

## Complete genome sequence of *Trueperella pyogenes* strain Arash114, isolated from the uterus of a water buffalo (*Bubalus bubalis*) in Iran

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### Abstract

**Objective:** *Trueperella pyogenes* has been considered a major causative agent of metritis, abortion, and death in a broad range of domestic and wild animals, including cattle, swine, sheep, goats, camels, buffalo, deer, antelopes, reptiles, and birds.

**Data description:** Here, we report the complete chromosome sequence of *Trueperella pyogenes* strain Arash114, isolated from the uterus of a water buffalo (*Bubalus bubalis*) died due to the infection caused by this pathogen. The genome assembly comprised 2,338,282 bp, with a 59.5% GC content. Annotation of the genome showed 46 tRNA genes, 6 rRNA, 1 CRISPR and 2059 coding sequences. Also, several genes coding for antimicrobial resistance such as *tetW* and virulence factor including *plo*, *nanH*, *nanP*, *cbp* and 4 fimbrial proteins were found. This study will advance our knowledge regarding the metabolism, virulence factors, antibiotic resistance and evolution of Arash114 strain and serve as an appropriate template for future researches.

**Keywords:** Complete genome sequencing; *Trueperella pyogenes*; Uterus infection; Water buffalo