Blood Transcriptome Analysis reveals Age-associated changes in Expression Profile of Immune-Related Gene in Golden snub-nosed Monkey (*Rhinopithecus roxellana*)

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Abstract

Background Golden snub-nosed monkeys (Rhinopithecus roxellana) are an endangered species in China. In the present study, the blood transcriptomes of nine monkeys were characterized by using RNA-Seq technology.

Results 57.31 Gb high-quality sequencing data was obtained. The clean data of each sample was >5 Gb, and 86.17% to 94.48% of the reads of each sample could be compared to reference genome of snub-nosed monkey. After assembly, we obtained 24,992 genes, including 3,917 new genes. Many genes were up-regulated or down-regulated with age. In adult group of R. roxellana roxellana, there were 76 differential genes, including 68 up-regulated and 8 down-regulated genes, compared with the young group. While, compared with the adult group, in the old group there were 58 differential genes, including 25 up-regulated genes and 23 down-regulated genes. In R. roxellana qinlingensis, compared with the young group, 117 differential genes were obtained, including 34 up-regulated and 83 down-regulated genes. Functional enrichment analysis indicated that the up-regulated genes were mainly related to innate immune response and T-cell activity, while the down-regulated genes were mainly involved in B-cell activity, suggesting that immune competence of adult group increased gradually compared to young group. However, the adaptive immune function declined gradually in the old group.

Conclusions Our findings will contribute to understand on the molecular mechanisms of age-related changes in immune system, which will provide a foundation for future study in snub-nosed monkey.

Full-text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed.

However, the manuscript can be downloaded and accessed as a PDF.

Tables

Table 1 statistics chart of the result of the sample sequencing

| Samples | Clean reads | Clean bases | GC Content | %≥Q30 | %≥Q20 |
|---------|-------------|-------------|------------|-------|-------|
| RRM1    | 23,861,189  | 6,013,019,628 | 50.03%     | 92.51%| 96.75 |
| RRM2    | 20,926,605  | 5,272,865,233 | 53.23%     | 85.79%| 94.86 |
| RRM3    | 19,923,730  | 5,007,878,795 | 48.57%     | 92.23%| 97.67 |
| RRM4    | 22,731,423  | 5,728,318,596 | 49.82%     | 91.76%| 96.43 |
| RRM5    | 21,821,696  | 5,492,240,374 | 52.06%     | 90.17%| 97.23 |
| RRM6    | 24,582,024  | 7,345,755,684 | 53.34%     | 94.78%| 97.92 |
| RRM7    | 22,932,075  | 6,842,882,592 | 52.44%     | 93.94%| 97.55 |
| RRM8    | 26,157,724  | 7,819,569,876 | 53.07%     | 94.97%| 98.11 |
| RRM9    | 26,071,517  | 7,792,132,466 | 53.19%     | 94.93%| 98.05 |
### Table 2 Number of genes annotated to each database

| Anno Database | Annotated Number | Percentage | 300<=length<1000 | length>=1000 |
|---------------|------------------|------------|------------------|-------------|
| COG           | 6668             | 27.6%      | 1958             | 4627        |
| GO            | 19705            | 81.6%      | 7045             | 12084       |
| KEGG          | 14345            | 59.4%      | 4773             | 9239        |
| KOG           | 14591            | 60.4%      | 4645             | 9634        |
| Pfam          | 19685            | 81.5%      | 6947             | 12234       |
| Swiss-Prot    | 18365            | 76.0%      | 6411             | 11447       |
| eggNOG        | 22659            | 93.8%      | 8189             | 13797       |
| NR            | 24102            | 99.8%      | 8891             | 14427       |
| All           | 24154            | 100%       | 8912             | 14445       |

### Table 3 The number of new genes annotated into each database and the total number of annotations

| Anno Database | Annotated Number | Percentage | 300<=length<1000 | length>=1000 |
|---------------|------------------|------------|------------------|-------------|
| COG Annotation| 122              | 3.2%       | 52               | 65          |
| GO Annotation | 2106             | 55.2%      | 622              | 1395        |
| KEGG Annotation| 609             | 16%        | 256              | 318         |
| KOG Annotation | 530             | 13.9%      | 228              | 268         |
| Pfam Annotation| 628             | 16.5%      | 264              | 337         |
| Swiss-Prot Annotation | 1807 | 47.4% | 485 | 1259 |
| eggNOG Annotation | 2006 | 52.3% | 655 | 1257 |
| NR Annotation | 2981             | 78.2%      | 1021             | 1821        |
| All Annotated | 3004             | 78.8%      | 1032             | 1831        |

### Table 4 the statistics chart of SNP site distribution and type

| Sample | SNP Number | Genic SNP | Intergenic SNP | Transition | Trans-version | Heterozygosity |
|--------|------------|-----------|----------------|------------|---------------|----------------|
| RRM1   | 183,516    | 137,919   | 45,597         | 72.78%     | 27.22%        | 38.24%         |
| RRM2   | 101,415    | 75,053    | 26,362         | 74.44%     | 25.56%        | 37.41%         |
| RRM3   | 127,059    | 94,321    | 32,738         | 72.45%     | 27.55%        | 31.60%         |
| RRM4   | 196,836    | 149,387   | 47,449         | 72.56%     | 27.44%        | 40.36%         |
| RRM5   | 115,005    | 85,469    | 29,536         | 74.59%     | 25.41%        | 42.85%         |
| RRM6   | 113,843    | 85,749    | 28,094         | 75.06%     | 24.94%        | 41.65%         |
| RRM7   | 85,522     | 64,936    | 20,586         | 73.73%     | 26.27%        | 42.70%         |
| RRM8   | 98,229     | 74,368    | 23,861         | 74.44%     | 25.56%        | 29.03%         |
| RRM9   | 130,970    | 99,644    | 31,326         | 74.27%     | 25.73%        | 41.43%         |

### Table 5 Age and gender of 9 snub-nose monkeys
| Sample | age            | Gender | subspecies                  | group           |
|--------|----------------|--------|-----------------------------|-----------------|
| RRM1   | 1.6 years old  | male   | *R. roxellana roxellana*    | Young           |
| RRM2   | 4 years old    | male   |                            |                 |
| RRM3   | 5.72 years old | male   |                            | Adult           |
| RRM4   | 6.6 years old  | female |                            |                 |
| RRM5   | 23 years old   | female |                            | Old             |
| RRM6   | 3.88 years old | male   | *R. roxellana qinlingensis* | Young           |
| RRM7   | 4.8 years old  | female |                            |                 |
| RRM8   | 10.8 years old | female |                            | Adult           |
| RRM9   | 10.9 years old | male   |                            |                 |

Figures
Figure 1

the GO annotation cluster of 19705 transcriptomes
Figure 2

COG function annotation classification of 19705 transcripts

Figure 3

SNP classification annotation map in all samples
Figure 4

SNP mutation type distribution map
Figure 5

Expression correlation heat map between samples

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