



Lecture 2:

Modes of academic communication

Course 501

Writing and Communication Skills

AIMS

- Learn the different forms of academic communication.



Modes communication



Oral



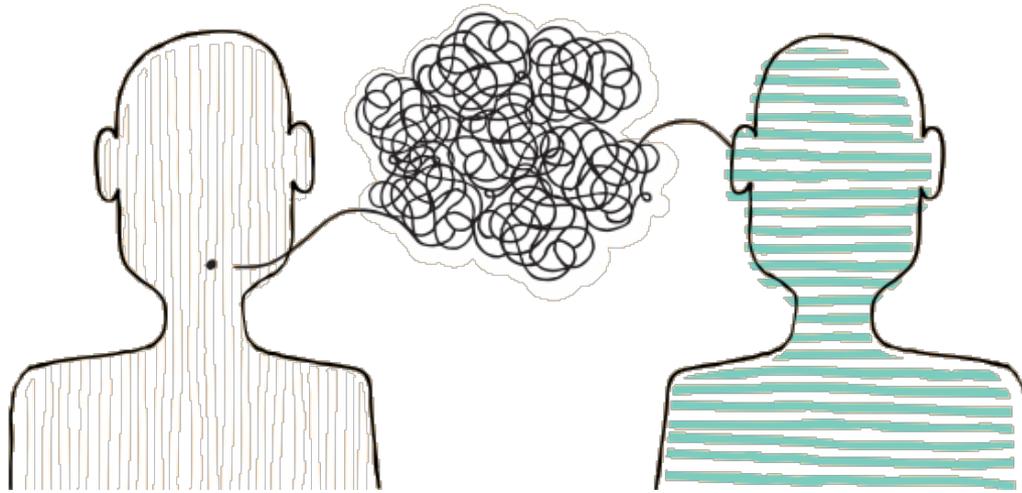
Visual



Written



What are the goals of communication?



Inform

Teach

Persuade

Debate

Report

Document

Take home message!

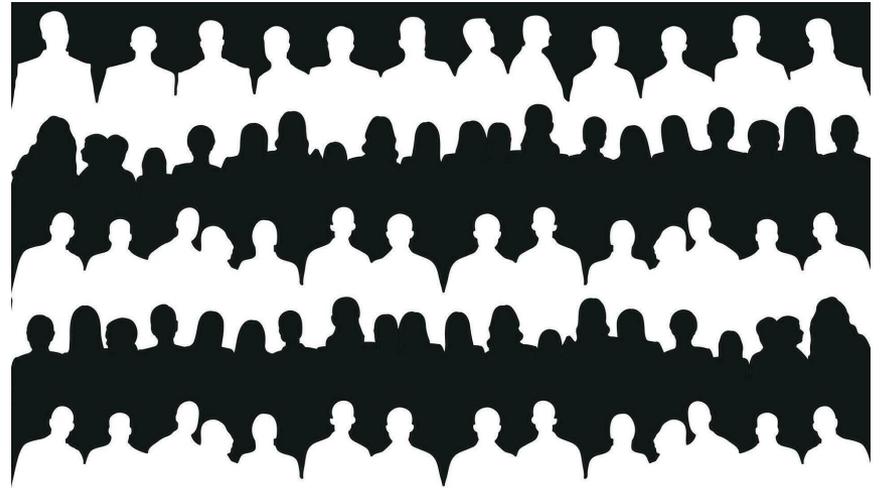


لكل مقام مقال



Who are you communicating with?

The public
Educated
Specialists
Students
Teachers
Policy makers



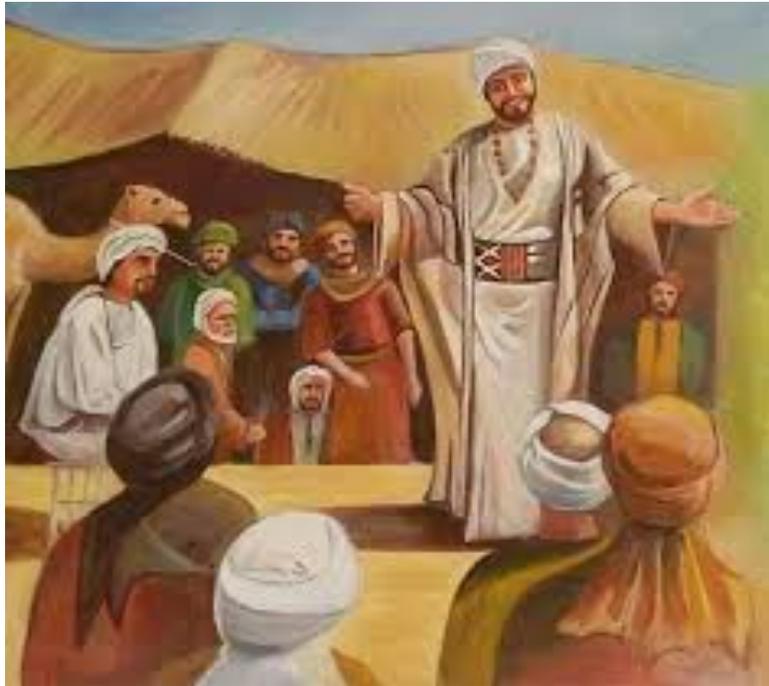
Take home message!



خاطبوا الناس على قدر عقولهم



Oral communication



Poetry

Sermons
Speeches
Forums
Debates
Lectures



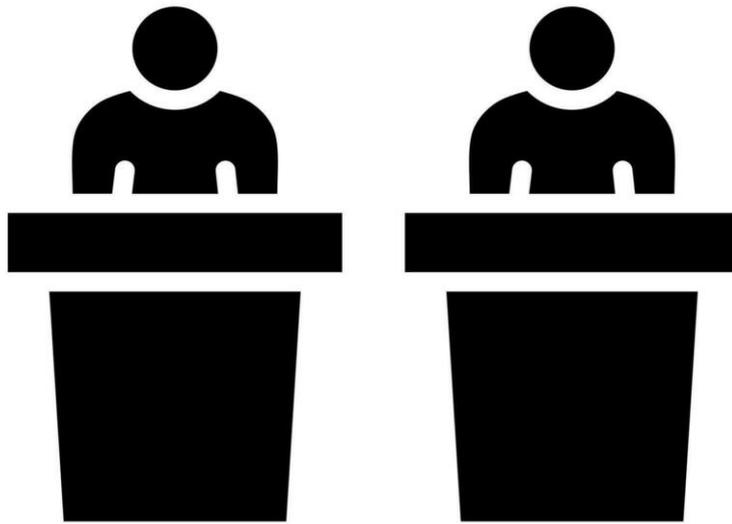
Poetry
Sermons
Speeches
Forums
Debates
Lectures



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Poetry
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Poetry
Sermons
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How hard?

How easy?





Visual communication

A Second Longhair Allele for Arabian Camels within the *FGF5* Gene

Tasneem Maraga, Bader H. Alhajeri, and Hasan Alhaddad
Department of Biological Sciences, Kuwait University, Kuwait

Objectives

- Study hair distribution and variance in length across different parts of camels' bodies (Figure1).
- Sequence the three exons of the *FGF5* gene and determine polymorphism that may be associated with a new hair phenotype.

Materials and Methods

- DNA samples were extracted from 30-40 tail-hair roots from 32 dromedary camels. Photos of each camel were taken from different body parts (Figure1).
- PCR reaction was applied on the three exons, each with its specific primer pairs at specific conditions, followed by sequencing reactions using the Sanger sequencing method (for more details see Maraga et al. 2021).
- The DNA sequences of the three *FGF5* exons were aligned together to detect the previous *FGF5* SNP in exon3 (c.779 C>T) and its association with hair length across different parts of camel body. And to screen for any other polymorphism using BioEdit and FitchTV softwares.

Abstract

Mutations in the *FGF5* gene influence the hair growth cycle causing different hair lengths. Variation in hair length is found in many domestic animals including New World camelsids. The dromedary camel was investigated in our previous study with breeds exhibiting marked variation in hair length. The dromedary different hair length is associated with a nonsynonymous mutation (c.779 C>T) that changes the amino acid from proline to leucine allowing for having three hair length phenotypes: short (C/C), intermediate (C/T), and long (T/T). However, some camels were found to have a unique hair length (very long hair) despite having the short *FGF5* allele (c.779 C). Therefore, the hair of those unique camels was studied from different body parts. And to study the three *FGF5* exons including the splicing sites. As a result, we were able to identify a second *FGF5* mutation represented by a deletion of four nucleotides exactly after the splicing site of exon1 (g.364-366delAAGT). The camels with the homozygous genotype of the deletion have the longest hair length across the body. The camels with the heterozygous genotype for the deletion also have very long hair that cannot be clearly distinguished from the homozygous camels, which suggests an incomplete dominance mode of inheritance.



Figure 1. The distribution of the unique hair length across different body parts. 1: hair around the eyes; 2: hair around the ears, in which both the eyes and ears are almost covered with the hair; 3: neck, where the hair length is moderate; 4 and 5: are different parts of shoulder with different hair lengths; 6, 7, and 8: are different parts of torso, the longest hair found at the highest part of the torso (6); 9 and 10 are the forehead limbs that are almost cover with hair; 11 lowest part of torso; 12, 13 and 14 are the back-limbs which are covered by shorter hair than the front-limbs. Photos by Alhaddad, 2022.

Results

- Different hair lengths were observed across different camel body parts (Figure 1).
- A second polymorphism was identified in the *FGF5* gene: a deletion of four nucleotides in intron1 after the splicing site (g.364-366delAAGT) (Figure 2).

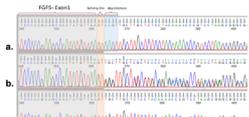


Figure 2. Chromatograms graphs of *FGF5* exon1 and the splicing site, which shows a four nucleotides deletion in intron1 (g.364-366delAAGT). a. *FGF5* exon1 and the splicing site reference. b. heterozygous for the deletion which is associated with the very long hair phenotype, and c. homozygous for the deletion which associates with a unique hair length (longest) in dromedary camels.

Acknowledgments

We would like to thank local Kuwaiti camel breeders especially Mohammed Farhan Alfanoush, Mubarak Humoud Almutairi for supplying the camel hair samples continuous support.

References:
Maraga, T., Alhajeri, B. H., & Alhaddad, H. (2021). *FGF5* missense mutation is associated with dromedary hair length variation. *Animal Genetics*, 52(6), 848-856.



Figure 3. A comparison of camel hair length phenotypes. a. homozygous (C/C) camel at c.779. b. homozygous camel for (T/T) genotype at c.779. Both a. and b. are homozygous camels for non deletion g.364-366delAAGT genotype. c. homozygous camel for (C/T) genotype at c.779 and a homozygous for the deletion (g.364-366delAAGT). d. homozygous camel for (C/C) genotype at c.779 and a heterozygous for the deletion (g.364-366delAAGT). Photos by Alhaddad, 2022.

Conclusion

A new polymorphism in the dromedary *FGF5* gene is found, represented by four nucleotides deletion in intron1 after the splicing site (g.364-366delAAGT), which could be responsible for the unique hair length.

Characterization of camel ear variation

Amr A. Alsharif, Bader H. Alhajeri, and Hasan Alhaddad
Department of Biological Sciences, Kuwait University, Kuwait

Background
Camel shows diversity for ear variation. However, a relatively low number of studies have been conducted on the ear variation in camels. The aim of this study was to characterize the ear variation in camels and to identify the genetic factors associated with it.

Methods
A total of 100 camels were sampled from different regions in Kuwait. The ear variation was characterized by measuring the ear length, ear width, and ear area. The genetic factors associated with ear variation were identified using PCR and sequencing techniques.

Results
The study identified several ear phenotypes, including short, intermediate, and long ears. The genetic factors associated with ear variation were identified as SNPs in the *FGF5* gene.

Conclusion
The study provides a comprehensive characterization of camel ear variation and identifies the genetic factors associated with it. This information is valuable for breeding programs and for understanding the evolution of ear variation in camels.

Keywords
Camel, ear variation, *FGF5* gene, SNP, ear length, ear width, ear area.

Phenotypes of Mezeayan (Mezayan) Camel-types

Elmehdi Samad, Tasneem Maraga, Bader H. Alhajeri, and Hasan Alhaddad
Department of Biological Sciences, Kuwait University, Kuwait

Background
Mezeayan camels are a unique breed of camels found in the Mezeayan region of Kuwait. They are characterized by their long hair and unique ear shapes. The aim of this study was to characterize the phenotypes of Mezeayan camels and to identify the genetic factors associated with them.

Methods
A total of 50 Mezeayan camels were sampled from the Mezeayan region. The phenotypes were characterized by measuring the ear length, ear width, and ear area. The genetic factors associated with the phenotypes were identified using PCR and sequencing techniques.

Results
The study identified several Mezeayan phenotypes, including long hair, short hair, and intermediate hair. The genetic factors associated with the phenotypes were identified as SNPs in the *FGF5* gene.

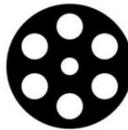
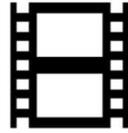
Conclusion
The study provides a comprehensive characterization of Mezeayan camel phenotypes and identifies the genetic factors associated with them. This information is valuable for breeding programs and for understanding the evolution of Mezeayan camels.

Keywords
Mezeayan camel, ear variation, *FGF5* gene, SNP, ear length, ear width, ear area.

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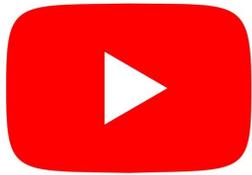
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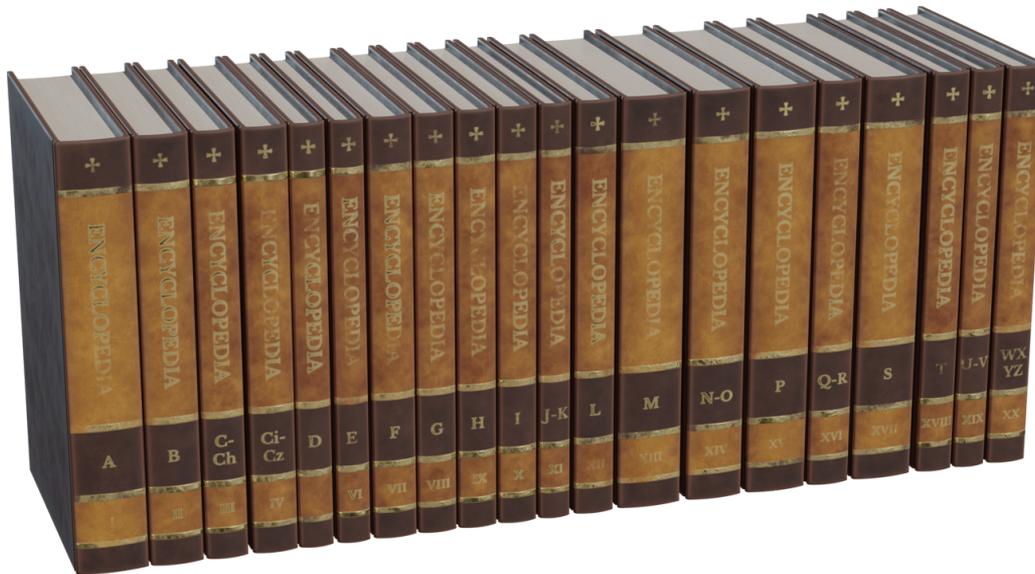
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ABSTRACT

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Introduction

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* Corresponding author. Tel.: +33 4 67 50 50; fax: +1-123-345678.

E-mail address: example@examplemail.com (E. Author One).

¹ UFR 208 Biopolymères Interactions Assemblages, INRA, F-44116 Nantes, France

² CNRS-IOM-OGG, c/o Institut Laue-Langevin, 6 rue Jules Horowitz, BP 156, 38042, Grenoble Cedex 9, France.

³ Institut Laue-Langevin, 6 rue Jules Horowitz, BP 156, 38042 Grenoble Cedex 9, France.

⁴ Université Joseph Fourier UFR PHTM, BP 53, 38041 Grenoble Cedex 9, France.

⁵ Institut de Biologie Structurale, 41 rue Jules Horowitz, 38027 Grenoble Cedex 1, France.

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