

1 Introduction

2 Aims & Hypotheses

3 Methods & Materials

4 Results

5 Discussion

6 Conclusions & Suggestions



**Thesis
presentation
outline**

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**Thesis
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1 The sixth most common cancer

2 More than one million new cases each year

3 Poor prognosis with 10–12 months median overall survival

4 The fourth most leading cause of cancer-associated mortality

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Gastric Cancer

in the world

1 The fifth most common cancer

2 The fourth place based on the incidence rate

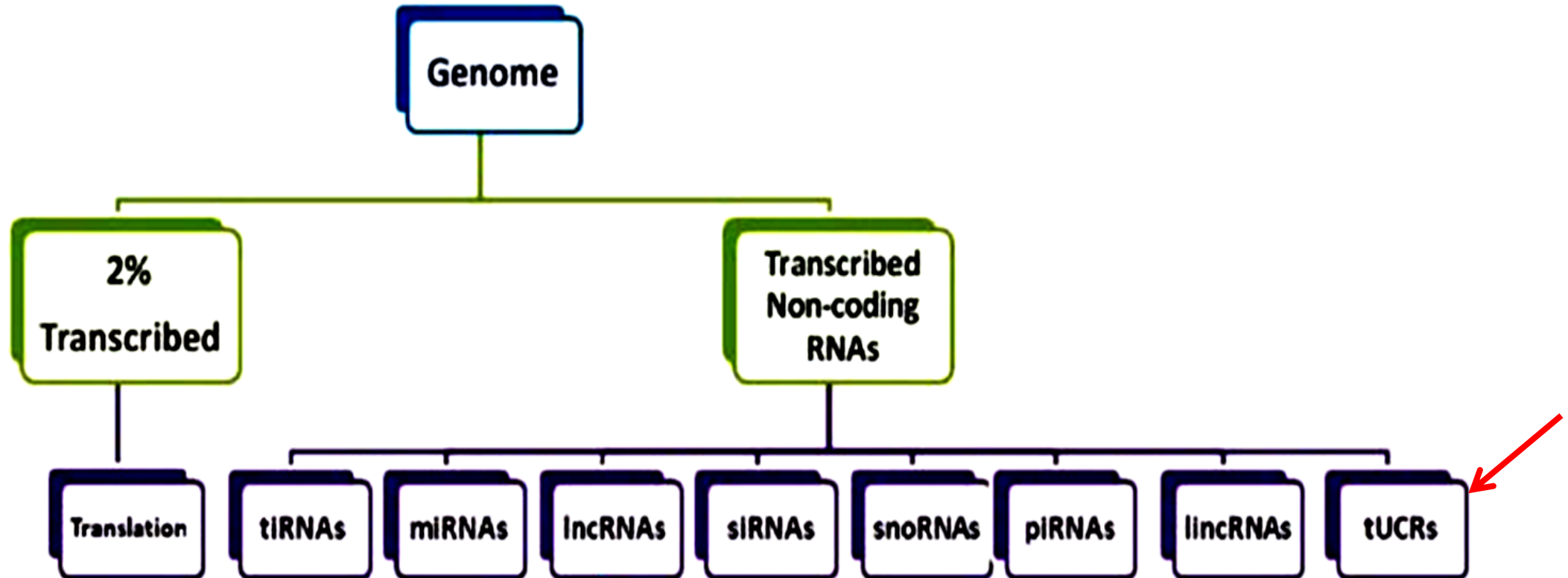
3 The fourth most leading cause of cancer-associated mortality



Gastric Cancer

in Iran

Non-coding RNAs and their classification



1 A new type of lncRNAs

2 Discovered in 2004 through bioinformatics comparisons of the mouse, rat and human genomes

3 100% identity between orthologous loci of the human, mouse and rat genomes

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Transcribed
ultraconserved
regions (T-UCRs)

4 481 genomic elements longer than 200 bp (range: 200–779 bp)

5 Mostly in the fragile sites and cancer-associated genomic regions (CAGRs)

6 Acting as oncogenes or tumor suppressors

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Transcribed
ultraconserved
regions (T-UCRs)

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Literatures Review


1


2007

2

3

4

- 
- 1 Diagnosis of the disease in the advanced and metastatic stages
 - 2 The cause of the disease is unknown.
 - 3 Investigation of the pathways involved in gastric cancer in order to better understand the pathogenesis
 - 4 Thus far, no comprehensive analysis has been performed on the expression of all T-UCRs in gastric cancer.



**Importance
of
the study**

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2 **Aims & Hypotheses**

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**Determination of transcribed ultraconserved regions (T-UCRs)
involving in the gastric cancer by applying a system biology
approach and expression study of a candidate T-UCR**



**General
Aim**

Specific Aims



- 1 Determination of differentially-expressed T-UCRs in gastric cancer samples of TCGA cohort
- 2 Determination of differentially-expressed mRNAs in gastric cancer samples of TCGA cohort
- 3 Selecting a candidate T-UCR by constructing a network including differentially-expressed T-UCRs and mRNAs
- 4 Determination and comparison of the candidate T-UCR's mean expression in tumoral *vs* non-tumoral GC tissues