

INVESTIGATION INTO VIRULENCE GENES AND ANTIMICROBIAL SENSITIVITY OF FIELD ISOLATES OF BRUCELLA FROM INDIA

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One of the most serious zoonotic disease for human and animals throughout the world Brucellosis has been listed by WHO as one of the seven neglected zoonoses in the developing countries. The disease has been reported from almost all states in India. Devoid of classical virulence markers, the *Brucella* genome inhabits several putative virulence genes identification of which is important for better understanding of pathogenesis. These genes regulate their intracellular trafficking and survival to establish a chronic infection protected from immune and antibiotic arsenals. Prolonged treatments with combination antibiotics like doxycycline, rifampicin and streptomycin, which are active intracellular besides others, have been recommended to treat cases of human brucellosis. In general, antibiotic resistance in *Brucella* is not observed though sporadic cases of antibiotic resistance have been reported. The present study was undertaken to detect the putative virulence genes and *in vitro* antimicrobial sensitivity pattern of *Brucella* isolates from India. Totally, 45 isolates of *Brucella* spp. (*B. abortus* 16; *B. melitensis* 29) from human and animals from different regions of India namely Himachal Pradesh, Jammu & Kashmir, Punjab, Karnataka, Tamil Nadu, Maharashtra, West Bengal, Assam and Meghalaya were used. Virulence gene profiling for nine genes, viz., VirB5, BtpA, BtpB, VecC, BetB, BPE275, VirB2, BSPB and PrpA by polymerase chain reaction (PCR) and minimum inhibitory concentration (MIC) of seven antibiotics, viz., rifampicin, azithromycin, tetracycline, ciprofloxacin, streptomycin, ofloxacin and co-trimoxazole using the gradient diffusion susceptibility method (HiComb strips, HiMedia) was estimated. Virulence genes like VirB5 (37.77%), BtpA (73.33%), BtpB (68.88%), VecC (55.55%), BetB (82.22%), BPE275 (77.77%), VirB2 (97.77%), BSPB (82.22%) and PrpA (71.11%) could be identified among isolates. All the isolates were found sensitive to azithromycin, tetracycline, ciprofloxacin, streptomycin and ofloxacin. Of these, 10 (*B. abortus* 4; *B. melitensis* 6) isolates exhibited intermediate sensitivity to co-trimoxazole. Resistance to co-trimoxazole was found in 20 of which, 14 were *B. abortus* and 6 were *B. melitensis*. Similarly, 15 isolates were resistant to rifampicin, which include *B. abortus* (10) and *B. melitensis* (5). Significantly, six isolates (*B. abortus* 5; *B. melitensis* 1) were found resistant to both rifampicin and co-trimoxazole. While presence of combination of virulence genes may have influence on the pathogenesis, resistance to antibiotic(s) of choice used to treat human cases needs attention. Implication of these would be discussed.

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