**Titre d’article :** The characterization of Brucella strains isolated from cattle in Algeria reveals the existence of a B. abortus lineage distinct from European and Sub-Saharan Africa strains

**Résumé :**

Brucellosis is a zoonosis caused by bacteria of the genus Brucella that causes important economic losses and human suffering worldwide. Brucellosis control requires an understanding of the Brucella species circulating in livestock and humans and, although prevalent in African countries of the Mediterranean basin, data for this area are mostly restricted to isolates obtained from humans and small ruminants. Here, we report the characterization of twenty-four Brucella strains isolated from Algerian cattle. Bruce-ladder multiplex PCR and conventional biotyping showed that Algerian cattle are infected mostly by B. abortus biovar 3, and to less extent by B. abortus biovar 1 and B. melitensis biovar 3. Extended AMOS-ERY PCR showed that all Algerian B. abortus biovar 3 strains were of the subgroup 3b. Although by multi locus variable number of tandem repeats analysis (MLVA) most isolates were closer to the European counterparts, five strains displayed characteristics distinct from the European isolates and those of countries across the Sahara, including three repetitions of marker Bruce55. These five strains, plus an earlier isolate from an Algerian human patient, may represent a lineage close to clades previously described in Africa. These data provide the basis for additional molecular epidemiology studies in northern Africa and indicate that further bacteriological and molecular investigations are necessary for a complete understanding of the epidemiology of cattle brucellosis in countries north an