**Table 1 Features of *S. ricini* genome.**

|  |  |
| --- | --- |
| Statistics |  |
| Total bases | 450,479,495 |
| No. of chromosomes | 14(male)/13(female) |
| No. of scaffolds | 155 |
| The longest scaffold [bp] | 33,970,159 |
| Average scaffold length [bp] | 2,906,319 |
| scaffold N50 [bp] | 21,366,385 |
| Heterozygosity [%] | 0.0466–0.0472 |
| Genomic Features |  |
| Protein coding gene | 16,702 |
| G + C [%] | 34.3 |
| Repetitive elements [% (bp)] | 43.5 (196,045,652 bp) |

**Table 2 The result of linkage analysis.**

|  |  |
| --- | --- |
| Chromosome | Scaffold |
| Z | 13,30 |
| 1 | 2,26 |
| 2 | 10,17,21,24 |
| 3 | 8,14,19 |
| 4 | 4,25 |
| 5 | 1,23,27 |
| 6 | 6,35 |
| 7 | 11,15 |
| 8 | 3 |
| 9 | 7 |
| 10 | 9,18 |
| 11 | 22,28,31,32,33,34 |
| 12 | 12,16,30 |
| 13 | 5,29 |

**Table 3 The presence of *Fib-H*, *Fib-L*, *fibrohexamerin*, *p25* and *sericin* genes in 5 lepidopteran genomes.**

The numbers in the column of *S. ricini* and *B. mori* stand for copy number of each genes. The accession numbers in the column of *P. xuthus* were derived from the transcripts of the corresponding genes, registered at Genbank. Circles in the columns of *P. xylostella* and *D. plexippus* indicate that genome assembly of each species has at least one genomic region showing high similarity to the *B. mori* silk proteins with an e-value less than 1e-5. Question marks means BLAST search failed to identify any region with high similarity.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | *S. ricini* | *B. mori* | *P. xylostella* | *P. xuthus* | *D. plexippus* |
| Fib-H | 1 | 1 | ○ | NP\_001299362.1 | ○ |
| Fib-L | 0 | 1 | ○ | NP\_001299492.1,BAB39503.1 | ? |
| fibrohexamerin (p25) | 3 | 8 | ○ | NP\_001299201.1,BAB39504.1 | ○ |
| Ser1/Ser3 | 6 | 2 | ○ | ? | ? |
| Ser2 | 1 | 1 | ? | ? | ○ |