutes the main pathogen responsible for DD, independent of the environment and region where cows are kept, and it further suggests D. nodosus as another potentially important pathogen.