**附件一 论文、墙报格式**

**1. 论文格式及排版要求**

（1）论文大小要求：提交word 文档，A4纸页面不超过6页。

（2）论文内容要求：所有论文应有文题，作者姓名(多个作者用逗号隔开)及其单位名称（做各单位标明单位阿拉伯数字顺序码，包括单位名称、所在城市、邮政编码），中文摘要和关键词，引言，材料与方法（材料与方法为同一个部分），结果，讨论，参考文献，以及英文的文题、单位名称、摘要与关键词。论文标准层次按1，1.1，1.1.1，1.1.1.1，…的形式排列。

（3）论文排版要求：①字体要求：题目用4号黑体，作者、单位及邮编用5号楷体，正文用5号宋体，其中正文中的标题用黑体；②字数要求：字数6000字以内；③格式要求：请不要使用双栏或者多栏排版。

（4）论文脚注中需标明第一作者身份、项目资助（项目编号）、通讯作者与mail地址。

**2. 论文大摘要格式及排版要求（A4纸，一个版面）**

（1）摘要大小要求：提交word 文档，大小不超过1M。

（2）摘要内容要求：摘要包括题目、作者（多个作者由逗号隔开）、工作单位（单位名称、所在城市、邮政编码）、引言/目的、材料方法、结果、讨论、主要参考文献（限5篇以内，可省略）等内容。

（3）摘要排版要求：①字体要求：摘要题目用4号黑体，作者、单位及邮编用5号楷体，正文用5号宋体，其中正文中的标题用宋体加粗；②字数要求：摘要字数1000字以内；③格式要求：使用A4纸，排版不超过1页（单倍行距），请不要使用双栏或者多栏排版，可参考附件二-3中的模板格式；④原则上摘要中应无图表，如若有图表，最多1～2个。

（4）论文脚注中需标明第一作者身份、项目资助（项目编号）、通讯作者与mail地址。

（5）已发表的论文可投稿（2018年10月后发表），但在论文脚注中需标明发表时间和期刊名称等。

**3. 论文大摘要格式模板**

**水牛泌乳期与非泌乳期乳腺组织miRNAs差异表达研究**

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**引言**

水牛作为发展中国家重要的乳、肉、役兼用畜种，被国际粮农组织（FAO）认为是最具开发潜力和开发价值的家畜。高通量测序技术已成功运用于人、奶牛、奶山羊等生物miRNA研究，发现差异表达miRs的靶基因主要参与乳腺发育、细胞增殖和乳脂合成等重要代谢过程[1,2]。但是水牛乳腺组织miRNA测序与表达谱的相关研究较少。因此，本试验通过对本地水牛泌乳中期和非泌乳期乳腺组织小RNA进行序列测定，探究乳腺特异表达miRNA，并进行生物信息学分析，为研究水牛乳腺发育和泌乳提供理论参考。

**材料方法**

采集水牛泌乳期和非泌乳器乳腺组织，利用Solexa测序技术构建两个时期miR表达谱，鉴定前体miR、成熟miR和新miR，分析miR的第一普遍核苷酸和染色体分布，发掘水牛泌乳期和非泌乳期高表达及差异表达miRs。

**结果与讨论**

构建了水牛泌乳期以及非泌乳期乳腺组织2个miRNA表达谱，分别获得非泌乳期和泌乳期12,569,467和12,768,110 条18nt-31nt 的高质量序列。分析鉴定出259个miRNAs家族的359个成熟miRs和363个pre-miRs及5个水牛特有的miRs。Bbu-let-7b, bbu-let-7a, miR-26a和miR-21等5个miRs在两个时期均呈现高表达；Bbu-miR-148a,143, 200c,200a和bbu-let-7f等5个miRs在非泌乳期特异性高表达。Bbu-miR-125b,29a和 bbu-let-7c等3个miRs在泌乳期特异性高表达。Bbu-miR-148a,143,200a,141和30a-5p 等5个miRNAs在泌乳期的表达量下降为非泌乳期的1/2以下。而bbu-miR-26a, 29a, 125b, 99a和let-7c等5个miRs在泌乳期表达量大于或等于2倍非泌乳期丰度。本研究为进一步阐明奶水牛泌乳关键miRs作用机制奠定了基础。

**主要参考文献**

[1] Lin XZ, Luo J, Zhang LP, Wang W, Gou DM. MiR-103 Controls Milk Fat Accumulation in Goat (Capra hircus) Mammary Gland during Lactation. PLoSOne, 2013, 8(11): e79258.

[2] Kosaka N,Izumi H,Sekine K,Ochiya T. microRNA as a new immune-regulatory agent in breast milk. Silence, 2010, 1(1): 7-7.

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**4. 英文论文摘要格式模板**

**Identify and** [**analyze**](http://www.so.com/link?url=http://dict.youdao.com/search?q=analyze&keyfrom=hao360&q=%E5%88%86%E6%9E%90+%E8%8B%B1%E6%96%87&ts=1487584588&t=18e9264089578b5546657d17d590cc2) **the expression profile and mechanism of buffalo mammary gland miRNAs in the lactation and non-lactation periods**

CAIXiaoyan1，2, BAO Zhengpan1, ZHANG Xiaoxi1, REN Yanping1, SHENG Penglei1, SHI Deshun1\*

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**Objective:** This study aimed to identify and [analyze](http://www.so.com/link?url=http://dict.youdao.com/search?q=analyze&keyfrom=hao360&q=%E5%88%86%E6%9E%90+%E8%8B%B1%E6%96%87&ts=1487584588&t=18e9264089578b5546657d17d590cc2)the expression pattern and mechanism of buffalo mammary gland miRNAs in the lactation and non-lactatation periods.

**Method:** Buffalomammary gland tissuesof lactation and non-lactation periods were collected, their miRNAs expression profiles were analyzed by Solexa sequencing technology, pre-miRNAs, mature miRNAs and novel miRNAs were identified separately, the first preference nucleotide and Chromosome distribution were analyzed. The highly and differentially expressed in the lactation and non-lactation periods were detected.

**Result:** The results showed that two miRNAs expression profiles from buffalo lactation and non-lactation mammary gland were constructed. 12,569,467 and 12,768,110 high-quality reads between 18nt and 31nt were obtained separately. Three hundred fifty-nine mature miRNAs, 363 pre-miRNAs belonged to 259 miRNAs families and 5 buffalo-specific miRNAs were confirmed. U was the most common nucleotide at the 5 'end of 19nt and 25nt miRNAs. The bbu-let-7b, bbu-let-7a, miR-26a and miR-21 showed high expression in both periods. Bbu-miR-148a, 143, 200c, 200a and bbu-let-7f were highly specificially expressed in non-lactation period., bbu-miR-125b, 29a and bbu-let-7c were highly specifically expressed in lactation period. The bbu-miR-148a, 143, 200a, 141 and 30a-5p decreased the expression in the lactation period to less than 1/2 of the non-lactation period, bbu-miR-26a, 29a, 125b, 99a and let-7c were highly expressed more than or equal to 2 times of the lactation period.

**Conclusion:** The results indicate that Two miR profiles of buffalo lactation and non-lactating mammary gland tissues were constructed. 359 mature microRNAs and 363 pre-microRs of 259 buffalo miRNAs were identified.5 buffalogenome-specific miRNAs, 8 specially high expression miRNAs and 10 high expression differently miRNAs were obtained, which laid the foundation for further elucidating the mechanism of key miRs in lactating buffalo.

**Key Words:**buffalo;lactation and non-lactation; mammary gland tissues;miRNA expression pattern;signaling pathways

**Reference:**

[1] Lin XZ, Luo J, Zhang LP, Wang W, Gou DM. MiR-103 Controls Milk Fat Accumulation in Goat (Capra hircus) Mammary Gland during Lactation. PLoS One, 2013, 8(11): e79258.

[2] Kosaka N, Izumi H,Sekine K,Ochiya T. microRNA as a new immune-regulatory agent in breast milk. Silence, 2010, 1(1): 7-7.

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**5. 墙报格式及排版要求**

墙报要求：墙报大小：90cm宽×120cm长；题目与小标题至少为80号字体，正文字号不小于36号；内容应包括：题目、姓名、单位地址、引言、材料与方法、结果与讨论、结论、致谢或参考文献；图表数量不限、形式多样、颜色搭配合理。

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