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## BAU scientist reveals genome sequence of Brucellosis bacteria

BAU Correspondent . Mymensingh | Published at 02:03am on June 30, 2019

A Bangladesh Agricultural University scientist successfully revealed the genome sequence of the bacteria that causes Brucellosis, a highly contagious zoonotic disease, in farm animals.

At a press conference at BAU, Professor Dr Ariful Islam of Microbiology and Hygiene, Dr Mst Minara Khatun of Microbiology and Hygiene with PhD student Md Sadequl Islam said that they revealed genome sequence of Brucella abortus biovar 3 Strain BAU21/S4023, isolated from a dairy cow in Bangladesh.

Brucellosis has eight biovars responsible for the infection in Bangladesh but it is not known to all.

Prof Ariful isolated the brucella biovar from a cow and submitted the complete genome sequence in the genome database at National Center for Biotechnology Information.

Prof Ariful had successfully done the research with the financial support from Bangladesh Academy of Sciences and USA department of agriculture.

His team found the relationship of Brucellosis biovar of our country with Brazilian, France Brucellosis biovar because we used to import cows from these countries.

The genome sequencing will help us to know the genomic structure, understanding its virulence, pathogenesis, host specificity, biotyping difference and relationships with other disease and finally it would help in developing vaccines to prevent and control brucellosis, said Prof Ariful Islam at the press conference.

Brucellosis is typically transmitted from affected animal to human by ingestion of unpasteurised milk or undercooked meat. Due to this disease a substantial economic loss occurs in dairy animals through stillbirths and decreased milk production.

Veterinarian in the time of treatment and the farmers in the time of rearing can get affected by Brucellosis being close to the affected cattle.

The unfolding of the genome sequence will assist in tackling the disease in Bangladesh.



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