

Computational prediction of interactions of long non-coding RNAs and micro RNAs in maize

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Motivation and Aim: Only 1 to 2 % of the genome sequences in the human body have protein-coding functions, and the content of non-coding regions without protein-coding capabilities is as high as 98 % [1]. The remaining expressed genes are likely to be transcribed into non-coding RNA (ncRNA). However, the research on long non-coding RNA (>200 nt, lncRNAs) has just entered the development stage, and the research on plant lncRNA started even later. Therefore, the research on plant lncRNA may reveal unknown new mechanisms controlling plant growth and differentiation [2]. Micro RNA (miRNAs) are small (22–24 nt) ncRNAs that can interact with protein-coding transcripts (mRNAs) providing their subsequent degradation and regulating their functioning. Interactions between miRNAs and mRNAs has been studied in detail [3]. However, the interaction between miRNA and lncRNA has rarely been studied in plants. So identification of potential MIRNA-lncRNA interactions in various plant species remains a challenging task. Furthermore, among the identified miRNA-lncRNA interactions, only a few have been analyzed for biological significance experimentally. The detailed functional mechanisms of these interactions remain unclear. It will also be interesting to understand whether these miRNA-lncRNA interactions, related functions, and mechanisms are conserved between different plant species. At present, lncRNA and miRNA discovered in animals and plants are difficult to verify through large-scale biological experiments. Therefore, there is an urgent need to use computational methods to reveal the characteristics of lncRNAs and miRNAs to guide those expensive and laborious laboratory experiments [1].

Methods and Algorithms: Most research on the mutual regulation mechanism between miRNA and lncRNA focuses on animal and human cancers, with relatively few studies on plants, and even less on corn. In order to deeply explore the interaction between corn miRNA and lncRNA, this article uses the PmliPred method [4]. This method is based on hybrid models and fuzzy decision-making, combines deep learning and shallow machine learning, and uses original sequences and artificial extraction of characteristic plant miRNA-lncRNA to achieve classification prediction of miRNA-lncRNA interaction relationships. Through the PmliPred method, the interaction information between miRNA and lncRNA can be used to predict potential relationships in the maize gene regulatory network. In order to achieve this goal, we first collect data, then preprocess the data and write a series of python programs to extract features from the data. PmliPred is then run for predictive analysis based on their sequences and features. As an effective tool, PmliPred helps us deeply explore the complex mechanisms of gene regulation in

maize, better predict the interaction between miRNA and lncRNA in maize, and provide an important reference for further functional research and breeding.

Results: Using PmliPred software, we predicted putative interaction between maize lncRNAs [5] and miRNAs. This allowed to reconstruct graph of the miRNA-lncRNA interacting pairs. Analysis of co-expression of the lncRNAs involved in the various interactions with miRNAs was also performed.

Conclusion: Our research provide new information about miRNA-lncRNA interaction in maize.

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