

Size doesn't matter: integrative taxonomy shows Crepidula adunca and Crepidula norrisiarum have overlapping shell size and broadly concordant distributions

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Size doesn't matter: integrative taxonomy shows Crepidula adunca and Crepidula norrisiarum have overlapping shell size and broadly concordant distributions. --Manuscript Draft--

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Abstract:	The calyptraeids Crepidula adunca and Crepidula norrisiarum, both direct-developers, are abundant in the shallow waters of the northeastern Pacific. They have long been considered as two allopatric species that live on different hosts and differ in body size. In this study, we rigorously test this historical hypothesis by assessing molecular taxonomy, museum records, new morphological and host observations, and population genetic structure along the northeast Pacific coast. Results show that contrary to previous understanding, the distributions of the two species largely overlap, and that size does not effectively distinguish them, especially in the northern part of the range where the nominal "C. adunca" has been studied. Newly recognized northern occurances of C. norrisiarum demonstrate that both species have similar, disrupted distributions that range from British Colombia through Southern California. Neither species is reported to occur on the outer shores of Southern Washington or Oregon, the exception being records of C. adunca at Cape Arago, Oregon. Despite this apparent geographic gap, neither species shows appreciable genetic differentiation between the northern and southern parts of their ranges. Despite that body size has been used to distinguish these species, our observations do not support body size as a species-specific trait; rather, they support a new hypothesis that body size variation			

reflects regional differences in host use and host availability.

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- 19 **Abbreviations**:
- 20 ABGD: Automatic Barcode Gap Discovery
- 21 CAS: California Academy of Sciences: San Francisco
- 22 CASIZ: Unique voucher identifier of Invertebrate Zoology collections at the California Academy
- 23 of Sciences: San Francisco
- 24 CMN: Canadian Museum of Nature: Ottawa

cox1: Cytochrome c oxidase I 25 26 DFO: Fisheries and Oceans Canada: Canada 27 FMNH: Field Museum of Natural History: Chicago 28 LACM: Natural History Museum of Los Angeles County: Los Angeles 29 NHMUK: Unique voucher identifier at Natural History Museum: London 30 RBCM: Royal BC Museum: Victoria USNM: National Museum of Natural History: Smithsonian Institution: Washington: D.C. 31 32 AK: Alaska 33 BC: British Columbia 34 WA: Washington 35 OR: Oregon 36 CA: California 37 **Keywords**: slipper limpets; northeastern Pacific; *cox1*; systematics; phylogeography; mutualism. 38 39

Abstract

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The calyptraeids Crepidula adunca and Crepidula norrisiarum, both direct-developers, are abundant in the shallow waters of the northeastern Pacific. They have long been considered as two allopatric-species that live on different hosts and differ in body size. In this study, we rigorously test this historical hypothesis by assessing molecular taxonomy, museum records, new morphological and host observations, and population genetic structure along the northeast Pacific coast. Results show that contrary to previous understanding, the distributions of the two species largely overlap, and that size does not effectively distinguish them, especially in the northern part of the range where the nominal "C. adunca" has been studied. Newly recognized northern occurances of *C. norrisiarum* demonstrate that both species have similar, disrupted distributions that range from British Colombia through Southern California. Neither species is reported to occur on the outer shores of Southern Washington or Oregon, the exception being records of C. adunca at Cape Arago, Oregon. Despite this apparent geographic gap, neither species shows appreciable genetic differentiation between the northern and southern parts of their ranges. Despite that body size has been used to distinguish these species, our observations do not support body size as a species-specific trait; rather, they support a new hypothesis that body size variation reflects regional differences in host use and host availability.

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Introduction

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Species that form mutualistic relationships are subject to selective pressures imposed by their host and environment, and this can have an important impact on their phenotypic traits, behavior, and geographic range (Boucher, 1982; Afkhami et al., 2014, Pechenik et al., 2020). Well-studied examples of eco-evolutionary changes induced by mutualism are found in terrestrial and marine systems, from viruses to large mammals, including flowering plants and their animal pollinators or seed dispersers (Fleming and Estrada, 1993; Moeller et al., 2012). Marine examples have also been explored and include fish-cleaning shrimps that develop specific behavioral and morphological traits to attract their fish customers (Vaughan et al., 2017; Horka et al., 2018), and partner fidelity between sponges, corals and their symbiotic bacteria and zooxanthellae (Muller-Parker et al., 2015). Mutualism can involve close associations or more diffuse ones that allow switches to novel partners, or even to abandonment of mutualism (Toby Kiers et al., 2010; Freeman et al., 2015; Fang et al., 2017). Such processes can impact the geographic range of each mutualistic partner. In some cases, habitat fragmentation, population structure, and mode of dispersal may also impact whether the form of mutualism is close versus diffuse and affect the spatial dynamics of the interaction (Amarasekare, 2004).

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The sedentary, suspension-feeding gastropod mollusks known as slipper limpets (Calyptraeidae: Crepidula) provide a useful system for studying the impact of mutualism on phenotypic traits, behavior, and species distribution patterns. Numerous species in this group form long-term epibiotic associations with other invertebrates but many can also be opportunistically found on rocks and other hard substrates (Vermeij, 2020). Because the slipper limpet lacks an operculum and has a large aperture, the edges of the shell must grow to closely fit the curvature and irregularities of the substrate in order to protect the internal body.

Consequently, shell shapes and body size of calyptraeids often vary within species and among regions, being flat, arched, concave, scalloped, or twisted, depending on substrate shape and host identity (Coe, 1942; Vermeij *et al.*, 1987; Von Tungeln and Pernet, 2017). The phenotypic plasticity of slipper limpets has led to considerable taxonomic confusion and consequent misleading or ambiguous results of ecological studies, when the taxonomy is poorly resolved. Here we apply an integrative taxonomic approach to resolve one such taxonomic problem.

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For over 100 years, Crepidula adunca and Crepidula norrisiarum, both abundant shallow water calyptraeids of the northeastern Pacific, have been thought to have mostly allopatric distributions, to live on different hosts, and to have different shell morphologies and body sizes. Crepidula adunca is known for being a small, dark brown species found mostly intertidally on the gastropod Tegula funebralis in central California, or intertidally on Calliostoma ligatum as well as on T. funebralis in Washington State and British Columbia. Crepidula norrisiarum is known for being a large subtidal species, light rust-brown in color with brown radiating lines, that lives primarily on the large gastropod *Norrisia norrisii* in Southern California. Recently, a largescale assessment of biodiversity and community dynamics of littoral gastropods in British Columbia, Canada, showed two species with similar body size and shell morphologies co-occur there (Castelin et al., 2016). Individuals from the same sites could not be differentiated by shell morphology and had mitochondrial DNA and a nuclear marker divergence levels similar to those observed between other congeneric gastropods (Castelin et al. 2016). These observations challenged the species concepts and the historical hypothesis of two allopatric species varying in size and morphology, and raised questions regarding host-specificity, as the large, Californian host of C. norrisiarum, N. norrisii, is not present as far north as British Columbia. These observations led to an alternative hypothesis that shell morphology and body size are misleading

with respect to species identity and instead reflect regional differences in host use and host availability.

The present study investigates the geographic distributions and population genetic structure of *C. adunca* and *C. norissiarum* along the Northeast Pacific coast, and documents new morphological diagnostic traits to distinguish them. We also report host records based on available museum records and field observations to enable future investigation on the spatial dynamics of mutualism in these species. Our aim was to redress the relative lack of available data from the north (British Columbia), but we also conducted new collecting in the south (Washington to California) to add to existing samples. Finally, by re-describing the two species, we provide key diagnostic characters to distinguish them and give a more precise description of their respective distribution, habitats, and host preferences. The present study enables and encourages marine ecologists to: (i) accurately distinguish between *C. adunca* and *C. norrisiarum*; (ii) consider their co-occurrence when planning sampling strategies along the northeast Pacific coast; (iii) carefully document host use; (iv) pay extra attention to potential taxonomic misidentifications in the scientific literature.

Materials and Methods

Study area and specimen collection

Slipper limpets *C. adunca* and *C. norrisiarum* were collected between 2012 and 2019 (Table 1). Samples collected along the coast of British Columbia (BC) were obtained by hand either during dive surveys to 10 m depth or shore-based expeditions directed by Fisheries and Ocean Canada (DFO) and the Royal British Columbia Museum (RBCM), Victoria, BC, Canada. Samples from Washington (WA) were collected by hand at low tide from the intertidal zone by Collin (2000a;

2000b; 2004) (Fig. 1A). Animals were sampled in California (CA) in the intertidal by Eernisse, by dive surveys by personnel of the Channel Islands National Park (Fig. 1B), and material collected for past projects was also used (Collin (2000a; 2000b; 2004). In addition to the 35 specimens of *C. adunca* and *C. norrisiarum* available from Castelin *et al.* (2016), 12 individuals from BC (Ucluelet and Tofino) and 19 individuals from CA (San Simeon, Yellow Bank, and Santa Barbara) were newly-collected in this study for DNA sequencing. Two additional specimens, one from WA and one from CA with previously published sequences (Collin, 2003a), were added to the final dataset (Table 1).

After collection, all specimens were preserved for molecular analysis. Soft tissues were preserved in 95% ethanol, while shells were dried and kept intact for further study. Vouchers from Canadian samples were deposited in the biological collections of the RBCM, and those from the CA samples were deposited in the Natural History Museum of Los Angeles County (LACM) (Table 1).

PCR amplification and DNA sequencing

Total genomic DNA was extracted using the NucleoSpinR 96 Tissue kit (Macherey-Nagel, Allentown, PA, United States) following manufacturer's instructions. A fragment of the mitochondrial *cox1* was amplified using universal primers LCOI1490 and HCO2198 (Folmer *et al.*, 1994) using conditions described in Castelin *et al.* (2016). PCR products were purified with ExoSAP-IT (Affymetrix, Santa Clara, CA, United States) prior to bidirectional sequencing using PCR primers and BigDye Terminator v3.1 chemistry. Cycle sequencing reactions were purified using ethanol/EDTA precipitation followed by an additional ethanol wash and were electrophoresed using an ABI 3730xL DNA Analyzer (Applied Biosystems, Waltham, MA,

155 United States). Double stranded sequences were assembled and edited using CodonCode Aligner 156 v. 4.1.1 (CodonCode Corporation, Dedham, MA, United States). 157 158 DNA sequence alignment and molecular analysis 159 Alignments were generated using MAFFT v. 7 (Katoh et al., 2002; Katoh and Toh, 2010). 160 Sequences were aligned using the FFT-NS-I option, which is recommended for alignments of 161 closely-related sequences with global homology (Katoh and Toh, 2008). The offset value was set 162 at 0.1, as gaps were not expected. The accuracy of automatic alignments was confirmed by eye 163 and protein coding sequences were translated into amino acids using MEGA v. 5.05 (Tamura et 164 al., 2011) to check for gaps and stop codons. Newly produced sequences from Canada were 165 deposited in BOLD Systems in the project DS-CREPID West Coast Crepidula (SGPBS001-20 to 166 SGPBS011-20) and in GenBank (MN992952 - MN992958, MN992960 - MN992961). Those

The Automatic Barcode Gap Discovery (ABGD) method of Puillandre *et al.* (2012) was applied to our *cox1* dataset to assign newly-sampled specimens to species (i.e., to *C. adunca* or *C. norrisiarum*) using sequences from existing phylogenies (Collin, 2003a; Castelin *et al.*, 2016). The ABGD method was implemented using the online version of the program with the relative gap width (X) set to 10.

from CA were deposited directly in GenBank (OK526437 - OK526467) (Table 1).

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Within each species, identical sequences were identified using DnaSP version 6 (Librado and Rozas, 2009). To visualize the genealogical relationships among haplotypes and geography, median-joining networks (MJN) were constructed for both species using the program NETWORK 10.2 (Bandelt *et al.*, 1999) with equal weights for variable sites (epsilon = 0) using

the connection cost calculation method. To delete superfluous median vectors and links that are not contained in the shortest tree, we ran a postprocessing maximum parsimony calculation.

Genetic differentiation within each species was assessed using Arlequin 3.5.2.2 with an analysis of molecular variance (AMOVA; Excoffier *et al.*, 1992). Individuals within each species were partitioned into northern (BC, WA) and southern (CA) localities. Estimates of Φ_{ST} were conducted using a distance matrix with 10,000 permutations and the pairwise difference model. Significance of Φ -statistics was calculated from 10,000 replicate analyses based on samples drawn randomly and an alpha value of 0.05 (Excoffier and Lischer, 2010). In addition, within-species, genetic diversity between northern and southern populations was assessed using number of segregating sites (S), nucleotide diversity (π , mean number of pairwise differences), and haplotype diversity (Hd).

Morphological observations

Shell morphology of individuals in each genetic group (as identified by the ABGD method) was examined and overall shape and size of each individual were recorded as was their color, shell apex morphology, and extent of excavation of the apex below the shelf. Maximum shell length was measured using a precision caliper. The following features of the soft anatomy: osphradium morphology, penis morphology, and the shape of the female genital papilla were examined for a subset of individuals as these features have previously been shown to vary among closely related calyptracid species (Collin, 2000a; 2003b; 2019). The soft anatomy was examined for animals from both species, collected from south central CA and from *C. norrisiarum* from San Juan Island, WA. The shells of the type material of *C. adunca*, *C. norrisiarum*, and all species commonly synonymized with either species were examined either in person or using digital images requested from curators. If the type could not be found, we examined the illustrations in

the original description. Shell morphology was examined for more than 100 specimen lots from the Los Angeles County Museum, Invertebrate Zoology collections of the California Academy of Sciences (CASIZ), RBCM and Canadian Museum of Nature (CMN), including the syntypes of *C. norrisiarium* (LACM 1027).

Host observations

Records, including our own, were reviewed to determine what host species were used by the two *Crepidula* species. These included museum records and *in situ* images of *C. adunca* and *C. norrisiarum* posted on iNaturalist (2021) when diagnostic features including apex position, posterior slope shape (hooked or blunt), and/or shell color were clearly-identifiable.

Results

Molecular results

A total of 68 *cox1* sequences of 657 bp length were analyzed, of which 31 were newly-produced in this study (Table 1) and 37 were obtained from previous studies (Collin, 2003a, b; Castelin *et al.*, 2016). We found no evidence of *cox1* pseudo-gene amplification; no sites were scored as ambiguities by the software and no translations contained any stop codons. The ABGD method estimated 10 *a priori* thresholds, 9 of which led to partitions that split individuals into two groups separated by 11% divergence and associated with morphological differences (see taxonomic section). A total of 48 individuals were attributed to a mtDNA clade corresponding to *C. adunca* and 20 individuals to the reciprocally monophyletic group for *C. norrisiarum*.

The 48 individuals of *C. adunca* comprised 9 haplotypes, with 40 individuals sharing 4 haplotypes in the north (BC = 36 individuals, 4 haplotypes; WA = 4 individuals, 1 haplotype), and 8 individuals sharing 5 haplotypes in the south (CA). Consequently, although more individuals

were collected in the north, haplotype and nucleotide diversity was lower in the north (Hd = 0.146, π = 0.2) than in the south (Hd = 0.857, π = 2.07) (Table 2). No haplotypes were shared between the north and south.

The 20 individuals of *C. norrisiarum* displayed 13 haplotypes, with 12 individuals sharing 7 haplotypes in the north (BC = 11 individuals, 7 haplotypes; WA = 1 individuals, 1 haplotype), and 8 individuals sharing 6 haplotypes in the south (CA). Contrary to *C. adunca*, haplotype and nucleotide diversity was high both in the north (Hd = 0.833, π = 1.68) and south (Hd = 0.892, π = 2.14). No haplotypes were shared between the north and south.

In both species, haplotype networks showed geographic structure between northern and southern regions (Fig. 2-3). In *C. adunca*, a major northern haplotype was shared among individuals from the west coast of Vancouver Island, BC (Brooks Bay, Ucluelet, Port Renfrew) and individuals from the Pacific coast of the Olympic Peninsula, WA (Cape Alava). This major haplotype was separated by one to two mutations from four single haplotypes from Brooks Bay and Ucluelet (BC) and from one haplotype from San Simeon (CA), itself separated by one to four mutations from three haplotypes from the same area (CA) (Fig.2). In *C. norrisiarum*, three groups could be distinguished: a main central group including five haplotypes shared among individuals from Yellow Bank and Santa Barbara (CA), Tofino-Ucluelet and Brooks Bay (BC), from which derived a second group including only individuals from Vancouver Island (BC), and a third including only genetically distant individuals from Yellow Bank (CA) (Fig. 3).

Within each species, significant levels of genetic heterogeneity were detected between northern and the southern localities. In *C. adunca*, genetic heterogeneity between northern and southern regions ($\Phi_{ST} = 0.686$, $P < 10^{-5}$) accounted for 69% of the total variance and variation within regions accounted for 31% ($P < 10^{-5}$). In *C. norrisiarum*, genetic heterogeneity between

northern and southern regions ($\Phi_{ST} = 0.369$, $P < 10^{-5}$) accounted for 37% of the total variance, and variation within regions accounted for 63% ($P < 10^{-5}$).

Morphology

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Detailed examination of our samples and type material shows that C. adunca and C. norrisiarum can be distinguished based on internal shell characters, and that these diagnostic features are present in the holotype of C. adunca and four syntypes of C. norrisiarum. Crepidula adunca (Fig. 4) is characterized by an elevated, hooked, shell apex, which often creates a strongly concave vertical posterior shell outline, and a clear excavation or dimple in posterior portion of the shelf when the cleaned shell is viewed from the aperture. This is consistent from small juveniles (<3mm) to adult specimens. Crepidula norrisiarum (Fig. 5) is characterized by a more appressed and somewhat blunt and more rounded apex which may be either at the level of the aperture or somewhat above the aperture. When elevated, the apex is less high and less distinct than that observed in C. adunca, and has a relatively straight vertical posterior shell outline. Crepidula norrisiarum also lacks the excavation or dimple in the shelf and the shell exterior often has a pinkish tint and a somewhat checkered pattern (Fig. 5). Nearly all shells have either one or the other of these suites of characters, although some samples are intermediate in morphology, making it difficult to distinguish some living individuals with certainty. The presence or absence of the dimple on the shelf, which can only be observed on dead shells, appears to be the most reliable feature to distinguish them.

The two species show distinct inter- and intra-specific variation in body size. *Crepidula adunca* reach sizes up to 27mm (depending on the host used) and the largest sizes seem to be attained subtidally. In contrast *C. norrisiarum* shows size dimorphism. In the San Juan Islands, WA, where this species is common on *Calliostoma ligatum*, *C. norrisiarum* usually does not

exceed 15mm (Collin, 2000b, 2003b; 2019), while it often reaches 30 to 40mm in the southern CA part of the range where it lives on *N. norrisii* (Collin, 2003c).

With respect to the soft parts, there are very slight differences in overall body color (Fig. 6) and in the morphology of the osphradia. The head, body, mantle, and foot of C. adunca is bright white with fine opaque white speckles, while the body of *C. norrisiarum* is a cream color. The difference is not obvious unless the animals are observed side-by-side. Both usually have some black pigment on the mantle and dorsal area of the food pouch and head, but this is usually more pronounced in C. adunca. In C. norrisiarum from both northern and southern localities the osphradial leaflets are unevenly spaced (which is unusual in *Crepidula* species), with a central leaflet flanked on each side by a gap and lateral to that a small cluster of leaflets with a total of no more than 19 (see Fig. 6A and Fid. 7B in Collin, 2003b). The gap is very pronounced in large animals and less obvious or absent in smaller ones. The osphradium in C. adunca shows a similar arrangement with one central leaflet flanked by a gap on each side and then a cluster of leaflets, but the leaflets are relatively longer and the gap seems relatively shorter than in *C. norrisiarum*. In both species the number of leaflets increases in a similar way with shell length (data not shown). Other features of the soft anatomy that have been used to distinguish closely related species of Crepidula, like mode of development and gross morphology of the female genital papilla, did not show obvious differences between these two species.

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Hosts

Crepidula adunca and C. norrisiarum have been observed on various hosts, including a number of occasional hosts (Table 3, Fig. 7). Of the many host species, only Tegula pulligo, Tegula brunnea, Calliostoma ligatum, and Alia carinata have so far been associated with both C. adunca and C. norrisiarum (Table 3).

In the northern part of the range and in central CA, specimens of *C. adunca* were collected intertidally on their typical host, *Tegula funebralis*. Interestingly, it has not been reported from *T. funebralis* in southern CA, even though this species is relatively common there in the intertidal, nor does *C. adunca* seem to occur on the similar intertidal species, *T. gallina*, which replaces *T. funebralis* to the south. In California *C. adunca* is known from the subtidal on *Tegula* spp. around Santa Barbara and on *Mitra idae* (Figure 7; R. Collin pers. obs.). In the northern part of the range, *C. adunca* was also commonly collected on *Lirabuccinum dirum* and occasionally on a number of other species. In BC, *C. adunca* has also been observed on snail shells occupied by hermit crabs as well as empty shells, as it has been in Oregon (R. Emlet, pers. com. 2019). *Crepidula adunca* was also sometimes found on rock in WA (RBCM 21-53-1) and the west coast of Vancouver Island (LACM 26030).

Southern CA specimens of *C. norissiarum* typically occurs subtidally attached to *Norrisia norrisii*, but we also observed some *C. norrisiarum* on low intertidal specimens of *Tegula brunnea* and subtidal specimens of *T. pulligo* in central CA as far north as Monterey Co. In central CA, *C. norrisiarum* was never observed on *Calliostoma ligatum*, while in WA and BC, it was most commonly collected attached to *Calliostoma ligatum* and occasionally *Tegula pulligo*.

Taxonomic Section

Crepidula Lamarck, 1799

- Crepidula Lamarck, 1799: 78. Type species: Patella fornicata Linnaeus, 1758.
- 315 Ianacus Mörch, 1852: 146. Type species: Crepidula unguiformis Lamarck, 1767.

317	Crepidula adunca G. B. Sowerby I, 1825
318	Crepidula adunca Sowerby I, 1825 (App.): 7. Holotype NHMUK 1997150. No locality. (Fig. 4).
319	Crepidula solida Hinds, 1844: 53, pl. 16, figs 7–8. Type lost, Bodegas, California. 10 fathoms.
320	Crepidula rostriformis Gould, 1846: 160, 1856, pl. 32, fig. 482. Holotype USNM 5872. Strait of
321	Juan de Fuca, Washington.
322	Crepidula adunca Sowerby I, 1825 Hoagland 1977 (in part)
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324	<i>Material sequenced</i> . KX069514 - KX069521; KX069523; KX069525 - KX069529; KX070349;
325	KX070351; MN992952 - MN992961; MT048416; OK526437 - OK526457 (Table 1). Other
326	material examined includes the entire dry collection at LACM and at CAS as well as material in
327	RC's personal collected from Diablo Canyon, California by Sean Andersen.
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329	Description
330	The shell is typically smooth, uniform chestnut to dark brown (Fig. 4). The shell can appear
331	ribbed when attached to a ribbed snail host, and the shape can take on the contours of the host.
332	The shell is typically oval but occasionally it is round when substrate is not limiting. The shell
333	length of animals living on other snails can reach 27 mm, and one particularly unusual individual
334	collected from a rocky substrate is 32.7 mm (LACM 26030). The apex is raised, usually nearly
335	as high or higher than the body of the shell, and sharply hooked or beaklike. The apex is rostrate,
336	often projecting beyond the posterior margin of the base (Fig. 4, Fig. 7A-C, Fig. 7E). The shell
337	interior is dark chocolate brown with a white shelf or septum. The septum is flat, extends
338	straight across, without a medial ridge, and extends anteriorly on both sides. There is a deep
339	cavity like a dimple extending into the spire where the septum meets the posterior margin of the
340	shell (Fig. 4). This cavity was clear in both juvenile (<3 mm) and adult shells, and is not observed

in *C. norrisiarum*. There are muscle scars adjacent to the anterior extensions of the septum on each side.

External Anatomy is overall similar to other *Crepidula* species. Observations reported here are for *C. adunca* from Diablo Canyon, CA. The body is white with small opaque white speckles on the mantle and the top of the neck. There is black pigment on the top of the tentacles, snout and lips, as well as on the osphradium and the tip of the gills. These markings are similar but more pronounced than in *C. norrisiarum*. The lips are almost symmetrical making this species easy to distinguish from *C. naticarum*, a species only reported to live on naticid gastropod shells occupied by hermit crabs, in which the lips, head and neck are asymmetrical. The foot is extensible but retains the oblong, blunt shape when extended and does not form propodial tentacles and there are no mesopodial flaps. The osphardium is monopectinate, the leaflets are somewhat unevenly spaced in all but small males. One central leaflet is flanked on each side by a gap, followed by a cluster of leaflets. Leaflets are longer in *C. adunca* than in *C. norrisiarum* and the gap is less pronounced in *C. adunca*. The food pouch is right of the midline (when viewed from the aperture) and the rim does not form a large flap as it does in some *Crepidula* species.

Development is direct from large eggs. Hatching length has been previously reported as 1.19mm from naturally hatching broods of 6 females from Central CA (Putnam, 1964) which can be clearly identified as *C. adunca* from the illustrations in the paper. Coe (1949) reported eggs size as 400-420 μm from southern CA but the identity of his material is less clear. Uncleaved eggs from 2 clutches of animals collected in Diablo Canyon had mean hatching sizes of 503μm and 486μm. The embryos from these animals have a large head vesicle which is not filled with yolk, the velum is a simple rudiment at the base of the tentacles. Only late stage embryos were

observed but they appear to have only a single large larval "kidney cell", as compared to C. norrisiarum, which has a cluster of cells. Mean hatching size per clutch from Diablo Canyon ranged from $1044\mu m$ to $1426\mu m$ for 8 clutches.

Notes: Animals collected from San Juan Island, WA and referred to as *C. adunca* in Collin (2000; 2003a,b; 2004) are actually *C. norrisiarum*. This is also likely the case for Herstoff and Iyengar (2011) who collected animals at the same site and partially for Vermeij *et al.*, (1987) who included material from both species, *C. norrisiarum* from San Juan Island, WA (Fig. 1 in Vermeijj *et al.*,1987) and *C. adunca* from Tatoosh Island, WA.

Examination of the types of *C. rostriformis* and the figures in the description of *C. solida* clearly show the rostrate apex and cavity or dimple in the shelf extending into the shell apex (Fig. 4), which supports the conclusion that they are junior synonyms of *C. adunca*. Hoagland (1977) lists *C. uncata* Menke 1847 from Panama as a synonym, but this is almost certainly one of the related southern species, like *C. incurva*, that also live on gastropod shells. The Miocene fossil *Crypta rostralis* Conrad 1865 from the Astoria formation in Oregon could be either *C. adunca* or *C. norrisiarum* (or an earlier distinct species) based on our examination of the dorsal view of the holotype (USNM 110447) published in Moore (1963). We were not able to examine this shell as it could not be located in the USNM collections.

Distribution: Museum samples with diagnostic shell features indicate that the range extends at least from Cohen Island, Kachemak Bay, AK (LACM 59-23.18) to Santo Thomas, northern Baja California, Mexico (LACM 161700). This species is rare in the intertidal in southern California, especially south of Santa Barbara Co. It is also rare between northern California and northern Washington state, where it has been reported only from Cape Arago, OR (e.g., LACM collections

389	AHF 1989-42 through AHF1491-42; AHF 1492-42 . In the Strait of Juan de Fuca, C. adunca was
390	found only on the outer shores, west of Victoria, BC and west of Tongue Pt., WA.
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393	Crepidula norrisiarum Williamson, 1905
394	Crepidula rugosa norrisiarum Williamson, 1905: 50. Syntypes LACM 1027. San Pedro Bay,
395	California.
396	Crepidula norrisiarum Williamson, 1905. Hoagland 1977 (In part)
397	Crepidula adunca Sowerby 1825. Hoagland 1977 (In part)
398	Crepidula norrisiarum Williamson, 1905. McLean (In part)
399	Crepidula norrisiarum Williamson, 1905. Collin 2003a, b
400	Crepidula adunca Sowerby 1825 Collin 2000; 2003a,b
401	Crepidula norrisiarum Williamson, 1905. Collin 2019
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403	<i>Material sequenced.</i> AF546047; AF550487; KX069531; KX069533; KX069535; KX069537;
404	KX070358; OK526458 - OK526467 (Table 1). Other material examined includes entire
405	collection at LACM and CAS and animals included in Collin 2003a,b represented by vouchers:
406	FMNH282185, FMNH282173 - FMNH282175 from Naples Reef, Santa Barbara county, CA and
407	animals included in Collin (2000a,b).
408	
409	Diagnosis:
410	The shell exterior is typically smooth, light rust-brown with brown radiating lines or checkers
411	and often with a pinkish apex (Fig. 5). The radiating lines are not evident in many northern
412	specimens of C norrisiarum. The thin periostracum is sometimes worn away. The shell can

appear ribbed when attached and growing on a ribbed snail host and the shape can take on the contours of the host. The shell is typically oval but occasionally it is round when substrate is not limiting. The shell length reaches 40 mm in the southern range where it is found on the larger snail host, N. norrisii. In the northern range the shell length is typically to 15 mm. The apex is soft-pointed to blunt, projecting less than in C. adunca, and often almost symmetrical, near the midline, with a slight curve or tilt to the right (Fig. 5; Fig. 7F, G). The apex extends slightly past the posterior margin, usually overhanging it. The apex is generally on the lower half of the shell, sometimes at the level of the aperture, and is seldom the highest part of the shell. **The interior** is pink to tan, with a white septum. **The septum** is broadly U-shaped, and the sides extend forward. There are two muscle scars, each adjacent to the anterior extensions of the septum. The septum does not have a cavity where the septum meets the posterior shell margin (Fig. 5). The lack of a cavity under the spire (apex) was remarked upon by Williamson, 1905 in his original description of C. norrisiarum. In the northern population, the shell is more arched, the apex moderately raised, typically higher than in the southern form, and projecting beyond the posterior margin (Fig. 7G). This is likely due to the animals growing to fit smaller hosts.

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External Anatomy is overall similar to other *Crepidula* species. Observations reported here are from *C. norrisiarum* from San Juan Island, WA and from Santa Barbara, CA. The body is cream-colored (Fig. 5A) with sparse small opaque white speckles on the mantle and the top of the neck. There is a dusting of black pigment on the top of the tentacles, snout and lips, as well as on the osphradium and sometimes on the tip of the gills. The lips are almost symmetrical making this species easy to distinguish from *C. naticarum*, in which the lips, head and neck are asymmetrical. The foot is extensible but retains the oblong, blunt shape when extended and does not form propodeal tentacles and there are no mesopodial flaps. The osphardium is monopectinate, the

437	leaflets are unevenly spaced in all but small males (see Fig. 7A in Collin 2003b). One central
438	leaflet is flanked on each side by a gap, followed by a cluster of leaflets. Leaflets are shorter than
439	in C. adunca. The food pouch is right of the midline (when viewed from the aperture) and the rim
440	does not form a large flap as it does in some Crepidula species. The penis is evenly tapered and
441	slightly flattened with a groove extending to the end. The female genital papilla extends free into
442	the mantle cavity, it is not grooved.
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444	Development is direct from large eggs. In the San Juan Islands, uncleaved egg size was reported
445	as 260-320 μm (Collin 2000) and 240 μm (Strathmann, 1987), and hatching size was 1.5-2.7 mm
446	(Collin 2000) or 1.0-2.0 mm (Strathmann, 1987). In southern California uncleaved egg size from
447	the single brood from a definitive C. norrisiarum collected from a N. norrisii from Santa Barbara,
448	CA was 496 μm . Mean hatching was 1250 μm and 1304 μm for 2 broods from animals from the
449	same Santa Barbara population (Collin 2003). The embryos have a large head vesicle which does
450	not contain yolk and multiple embryonic "kidneys" (see figures in Collin 2000).
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452	Distribution: From Hotspring Island (52° 35'N; RBCM 979-2392) and Hope Island, British
453	Columbia (50°54'N; RBCM979-4221) to at least Punta Banda, (LACM 63-42), Todos Santos
454	(LACM67-45), Boca del Playa (LACM H-532) and Arbolitos (LACM 65320) Baja California,
455	Mexico in the south. The observed distribution is disjunct with an apparent gap of ~1,000km
456	between northern CA and the outer coast of WA and the Strait of Juan de Fuca.
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458	Notes: See comments for <i>C. adunca</i> about past taxonomic confusion between the two species.
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Discussion

Taxonomic misidentifications and phenotypic variation

Contrary to the historical expectation that *C. norrisiarum* is mostly restricted to southern California, our study shows that the species occurs up to the northern tip of Vancouver Island and in Haida Gwaii. It therefore largely overlaps with the geographic range of its close relative C. adunca. We found that the taxonomy of C. adunca and C. norrisiarum has been consistently confused, especially in the northern part of the range where all small-bodied animals were previously identified as C. adunca. Both species occur in the region and the two species are found in sympatry in the outer and transition coasts of the Strait of Juan de Fuca separating BC and WA. To our knowledge, only C. norrisiarum is found in the inner, protected waters of Puget Sound, San Juan Islands, and the Gulf Islands, where various aspects of the biology of C. norrisiarum have been studied and published under the name "C. adunca" (e.g., Hoagland, 1977; Vermeij et al., 1987; Herstoff and Iyengar, 2011; Collin 2000b). For instance, Hoagland (1977) and Vermeij et al. (1987) stated that despite extensive dredging in the San Juan Islands, "C. adunca" was never found on any other substrate than the shell of other animals, which made that species one of the most specialized slipper limpets in terms of range of substrates occupied. In light of our findings, it appears that this refers to C. norrisiarum, which does occur in the San Juan Islands and has not yet been observed attached to rock, while C. adunca has been observed attached to rocks at Waddah Island, WA, and Barkley Sound, BC. It seems likely that this taxonomic confusion has also impacted reports of host use. Our revision of published and museum data provide a starting point for more thorough documentation of host use.

Results presented here show that shell morphology and body size of *C. adunca* and *C. norrisiarum* are highly variable across their geographic distributions. The ranges in shell shape and body size largely overlap between the two species and, in both species, size and shape differ among sampling localities and host use. Therefore, while it seems likely that shell morphology and body size are host-dependent, it is also possible that phenotypic variation is related to geographic or bathymetric factors, or that it is the result of genetic differentiation. However, the shell size of *Crepidula* is necessarily limited by host size (e.g., Pechenik *et al.*, 2020). As a result, and because subtidal host species are generally larger than intertidal ones, *C. norrisiarum* is twice as large when living on the large subtidal trochid *Norrisia norrisii* than when living on the small intertidal trochid *Calliostoma ligatum*. Likewise, *C. adunca* becomes much larger when on the large subtidal *Tegula pulligo* than on the smaller intertidal *T. funebralis*. These observations support the hypothesis that shell morphology and body size are not species-specific traits but reflect regional differences in habitat, host use, and host availability.

Geographic distribution, shell museum records, and population genetic structure

Our assessment of museum collections showed that shells of *C. norrisiarum* are relatively common in southern California, but also occur in parts of central and northern California, the protected coast of Washington, and the outer and protected coasts of BC. They are, however, virtually absent from the outer shores of Washington, Oregon, and northern California north of Marin County. Notably the most common Californian snail hosts, the trochid *N. norrisii* is rarely, if ever, found north of Point Conception. The very sparse representation in museum collections of *C. adunca* and other calyptraeids from areas between northern California and the outer coast of Washington suggests that this exposed stretch of the western coast of the United States has been

poorly sampled. On the other hand, this exposed shore may not offer many suitable habitats for slipper limpets or their hosts. Indeed, numerous studies of intertidal communities in Oregon and Washington have classified this stretch of shore - dominated by barnacles and mussels and marked by the Point Conception boundary - as one of the most important biogeographic breaks on the US west coast (Valentine, 1966; Briggs, 1974; Newman, 1976; Doyle, 1985; Gaylord and Gaines, 2000), with many widespread northeastern Pacific species being strikingly rare in or absent from the outer coasts of Washington, Oregon, and northern California (e.g., Kozloff, 2000; Keever et al., 2009). In spring and summer, strong southward winds along these coasts generate nearshore upwelling that constitute a strong physical barrier to gene flow in many intertidal species. For some species, notably those with a pelagic larvae, this biogeographic break is consistent with a phylogeographic break (e.g., Burton, 1998; Barshis et al., 2011; Wares and Skoczen, 2019), whereas in other species, this range disjunction does not correspond to any apparent phylogeographic structure (Keever et al., 2009). For instance, Marko (1998) and Wares et al. (2001) showed that for the direct-developing gastropod species Nucella emarginata, these ocean currents may not represent a physical barrier. Further work is needed to determine the cause of the apparent disjunct distribution of C. norrisiarum, C. adunca, and calyptraeids in general along these shores.

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A noteworthy result of this study is that two sedentary species with direct development show such large geographic spread with a surprisingly low level of genetic differentiation between the southern and northern parts of their ranges. Although genetic divergences between northern and southern populations were highly significant in both species, fixation indexes were below expected values for other *Crepidula* species lacking dispersal stages. For instance, along Atlantic coasts of Florida and Yucatan, *C. convexa* and *C. atrasolea*, two direct developers, show

extremely high genetic differentiation among localities less than 200 km distant (Collin, 2001). Although more intense geographical sampling may increase observed Φ_{ST} values, the spatial distribution of haplotypes and the genealogical relationships among them also indicated only moderate genetic structure between northern and southern regions in both species. Interestingly, similar population genetic patterns have been observed in other direct developers along the same shore, like *Nucella ostrina* and *N. lamellosa* (Marko, 2004).

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Despite our limited sampling, our results can suggest hypotheses for further investigation when viewed in the context of previous studies on post-glacial range expansions of northeastern Pacific shallow water species. Studies show that many rocky intertidal species have undergone large and rapid latitudinal shifts along the northeastern Pacific coast in response to the last glacial maximum (e.g., Marko et al., 2010; McGovern et al., 2010; Kelly and Palumbi, 2010). In C. adunca, the star-shaped haplotype network and the low genetic diversity observed in the northern region could reflect a recent bottleneck or founder event followed by a demographic expansion of northern populations. Such genetic patterns were evidenced in similar co-occurring sibling species (e.g., Nucella spp) and attributed to the effects of Pleistocene glaciation, which would have eliminated northern populations (Marko, 2004). Interestingly, this genetic signature is not observed in C. norrisiarum; despite their close phylogenetic relationship and ecological similarity, C. adunca and C. norrisiarum may have contrasting biogeographic histories. Further sampling of *C. adunca* and *C. norrisiarum* with larger sample size and more genetic markers enabling robust assessment of past demographic processes (e.g., Marko et al., 2010; McGovern et al., 2010), as well as in-depth comparisons of genetic diversity across host-use and between the intertidal and subtidal species, are needed to further understand the eco-evolutive phylogeographic history of these sibling species.

555	
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575	All material has been collected under appropriate collection permits and threated in compliance

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Table 1: List of individuals of *Crepidula adunca* and *Crepidula norrisiarum* analyzed on *cox1* gene.

Locality	GenBank # or BOLD#	Museum voucher #	Depth	Host	Study
C. adunca					
Port Hardy, Vancouver Island	MT048416 = SGPBS011-20	RBCM 012-00012-007	intertidal	no data	Castelin et al. 2016
Quatsino Sound, Strathcona, Vancouver Island	KX069527 = CAMIB070-16	RBCM 016-00194-001	10 m	no data	Castelin et al. 2016
	KX069525 = CAMIB017-16	RBCM 016-00194-004	10 m	no data	Castelin et al. 2016
Brooks Bay, Brooks Peninsula, Vancouver Island	KX069528 = CAMIB062-16	RBCM 016-00195-001	10 m	no data	Castelin et al. 2016
	KX069529 = CAMIB061-16	RBCM 016-00195-002	10 m	no data	Castelin et al. 2016
	KX069519 = CAMIB035-16	RBCM 016-00196-001	10 m	no data	Castelin et al. 2016
	KX069520 = CAMIB034-16	RBCM 016-00196-002	10 m	no data	Castelin et al. 2016
Little Beach, Ucluelet, Vancouver Island	OK526437	LACM 2015-23.1	intertidal	on Nucella lamellosa	This Study
	OK526438	LACM 2014-38.1	intertidal	on Tegula funebralis	This Study
	OK526439	LACM 2014-38.2	intertidal	on Tegula funebralis	This Study
	OK526440	LACM 2014-38.3	intertidal	on Tegula funebralis	This Study
	OK526441	LACM 2014-38.4	intertidal	on Tegula funebralis	This Study
	OK526442	LACM 2014-38.5	intertidal	on Tegula funebralis	This Study
	OK526443	LACM 2014-38.6	intertidal	on Tegula funebralis	This Study
Big Beach, Ucluelet, Vancouver Island	MN992959 = SGPBS001-20	RBCM 016-00197-001	intertidal	on Tegula funebralis	Castelin et al. 2016
	MN992958 = SGPBS002-20	RBCM 016-00197-002	intertidal	on Tegula funebralis	Castelin et al. 2016
	MN992954 = SGPBS003-20	RBCM 016-00199-001	intertidal	on Tegula funebralis	Castelin et al. 2016
	MN992955 = SGPBS004-20	RBCM 016-00199-002	intertidal	on Tegula funebralis	Castelin et al. 2016
	MN992956 = SGPBS005-20	RBCM 016-00199-004	intertidal	on Tegula funebralis	Castelin et al. 2016
	MN992952 = SGPBS006-20	RBCM 016-00199-005	intertidal	on Tegula funebralis	Castelin et al. 2016
	MN992960 = SGPBS007-20	RBCM 016-00199-007	intertidal	on Tegula funebralis	Castelin et al. 2016
	MN992957 = SGPBS008-20	RBCM 016-00199-008	intertidal	on Tegula funebralis	Castelin et al. 2016
	MN992961 = SGPBS009-20	RBCM 016-00199-009	intertidal	on Lirabuccinum dirum	Castelin et al. 2016
	MN992953 = SGPBS010-20	RBCM 016-00199-011	intertidal	on Lirabuccinum dirum	Castelin et al. 2016
Ucluelet, Vancouver Island	OK526444	LACM 2014-36.1	intertidal	on Tegula funebralis	This Study
	OK526445	LACM 2014-36.2	intertidal	on Tegula funebralis	This Study
Botanical Beach, Port Renfrew, Vancouver Island	KX069514 = CAMIB419-16	RBCM 016-00191-001	10 m	no data	Castelin et al. 2016
	KX069515 = CAMIB418-16	RBCM 016-00191-002	10 m	no data	Castelin et al. 2016
	KX069516 = CAMIB417-16	RBCM 016-00191-003	10 m	no data	Castelin et al. 2016

	KX069517 = CAMIB416-16	RBCM 016-00191-004	10 m	no data	Castelin et al. 2016
	KX069518 = CAMIB415-16	RBCM 016-00191-005	10 m	no data	Castelin et al. 2016
	KX069526 = CAMIB414-16	RBCM 016-00191-006	10 m	no data	Castelin et al. 2016
Botany Bay, Port Renfrew, Vancouver Island	KX070351 = CAMIB355-16	RBCM 016-00190- 002	10 m	no data	Castelin et al. 2016
	KX069523 = CAMIB354-16	RBCM 016-00190-003	10 m	no data	Castelin et al. 2016
	KX070349 = CAMIB353-16	RBCM 016-00190-004	10 m	no data	Castelin et al. 2016
	KX069521 = CAMIB330-16	RBCM 016-00191-007	10 m	no data	Castelin et al. 2016
Cape Alava, Clallam County, Washington	OK526446	LACM 2014-37.1	intertidal	on Tegula funebralis	This Study
	OK526447	LACM 2014-37.2	intertidal	on Tegula funebralis	This Study
	OK526448	LACM 2014-37.3	intertidal	on Tegula funebralis	This Study
	OK526449	LACM 2014-39.1	intertidal	on Tegula funebralis	This Study
San Simeon, San Luis Obispo, California	OK526450	LACM 2013-91.1	intertidal	on Tegula funebralis	This Study
	OK526451	LACM 2013-91.2	intertidal	on Tegula funebralis	This Study
	OK526452	LACM 2013-91.3	intertidal	on Tegula funebralis	This Study
	OK526453	LACM 2013-91.4	intertidal	on Tegula funebralis	This Study
	OK526454	LACM 2013-91.5	intertidal	on Tegula funebralis	This Study
	OK526455	LACM 2013-91.6	intertidal	on Tegula funebralis	This Study
	OK526456	LACM 2013-91.7	intertidal	on Tegula funebralis	This Study
	OK526457	LACM 2013-91.8	intertidal	on Tegula funebralis	This Study
C. norrisiarum				O V	
Brooks Bay, Brooks Peninsula, Vancouver Island	KX069535 = CAMIB060-16	RBCM 016-00195-003	10 m	no data	Castelin et al. 2016
	KX069530 = CAMIB033-16	RBCM 016-00196-003	10 m	no data	Castelin et al. 2016
Frank Island, Tofino, Vancouver Island	KX070355 = CAMIB474-16	RBCM 016-00189-002	10 m	no data	Castelin et al. 2016
	KX069533 = CAMIB473-16	RBCM 016-00189-003	10 m	no data	Castelin et al. 2016
	KX070357 = CAMIB286-16	RBCM 016-00189-004	10 m	no data	Castelin et al. 2016
	KX070358 = CAMIB285-16	RBCM 016-00189-005	10 m	no data	Castelin et al. 2016
	KX069531 = CAMIB241-16	RBCM 016-00189-006	10 m	no data	Castelin et al. 2016
	KX069537 = CAMIB237-16	RBCM 016-00189-010	10 m	no data	Castelin et al. 2016
Hyphocus Island, Ucluelet, Vancouver Island	OK526458	LACM 2016-16.1	10 m	on Tegula pulligo	This Study
	OK526459	LACM 2016-16.3	10 m	on Tegula pulligo	This Study
Dead Man's Bay, San Juan Island, Washington	AF546047	FMNH282185	intertidal	on Calliostoma ligatum	Collin (2003b)
Yellow Banks, Santa Cruz Island, California	OK526460	LACM 2014-34.1	subtidal	on Norrisia norrisii	This Study
	OK526461	LACM 2014-34.2	subtidal	on Norrisia norrisii	This Study
	OK526462	LACM 2014-34.3	subtidal	on Norrisia norrisii	This Study

	OK526463	LACM 2014-34.4	subtidal	on Norrisia norrisii	This Study
	OK526464	LACM 2014-34.5	subtidal	on Norrisia norrisii	This Study
	OK526465	LACM 2014-34.6	subtidal	on Norrisia norrisii	This Study
	OK526466	LACM 2014-34.7	subtidal	on Norrisia norrisii	This Study
Off Santa Rosa Island, Santa Barbara Co., California	OK526467	LACM 2014-35.1	subtidal	on <i>Norrisia norrisii</i>	This Study
Santa Barbara, California	AF550487	FMNH282173	subtidal	on Norrisia norrisii	Collin (2003a)

Table 2: Summary statistics for polymorphism at the coxI gene of 657 bp for each analyzed region within each species. N, number of sequences; Nh, number of haplotypes, S, number of segregating sites; π , nucleotide diversity (mean number of pairwise differences); Hd, haplotype diversity with standard deviation (S.D).

Localities	Nh	S	π	Hd S.D.
Crepidula adunca			S.D.	S.D.
Northeastern Pacific				
Ocean	4	4	0.2	0.146
N = 40	•	•	+/- 0.28	+/- 0.07
Southeastern Pacific				
Ocean	5	6	2.071	0.857
N = 8			+/- 1.47	+/- 0.10
Crepidula norrisiarum				
Northeastern Pacific				
Ocean	7	9	1.681	0.833
N = 12			+/- 1.19	+/- 0.1
Southeastern Pacific				
Ocean	6	6	2.214	0.892
N = 8			+/- 1.55	+/- 0.11

Table 3: List of the hosts associated with *Crepidula adunca* (Ca) and *Crepidula norrisiarum* (Cn). Host geographic range (AK, Alaska; BC, British Columbia; WA, Washington; OR, Oregon; CA, California). Host/Substrate on which *Ca* or *Cn* was found with location (north, N [from Alaska to Oregon]; south, S [along California State]) where association was found. List of sources for which association was personally confirmed and *Crepidula* species identity unambiguous.

Host range	Host/Substrate	Ca	Cn	Reference
	On rocks	N		R.H. pers. obs. Waddah Island, Neah Bay, WA, RBCM21-53-1; J.H. McLean, Barkley Sound, BC, LACM 26030
AK to CA	Tegula funebralis	N, S	S	Ca: LACM R-343; LACM 161708; CAS 231214; R.H. pers. obs. Ucluelet, BC; Putnam 1964 / Cn: CAS 55598
AK to CA	Tegula pulligo	N	N,S	Ca: RBCM 979-9595 / Cn: R.H. pers. obs. Ucluelet, BC; Monterey, CA, LACM 60-24.
AK to CA	Lirabuccinum dirum	N		R.H. pers. obs. Ucluelet, BC; Clover Pt., Victoria, BC; L. Schroeder pers. obs. Salt Creek County Park, W of Port Angeles, WA; N. Treneman, pers. obs. Cape Arago, OR.
AK to CA	Amphissa columbiana	N		R.H. pers. obs.; Ucluelet, BC; Vermeij et al. 1987.
AK to CA	Nucella lamellosa	N		R.H. pers. obs.; Ucluelet, BC; Victoria, BC; Slip Pt., Strait of Juan de Fuca, WA; Clover Pt. Victoria
AK to CA	Calliostoma ligatum	N	N	Ca: R.H. Ucluelet, BC; both Ca and Cn in the same sample RBCM979-4221. RC San Juan Island, WA
BC to CA	Alia carinata	N	S	Ca: R.H. Ucluelet, BC; Cn: MacGinitie and MacGinitie, 1964
AK to WA	Neostylidium eschrichtii	N		R.H. pers. obs. Ucluelet, BC
AK to CA	Pseudodiala acuta	N		R.H. pers. obs. Ucluelet, BC
AK to CA	Pomaulax gibberosus	N		R.H. pers. obs. Ucluelet, BC
	Homalopoma sp.	N		R.H. pers. obs. Ucluelet, BC
AK to CA	Philobrya setosa	N		R.H. pers. obs. Ucluelet, BC
CA	Tegula gallina	S		LACM 161700
CA	Tegula montereyi	S		R.C. pers. obs. Diablo Canyon, CA
OR to CA	Tegula brunnea	S		S. Lonhart, Monterey Co., California; N. Treneman Crescent City, CA 6-7-2019
CA	Atrimitra idae	S		LACM 161700; R.C. pers. obs. Diablo Canyon, CA
CA	Acanthinucella paucilirata	S		C.A. Clark record (iNaturalist 19263592) Princeton-by-the Sea, CA.

CA	Norrisia norrisii	S	Warner et al. 1996; Hobday et al. 1998; MacGinitie & MacGinitie 1964; R.C. pers. obs.; LACM 60278; LACM161798; FMNH 282173-175.
	Haliotis spp.	S	LACM 19435; Smith, 1946
BC to CA	Haliotis rufescens	S	CAS231212
AK to CA	Nassarius mendicus (N. cooperi)	S	MacGinitie and MacGinitie, 1964
AK to CA	Randallia bulligera (crab)	S	MacGinitie and MacGinitie, 1964
AK to CA	Calliostoma canaliculatum	S	Hazard Conyon, S of Morro Bay, CA
	Calliostoma sp.	S	CAS231213
OR to CA	Tegula brunnea	S	CAS231215; D.E. pers. obs. from San Luis Obispo and Monterey Counties, CA
CA	Tegula eisini	S	Alex Baristow, La Jolla, CA (iNaturalist 9652706)

Figure legends

Figure. 1: Map of the northeastern Pacific coast with magnification of sample localities of *Crepidula adunca* and *C. norrisiarum* from British Columbia and Washington State (A) and from California (B). Numbers on the map correspond to sample size per locality and per species.

Figure. 2: Median-joining network obtained from *cox1* sequences of *Crepidula adunca* in British Columbia and Washington State (A) and California (B). Circles are color coded based on sampling location and are sized according to the relative abundance of each haplotype. Each line connecting a circle or a small bar equals one mutational step.

Figure. 3: Median-joining network obtained from *cox1* sequences of *Crepidula norrisiarum* in British Columbia and Washington State (A) and California (B). Circles are color coded based on sampling location and are sized according to the relative abundance of each haplotype. Each line connecting a circle or a small bar equals one mutational step.

Figure. 4: The Holotype of *Crepidula adunca* Sowerby, 1825 (NHMUK 1997150) with arrow pointing out the dimple. Scale = 1 cm. © The Trustees of the Natural History Museum. Images by Phil Hurst, NHMUK Photographic Unit.

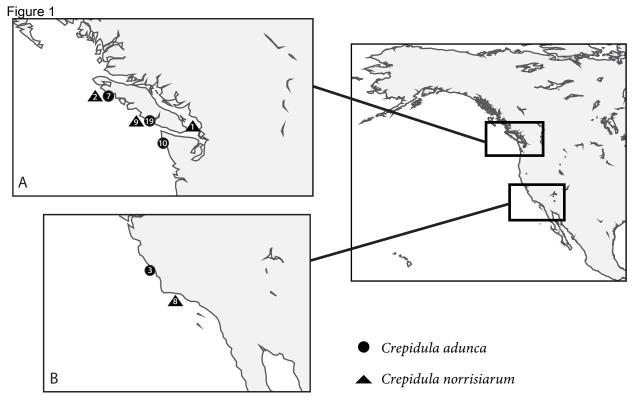
Figure. 5: Shells of *Crepidula norrisiarum*. (A) *C. norrisiarum* (LACM 182442) collected from *Calliostoma ligatum* on San Juan Island, Washington and (B) *C. norrisiarum* (LACM 182441) collected from *Norrisia norrisii* from Naples Reef near Santa Barbara, California (Photos by Maycol Maycol E. Madrid C.).

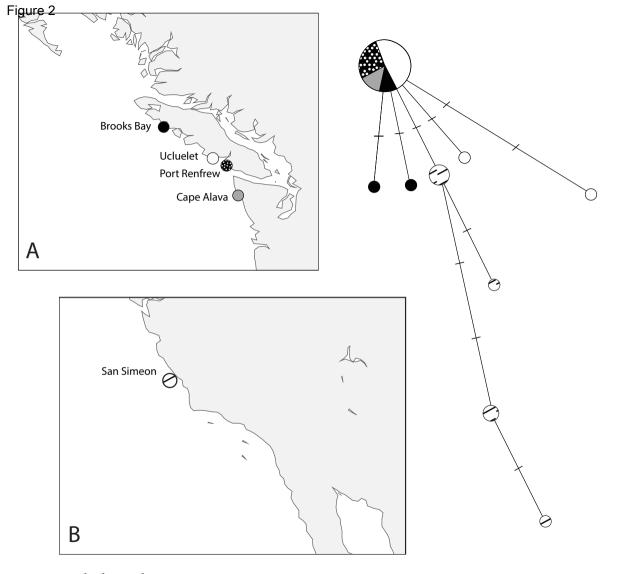
Figure. 6: Live *Crepidula norrisiarum* (A) and *C. adunca* (B) showing the difference in body color.

Figure. 7: *Crepidula adunca* and *C. norrisiarum* on different hosts. (A). *Crepidula adunca* on *Lirabuccinum dirum* from south Cove, Cape Arago, Oregon (Photo by: Nancy Treneman). (B)

Crepidula adunca on Tegula montereyi from Monterey Co., California (Photo by Steve Lonhart)

(C) Crepidula adunca on Pomaulax gibberosus from Ucluelet, British Columbia. (D) Crepidula norrisiarum on Norrisia norrisi from Los Angeles Co., California. (E) Crepidula adunca on Tegula funebralis. (F) Crepidula norrisiarum on Calliostoma ligatum from Keystone, Whidbey Island, WA (Photo by: Jan Kocian) (G) Crepidula norrisiarum on Calliostoma ligatum from Victoria, BC (Photo by: James Hester).





Crepidula adunca

