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Molecular identification of yeasts associated with raw cow milk from peri-urban farms in Kaduna State, Nigeria

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This study aimed to examine the diversity of yeasts associated with bovine mastitis by employing molecular techniques in yeast identification. A total of 300 composite milk samples were collected from 26 peri-urban dairy farms and examined. After culture, 37 (12.3%) fungal isolates were identified using the API 20C AUX. Polymerase chain reaction (PCR) and sequencing of the domains D1 and D2 of the 26S rRNA gene identified eleven (11) of these yeasts as *Candida albicans* (3 isolates), *Saccharomyces cerevisiae* (1 isolate) and *Pichia Kudriavzevii* (7 isolates). The D1/D2 26S rRNA gene sequences were 100% identical for the yeast isolates within the same species. It was found that all *C. albicans* had ability to produce germ tubes by incubation on human serum and chlamydospores. Antimycotic sensitivity showed that 78% fungal isolates were sensitive to amphotericin B. The presence of isolates of the pathogenic yeast, *C. albicans* in this study raises the possibility of cow milk being a vehicle of transmission of pathogenic yeasts.

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