88.9% of the workers had poor knowledge of brucellosis and 82.5% had poor practice towards prevention of brucellosis transmission. However, about 84.7% of the respondents deemed protective clothing was important; 78.8% claimed to actually use it while working and 71.4% personally indicated they owned protective clothing.

Conclusion: There was high seroprevalence of brucellosis among the abattoir workers screened. Age, length of occupation and level of education were significant associated factors to seropositivity to brucellosis using RBT and ELISA. Use of PPE proved to be protective against infection with brucellosis; though the knowledge and attitude towards its use was poor among the workers. It is recommended that health education should be routinely done for the abattoir workers to improve their knowledge on brucellosis and hence its prevention.

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Isolation of brucella strains in cattle from sedentary and nomadic communities and its public health implication

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Background: Brucellosis is a highly infectious disease caused by bacteria of the genus brucella affecting animals leading to high economic loss and an impediment to livestock exportation. It also infects man with serious public health consequences. The disease is one of the world's most important neglected tropical zoonoses. Brucellosis is considered endemic in Nigeria and current information on isolation in sedentary and nomadic cattle is required. We carried out an active surveillance in sedentary cattle in Kachia Grazing Reserve (KGR), Kaduna State and in nomadic communities on the Jos Plateau to isolate brucella organisms and carry out phenotypic and molecular characterization of the isolates to species level.

Methods & Materials: A total of 63 vaginal swabs, 36 milk samples, and 2 hygroma fluids were collected from cattle in KGR while 70 vaginal swabs, 50 milk samples and 2 hygroma fluids were collected from cattle on the Jos Plateau using a purposive sampling technique. Only animals that had history of abortion or infertility were sampled. They were cultured on serum dextrose agar with addition of antibiotic supplement (Oxoid) and incubated at 37 °C for 3 days in 5% CO_2 atmosphere. *Brucella* strains isolated were biotyped along with eight archived isolates according to classical *Brucella* biotyping method. Isolates were further subjected to Bruce-ladder multiplex PCR according to established protocol.

Results: Three and four *B. abortus* strains were isolated from KGR and Jos Plateau respectively. Biotyping revealed that all the 15 isolates were *B. abortus* biotype 3. Bruce-ladder multiplex PCR showed bands consistent with *B. abortus*.

Conclusion: The study established the endemicity of brucellosis due to *B. abortus* biotype 3 in the two study areas. These findings have great veterinary and public health implications as healthy animals and the farmers are at high risk of infection due to contact with infected animals, consumption of raw milk and other products. Farmers were advised to boil their milk before consumption, isolate infected animals, maintain good level of hygiene and use protective wears in handling their animals as preventive measures. The study recommends vaccination of cattle against brucellosis in the areas.

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Deciphering the differential virulence of leptospira interrogans by comparative transcriptomic study

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Background: Leptospirosis is the most common zoonotic disease worldwide. Humans get infected directly from animals or indirectly from contaminated water and soil. Human leptospirosis is mostly caused by *Leptospirosis interrogans (L. interrogans).* Despite its broad range of clinical presentations and severity, the molecular determinants of pathogenesis in human leptospirosis remain poorly understood. In this study, we elucidate associations of distinctive phenotypic features with genomic and transcriptomic characteristics of *L. interrogans*.

Methods & Materials: Six *L. interrogans* isolates from Malaysia were studied and compared clinically and tested for virulence in an animal model. SMRT sequencing was carried out on the PacBio *RSII* for long reads and complemented with Illumina MiSeq for short reads. The reads were de novo assembled with HGAP and VELVET and annotated with the PROKKA software tool. Two *L. interrogans* strains (strain Langkawi and 1530d) from both extremes of the virulence spectrum were subjected in triplicates to RNA-seq using Illumina HiSeq2500 Sequencer. Comparative genomics and transcriptomic studies were performed on the most virulent (Langkawi) and least virulent (1530d) strains.

Results: Findings of virulence testing in the guinea pig model correlated well with clinical findings. The two most and least virulent strains belonged both to serogroup Icterohaemorrhagiae and gene content and arrangement in the *rfb* locus were similar, however the genomic structure differed greatly. More than half of total genes associated with motility, chemotaxis and alginate biosynthesis were differentially expressed between these two extreme strains. At logarithmic phase culture, genes associated with chemotaxis were expressed significantly more highly in strain Langkawi than in strain 1530d, possibly reflecting differences in the capacity to enter and invade into host tissue.

Conclusion: Differences in pathogenicity of all the strains appeared to be largely determined by genomic make-up. This was evidenced by a substantial number of genes that were differentially expressed between the most and least virulence *L. interrogans* strains. Expression of chemotaxis-function genes may be one of the important parameters for virulence determinants in leptospirosis pathogenicity.

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