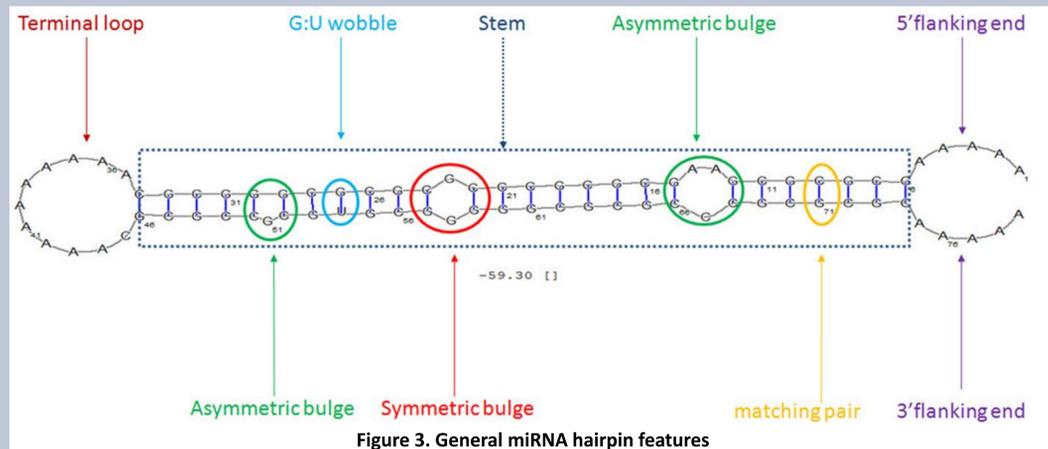
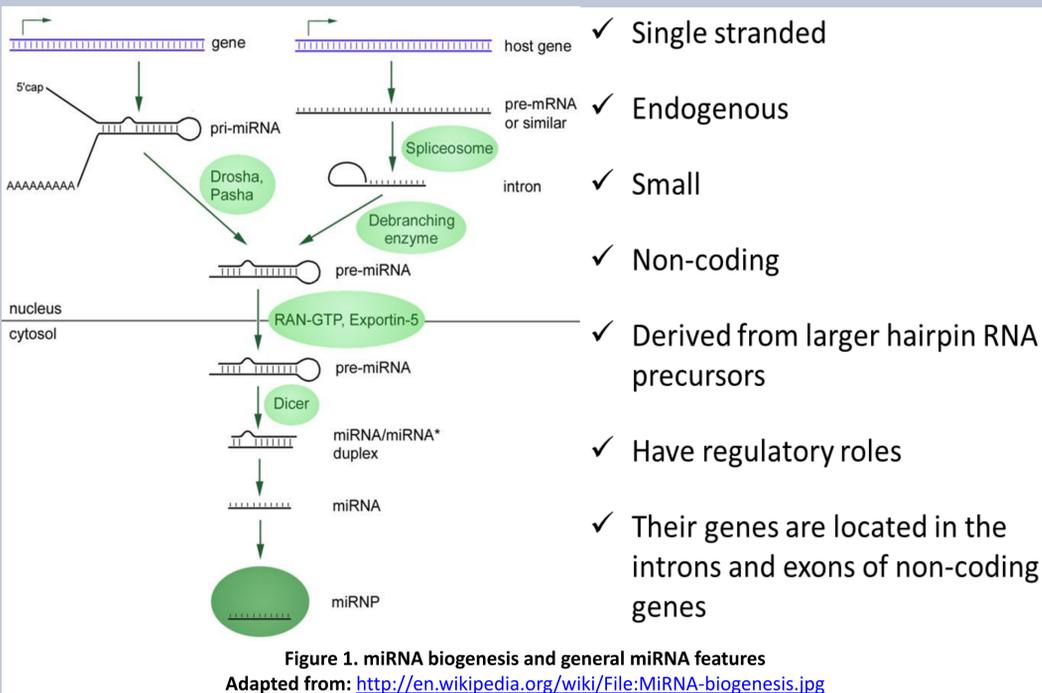


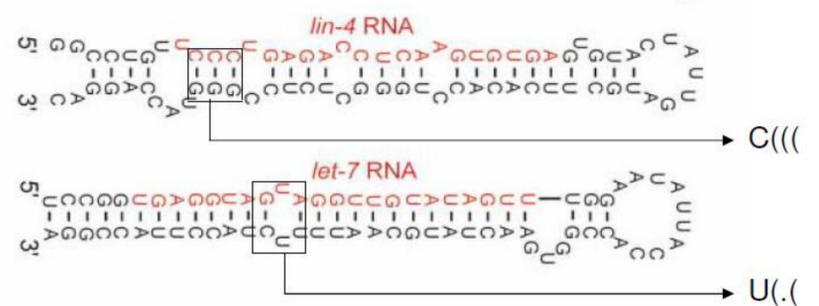
## Background

MicroRNAs (miRNAs) are single-stranded, small, non-coding RNAs of about 22 nucleotides in length that control gene expression at the post-transcriptional level through translational inhibition and destabilization of their target mRNAs (**Figure 1**). 20 to 30 percent of all human genes are controlled by miRNAs and relations between miRNA expression levels and human diseases such as Fragile X Syndrome (a type of mental retardation) and different types of cancers have been shown.



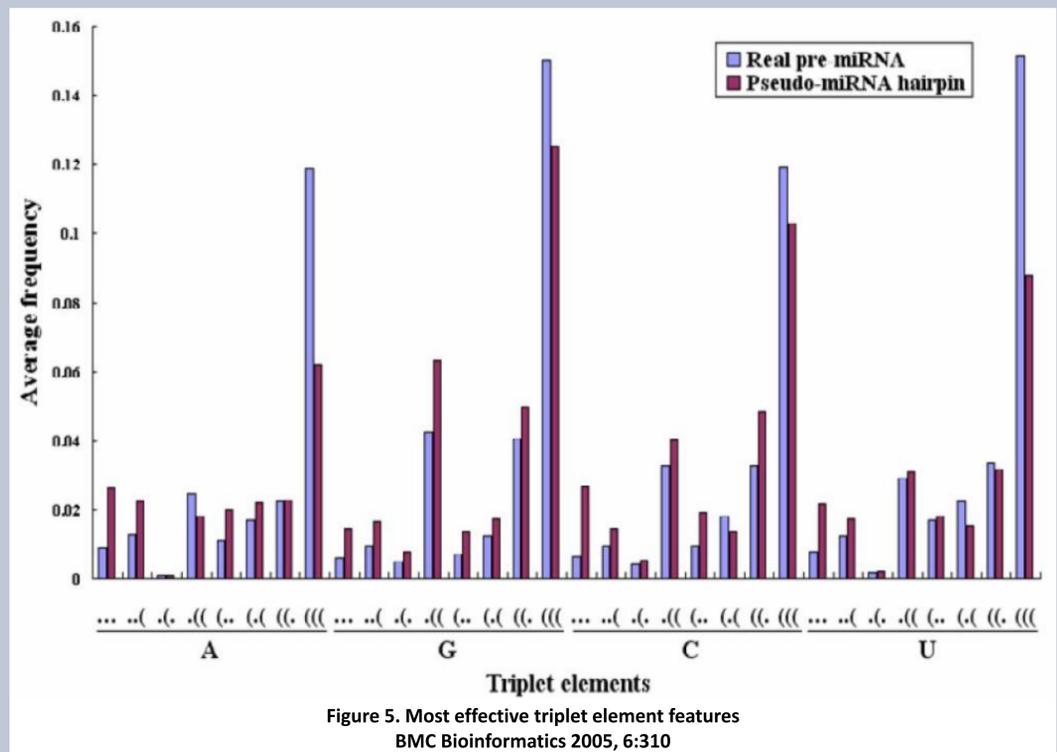
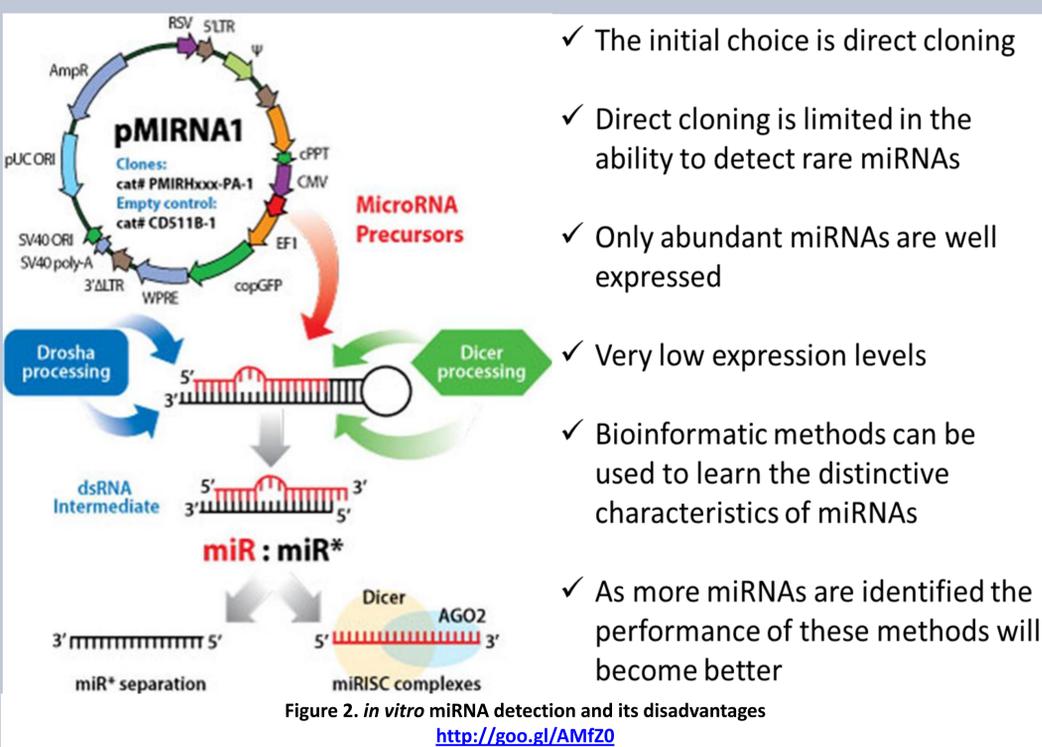
The triplet element is composed of the 3 adjacent nucleotides structures and the middle nucleotide type.

- paired sub-structure: brackets "(" or ")"
- unpaired sub-structure: dots "."
- nucleotide type: U/A/C/G



## Introduction

Many miRNAs have only recently been discovered and since laboratory methods for their detection are slow and expensive (**Figure 2**), bioinformatic studies have an undeniable importance in uncovering miRNAs and their roles and functions.



## Tools and Methods

Computational approaches benefit from some characteristic features of miRNA hairpins (**Figure 3**) including the GC content of the stem of the hairpin precursor which has proved to be a very important feature when looking to predict miRNAs, stem triplet elements (**Figure 4**), the number of unpaired nucleotides upstream of the 5' base (before the start of the stem), number of unpaired nucleotides downstream of the 3' base (following the end of the stem), size of the loop, stem length, hairpin length, free energy of the hairpin, number of mismatches in the stem, number of wobbles in the stem, number of unpaired nucleotides in the stem, average number of symmetrically occurring unpaired nucleotides and the free energy distribution over the stem.

## Outlook and Future Work

These and other features which may be presented in the future have to be taken into account in order to be able predict and present strong candidate miRNA hairpins for further *in vitro* and *in vivo* analyses.

## Contact Information

Jens Allmer, Associate Professor, IYTE, e-mail: [jens@allmer.de](mailto:jens@allmer.de)  
Müşerref Duygu Saçar, MSc. Student, IYTE, e-mail: [duygusacar@gmail.com](mailto:duygusacar@gmail.com)  
Hamid Hamzeiy, BSc. Student, IYTE, e-mail: [hamidhamzeiy@hotmail.com](mailto:hamidhamzeiy@hotmail.com)