The Relationship of polymorphism of the *SPEF2* gene to individual and mass motility in the semen of male Iraqi buffaloes

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Abstract

This study aimed to link the genetic variants of the sperm tail gene SPEF2 and both individual and mass motility to evaluate semen in male Iraqi buffaloes. This study was conducted in the College of Agriculture, University of Basrah, and the fields of the Artificial Insemination Centre of the Department of Livestock in the Abu Ghraib area/Ministry of Agriculture (25 km west of Baghdad), for the period from 11/15/2022 until 4/15/2023. The sequencing results were compared with the highest match rate in NCBI due to the occurrence of several different mutations, and the highest percentage of matching was with male Indian buffalo (Accession No. XM 025270630). The study's results clearly indicate a significant correlation between the polymorphism of the SBF2 gene and the rate of motility (individual and mass) in the semen of male buffalo. Therefore, this gene may be considered a molecular marker for selecting highly fertile males.

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Introduction

The Iraqi buffalo has great economic importance, but it suffers from many different problems that have led to a decline in its production for various reasons, the most important of which may be the lack of recent studies that address it (Rossi *et al*., 2018) [27]. The buffalo constitutes an important and effective part of the agricultural sector in particular and the economy in general. The country in general, but their production level does not cover the needs of the local market for many reasons, including mismanagement, poor nutrition, and genetic factors (Al- Rudha, *et al*, 2021) [1]. On the other hand, male fertility and semen quality are of vital importance to the livestock industry, as infertile males can cost producers large sums of money without any economic return (2008 Thundathil and Kastelic) [34], Semen characteristics have a moderate heritability coefficient, so there is a possibility of selection on the basis of semen characteristics (Gebreyesus *et al*., 2021) [5], several studies (Habib *et al*., 2017; Habib *et al*., 2018) [9-10] have indicated that there are many genes that can be molecular markers in semen. Modiba *et al*. (2022) [24] indicated that the SPEF2 gene is one of the candidate genes to be molecular markers associated with semen quality that may directly affect semen characteristics in cattle and therefore can be considered one of the molecular markers in selecting male cattle. The SPEF2 gene is one of the important genes that is directly related to the fertility of farm animals (Guo *et al*., 2014) [6], due to its work in producing a protein that contributes to the normal growth of the sperm tail and thus has a direct effect on sperm motility (Liu *et al*., 2020; Tu *et al*., 2020) [19, 36], poor sperm motility is associated with decreased fertility in buffaloes (Kumaresan *et al*., 2023) [17]. Individual sperm motility depends on the structure and function of the tail, as poor motility is significantly linked to genetic defects (Gupta *et al*., 2012) [7]. On the other hand, individual sperm movement is affected by several factors, including the season (Marai *et al*., 2010) [23], breed, and age of the animal (Kiani *et al*., 2014) [14], Low mass motility in buffalo bulls is an indicator of low sperm concentration and poor percentage of individual sperm motility (Muvhali *et al*., 2022) [25], this demonstrates the link between individual and mass motility. Because non-genetic factors (such as motility) are a very important indicator for measuring semen quality (Ramajayan *et al*., 2023) [26], this study aimed to link the genetic