

The complete mitochondrial genomes and phylogenetic analysis of four major *Panax* species

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ABSTRACT

Background: *Panax* species (ginsengs), which belong to the Araliaceae family, have been used as important medicinal plant worldwide for a long time. These plants have various pharmacological properties, and many studies have been performed on major metabolites. However, fundamental genetic studies for these valuable species are still limited and remained as a closed book.

Methods and Results: In this study, we completed mitochondrial genomes of four major *Panax* species including *P. ginseng* (Korean ginseng), *P. notoginseng* (Chinese ginseng), *P. quinquefolius* (American ginseng), and *P. vietnamensis* (Vietnamese ginseng) using hybrid assembly method. Korean ginseng showed a typical mitochondrial genome structure containing single circular form, but other three species had multipartite structure fragmented into 3-4 chromosomes. Mitochondrial genome of each species encoded 72 (45 protein-coding genes (PCGs), 24 tRNAs, and 3 rRNAs), 60 (38 PCGs, 19 tRNAs, and 3 rRNAs), 73 (44 PCGs, 26 tRNAs, and 3 rRNAs), and 94 (60 PCGs, 31 tRNAs, and 3 rRNAs) unique genes, respectively. Average GC contents were estimated as 45.1%, 45.19%, 44.32%, and 43.48%, respectively, which contained similar nucleotide compositions within *Panax* species. Phylogenetic analysis based on orthologous PCGs in mitochondrial genome with related species revealed that four *Panax* species clustered as a sister group and clearly distinguished from other families.

Conclusion: The first completed mitochondrial genomes of major *Panax* species will provide valuable information for further advanced studies involved with the important medicinal plants and the phylogenetic result will help to establish the obvious relationship among the related species.

METHOD & RESULTS



Fig. 1 Four major *Panax* species used in this study

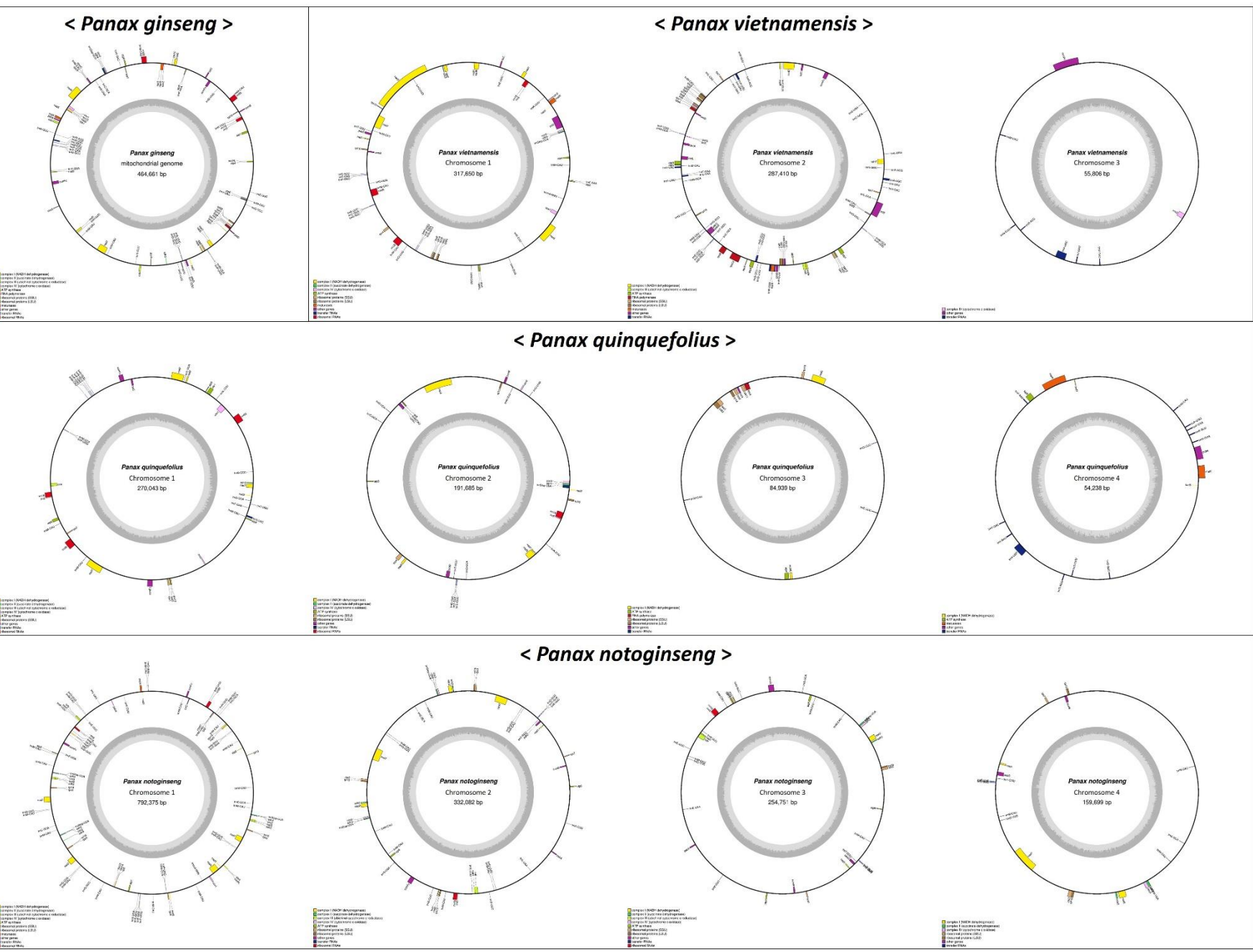


Fig. 3 The complete mitochondrial genome of four *Panax* species

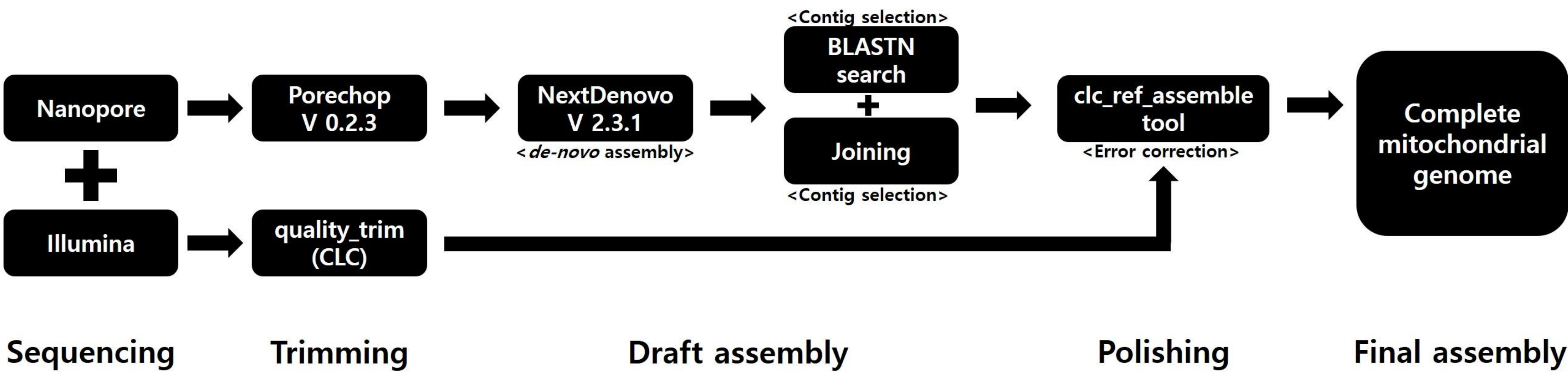


Fig. 2 Work-flow for mitochondrial genome assembly

Table 1 Statistics of raw and trimmed ONT reads for four *Panax* species

Sample name (SRA accession no.)	<i>P. ginseng</i>		<i>P. notoginseng</i>		<i>P. quinquefolius</i>		<i>P. vietnamensis</i>	
	Raw	After trimming	Raw	After trimming	Raw	After trimming	Raw	After trimming
Total read number	1,060,883	1,062,321	1,467,661	1,467,336	204,460	204,379	2,028,883	2,028,369
Total read bases (bp)	7,104,047,399	7,058,858,876	5,759,527,538	5,697,377,348	487,033,748	478,637,358	10,051,082,845	9,961,105,087
Max length (bp)	96,553	96,508	84,423	84,370	68,893	68,860	502,475	502,475
Average length (bp)	6.696	6.645	3.924	3.883	2.382	2.342	4.954	4.911
N50 (bp)	12,515	12,502	11,760	11,803	6,739	6,883	18,911	18,992
N90 (bp)	3,557	3,556	1,939	2,075	824	824	2,595	2,757
>1k reads No. / Base (bp) / Percent (%)	860,603 / 6,998,193,701 / 99	855,865 / 6,955,382,172 / 99	706,916 / 5,385,378,961 / 94	696,183 / 5,345,556,532 / 94	92,336 / 424,466,831 / 87	89,584 / 417,984,664 / 87	968,335 / 9,554,536,372 / 95	950,061 / 9,494,382,435 / 95
>5k reads No. / base (bp) / percent (%)	472,773 / 5,906,461,675 / 83	470,232 / 5,868,597,373 / 83	373,514 / 4,568,174,991 / 79	371,925 / 4,543,598,782 / 80	24,483 / 279,614,396 / 57	24,323 / 277,729,490 / 58	496,227 / 8,479,468,783 / 84	494,598 / 8,448,104,419 / 85
>10k reads No. / base (bp) / percent (%)	250,698 / 4,310,825,680 / 61	249,291 / 4,280,639,260 / 61	206,932 / 3,350,340,154 / 58	205,878 / 3,329,577,433 / 58	11,298 / 186,166,485 / 38	11,219 / 184,829,232 / 39	340,410 / 7,347,408,035 / 73	339,514 / 7,320,967,709 / 73
>20k reads No. / base (bp) / percent (%)	65,346 / 1,703,568,583 / 24	64,716 / 1,684,659,538 / 24	41,928 / 1,029,175,650 / 18	41,491 / 1,017,562,237 / 18	2,486 / 63,770,290 / 13	2,464 / 63,169,928 / 13	160,367 / 4,722,847,559 / 47	159,792 / 4,701,315,723 / 47

Table 2 Statistics of raw and trimmed Illumina reads for four *Panax* species

Sample name	<i>P. ginseng</i>		<i>P. notoginseng</i>		<i>P. quinquefolius</i>		<i>P. vietnamensis</i>	
	Raw	After trimming	Raw	After trimming	Raw	After trimming	Raw	After trimming
Total read number	57,844,148	50,404,922 (87.14%)	36,041,432	33,583,115 (93.18%)	57,063,762	51,315,911 (89.93%)	38,763,276	34,023,958 (87.77%)
Total read bases (bp)	8,734,466,348	7,164,444,434 (82.02%)	5,442,256,232	4,934,735,413 (90.67%)	8,616,628,062	7,338,594,828 (85.17%)	5,853,254,676	4,899,525,858 (83.71%)

Table 3 Characteristics of mitochondrial genome for four *Panax* species

Species name	Chromosome	Length (bp)	Aligned reads	Coverage (x)	Number of unique genes (PCG / tRNA / rRNA)	GC content (%)	GenBank accession no.
<i>P. ginseng</i> cv. 'Jakyung'	-	464,661	1,345,245	403.20	72 (45 / 24 / 3)	45.1	MZ389476
	1	792,375	899,860	163.90			MZ826156
<i>P. notoginseng</i>	2	332,082	183,524	79.60			MZ826157
	3	254,751	182,504	103.25	60 (38 / 19 / 3)	45.19	MZ826158
	4	159,699	94,899	86.20			MZ826159
	1	270,043	954,722	500.56			MZ826160
<i>P. quinquefolius</i>	2	191,685	895,552	657.95			MZ826161
	3	84,939	230,516	382.75	73 (44 / 26 / 3)	44.32	MZ826162
	4	54,238	398,235	1029.40			MZ826163
	1	317,650	240,237	107.37			MZ826164
<i>P. vietnamensis</i>	2	287,410	520,964	261.82	94 (60 / 31 / 3)	43.48	MZ826165
	3	55,806	60,158	149.66			MZ826166

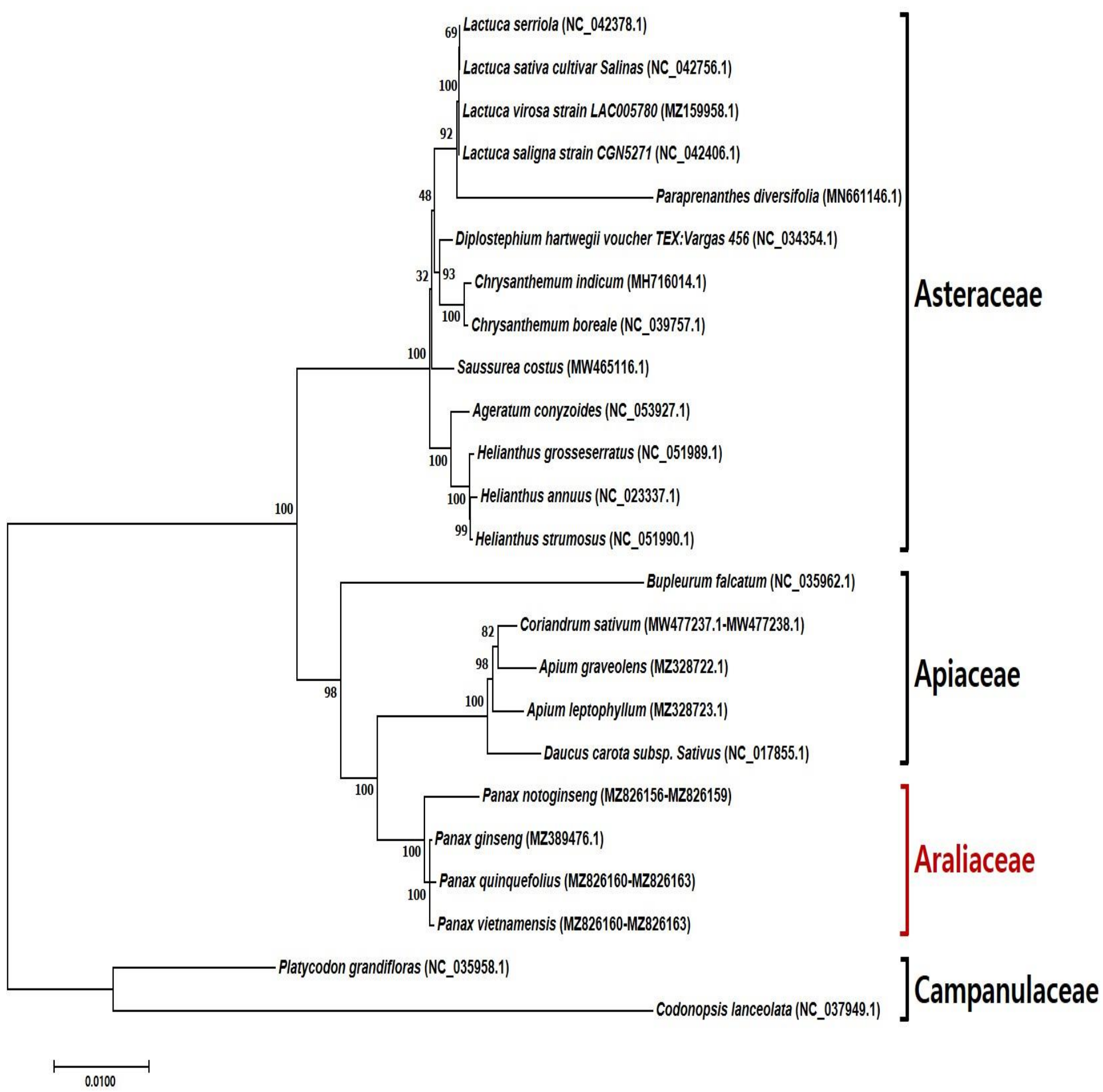


Fig. 2 Phylogenetic relationship among *Panax* and related species

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