The common sunstar, *Crossaster papposus* (Linnaeus 1767) is a conspicuous and ubiquitous starfish in the North Atlantic. *C. papposus* has a wide circumboreal distribution in all northern seas from the coastal region to oceanic depths (Clark and Downey 1992). The genus *Crossaster* belongs to the large family Solasteridae. Since Blake (1987) reinstated the order Valatida, the Solasteridae has long been regarded as a member of the order Valatida. However, based on the valvatacean phylogeny acquired using three genes (12S, 16S, and early-stage histone H3), Mah and Foltz (2011) assigned the Solasteridae to the order Valatida. In the recent phylogenetic analysis of seven asteroid orders (Linchangco et al. 2017), the Valatida appeared to be paraphyletic, and the members of the Solasteridae were not included in the tree. Here we present the complete mitogenome of *C. papposus*, which will be the first case within the Solasteridae. The whole mitogenome of *Crossaster* species will be useful to understand the phylogenetic context of the Solasteridae within the Asteroidea, as well as their diversity, taxonomy, and geographic distribution.

A specimen of *C. papposus* was collected in 2017 from the Beaufort Sea (82°46′1.7″N, 42°32′52.4″W) using a remotely operated underwater vehicle (ROV) of Monterey Bay Aquarium Research Institute (MBARI). The voucher specimen was registered both in the Research Institute of Basic Sciences of Incheon National University and in the Korea Polar Research Institute (Species ID: Echinodermata-01; Specimen ID: KOPRI-Benthos-01). Mitochondrial genomes were recovered by *de novo* assembling from Illumina shotgun sequence data. Genomic DNA was isolated using a QiAamp DNA Blood Mini kit (Qiagen, Hilden, Germany). Based on the manufacturer’s instructions (Illumina, San Diego, CA), a genomic library was constructed using SPAdes version 3.11.1 (Bankevich et al. 2012). Genomic features and annotations were performed using MITOS2 (Bernt et al. 2013) and tRNAscan-SE 2.0 (Lowe and Eddy 1997). The annotated gene structure was further confirmed using NCBI-BLAST (http://blast.ncbi.nlm.nih.gov). Mitochondrial genome of *C. papposus* was aligned with mitogenomes from other echinoderm genera, as well as two outgroup taxa from the genus *Balanoglossus*, and 13 PCGs were extracted for phylogenetic analysis (Nam et al. 2020). jModelTest version 2.1.10 (Darriba et al. 2012) was used to determine the best substitution model with an appropriate partitioning scheme, and a maximum likelihood phylogenetic analysis was conducted with 1000 bootstrap replicates in the PhyML version 2.4.5 (Guindon and Gascuel 2003).

The complete mitochondrial genome for *C. papposus* contained 13 PCGs, 22 tRNA genes, 2 rRNA genes, and a control region. The mitogenome for *C. papposus* (GenBank accession no. MW046047) was 16,335 bp long and had a GC content of 32.8% with an AT bias (A: 35.5%; T: 31.7%; G: 12.7%; C: 32.8%).
20.1%). The arrangement of genes and gene composition were identical to those of other starfishes. Our COI sequence was identical to the partial COI sequence (841 bp; GenBank accession no. MK270384) of *C. papposus* collected from the Baffin Bay (Ringvold and Moum 2020).

Although data for the order Velatida is lacking, our phylogenetic analysis using mitogenome data shows a similar ordinal relationship within the Asteroidea to the result of Linchangco et al. (2017). Our result resolved a close relationship of *C. papposus* to the derived cluster of the paraphyletic Valvatida, together which form a sister group to the order Spinulosida (Figure 1). This is in line with the previous suggestion that the Solasteridae belongs to the order Valvatida (Mah and Foltz 2011). Although different taxa of the

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**Figure 1.** Maximum-likelihood (ML) phylogeny of 38 echinoderms (15 asteroids including *C. papposus*, 7 crinoids, 5 echinoids, 5 holothuroids, and 6 ophiuroids) and two *Balanoglossus* mitogenomes as an outgroup based on the concatenated nucleotide sequences of entire protein-coding genes (PCGs). Numbers at nodes represent ML bootstrap percentages (1000 replicates). DDBJ/EMBL/Genbank accession numbers for published sequences are incorporated. The black arrow indicates the *C. papposus* analyzed in this study.
Valvatida were used for phylogenetic analysis, paraphyly of the order Valvatida was produced both in our study and in Linchangco et al. (2017). Future researches on the paraphyly of the Valvatida and the mitogenome data from the order Velatida are required.

Disclosure statement
No potential conflict of interest was reported by the author(s).

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Data availability statement
The data that support the findings of this study are openly available in the National Center for Biotechnology Information (NCBI) at https://www.ncbi.nlm.nih.gov, accession number MW046047.

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