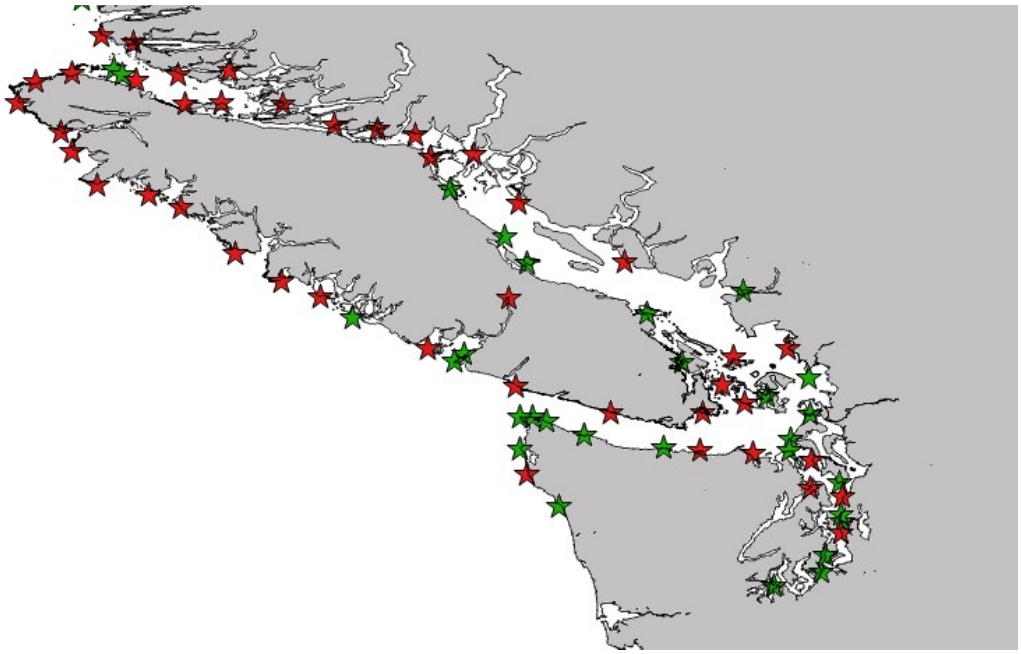

Figure S1. *Nereocystis luetkeana* sites used to model multiple generation oceanographic connectivity in the Salish Sea and adjacent North East Pacific coast sites (see main text). Sampled sites in green and non-sampled, stepping-stone connectivity (SSC) sites in red.

Table S1. Modeling genetic differentiation between *Nereocystis luetkeana* sites in the Salish Sea and adjacent North East Pacific coast. The response variable was pair-wise F_{ST} between sites. Table values are the percentages of variation in genetic differentiation explained independently by each predictor variable, using the R package hier.part and the optimized multiple regression model. The different columns show the effect of different periods where hydrodynamic transport was simulated. The date shown is the day in the middle of a 14 day period where particles were released. Pair-wise predictor variables were the following: oceanographic distance, the stepping-stone probability of hydrodynamic transport, the over the water spatial distance and a series of environmental variables (see paper methods). Environmental variables were averaged from 2002 to 2016 and the absolute difference between sites used as the pair-wise distance. Oceanographic distance is the only predictor which values change from column to column but percentages of explained independent variable for all other variables can change with changes of one of the predictors in multiple regression.

	Date											
Predictor	Jul-1	Jul-15	Jul-29	Aug-11	Aug-25	Sep-8	Sep-22	Oct-6	Oct-20	Nov-3	Nov-17	Dec-1
Oceanographic distance	18.2	21.4	20.2	22.2	20.5	23.1	18.9	18.5	16.6	20.9	19.3	21.1
Spatial Distance	12.9	12.2	12.4	12.0	12.3	11.8	12.7	12.7	13.2	12.2	12.7	12.2
Environmental distances												
Light penetration	9.6	9.3	9.5	9.3	9.3	9.4	9.4	9.5	9.6	9.3	9.4	9.4
PAR	6.4	6.0	6.1	5.9	6.08	5.9	6.3	6.3	6.5	6.0	6.2	6.0
POC	11.0	10.5	10.5	10.2	10.7	9.8	11.1	11.1	11.7	10.8	10.8	10.6
PIC	17.9	16.7	17.1	16.6	17.0	16.4	17.5	17.6	18.0	16.8	17.4	16.7
SST.Summer	13.6	13.58	13.7	13.6	13.7	13.6	13.6	13.7	13.7	13.7	13.6	13.8
SST.Fall	5.6	5.5	5.5	5.4	5.5	5.3	5.6	5.6	5.8	5.6	5.6	5.6
SST.Winter	4.8	4.7	4.7	4.7	4.8	4.6	4.8	4.8	4.9	4.7	4.8	4.8
Goodness of fit												
AIC	-2187.0	-2196.9	-2193.4	-2198.0	-2193.2	-2200.5	-2189.4	-2189.2	-2185.6	-2195.6	-2191.2	-2195.9
Adjusted R^2	0.382	0.395	0.390	0.397	0.390	0.400	0.385	0.385	0.380	0.394	0.387	0.394

Nereocystis luetkeana microsatellite marker isolation

We sequenced a pool of genomic DNA extracted from three *N. leutkeana* individuals from Alisomar (California, USA) using next generation 454 sequencing (Biocant, Cantanhede - Portugal), producing 150,000 reads, ranging from 80 to 900 bp. The sequences were scored for microsatellite motifs and primer design using the online program websat (http://wsmartins.net/websat/). We selected a total of 20 pairs of primers with different microsatellite motifs from di to hexanucleotides. A total of 17 primers amplified and were polymorphic after initial tests. We used fluorescent-dye labeled forward primers to test loci polymorphism in 40 individuals from three locations, Carmel Pinnacles +36°33'31.84", -121°58'4.34" (n=15), Cambria N. Onshore +35°32'38.58", -121°6'20.31" (n=13), Cambria Mid Upcoast +35°32'35.01, -121°6'2.23" (n=12).

Polymerase chain reactions were carried out in a total of 15 ul with 10 ng of DNA (extracted with Nucleospin Plant Kit, Macherey-Nagel, Germany), 0.1 uM of each primer (Table I), 0,8 mM odd NTPs (Promega), 1.5 mM of MgCl2, 3.0 ul of 5x Green Buffer and 0.5 U of GoTaq Polymerase (Promega, Madison, WI).

All PCR reactions were performed on a Eppendorf thermocycler (Eppendorf, USA) using the followed cycling conditions: initial denaturation for 5 min at 95ºC, 35 cycles of 20 s at 95ºC, 20 s at annealing temperature (Table I), 30 s at 72ºC and a final elongation of 20 min at 72ºC.

Allele sizes were accessed using a 48 capilar ABI PRISM 3130xl DNA analyzer and LIZ500 as size standard (Applied Biosystems) and the raw alleles were scored with the software STRand v2.4.59 (http://www.vgl.ucdavis.edu/informatics/STRand). The number of alleles, expected and observed heterozygosities, Hardy-Weinberg equilibrium and linkage disequilibrium tests were estimate with the software GENEPOP v4.1.4 (Raymond and Rousset 1995). Presence of null alleles was checked with MicroChecker software (http://www.microchecker.hull.ac.uk).

Across the three populations the number of alleles per locus ranged from 7 (locus Ner-06 and Ner-10) to 18 (locus Ner-11) with an average of 12.2. Expected heterozygosity varies from 0.6111 (locus Ner-06 in Population Cambria Mid Upcoast) and 0.9028 (locus Ner-11 for the same population) while observed heterozygosity ranged from 0.0909 (locus Ner-18 in Population Cambria N. Onshore) and 1.0000 (locus Ner-04 for Population Carmel Pinnacles).

References

Raymond, M., & Rousset, F., (1995). GENEPOP (version 1.2): population genetics software for exact tests and ecumenicism. *Journal of Heredity*, 86(3), 248-249.

Table S2 - Characterization of fifteen microsatellite loci for *Nereocystis leutkeana.*

Locus name (Access Number)	Primers Sequence (5'- 3')	Repeat motif	Clone size (bp)	PCR annealing (º C)	A	Size range (bp)
Ner-01 (AB0254152)	GTCAACGGCAAGGGCAAG ACCGTCACCCTCGTCACC	$(ACGGTG)_6$	107	61	9	64 – 111
Ner-02 (AB0254152)	GAAGAGGTGCGGTGGCTT GGAATCGGAACCCAAAATTAGT	$(ATTCGG)_6$	266	58	9	249 – 284
Ner-04 (AB0254152)	GTCATGTCCTTTACGTTCGGAG CCATCATCATCACCATCATCA	$(GAT)_{12}$	282	59	15	268 – 311
Ner-06 (AB0254152)	CGAGGAACAACAACAAGAACAA CGGGGTAGGAAACAAATGTAAA	$(AAC)_{12}$	182	58	7	160 – 180
Ner-07 (AB0254152)	CATGGGGAAGAGTAAAGTGAGG ACGGACTGCATTGTATTGTGAG	$(TTG)_{20}$	212	58	14	164 – 230
Ner-09 (AB0254152)	CACAAAACCCATGTCTCACG ATGATCTGGCGGACTAAGGTAT	$(GGGTC)_9$	256	61	16	218 – 320
Ner-10 (AB0254152)	GTCAGCACAGGACAGGACATTA GTCAAGCATCGGAACTAGATGG	$(GACAG)_7$	128	58	7	119 – 151
Ner-11 (AB0254152)	AAGTTGTTGCACATGAACCCC AGCTCTTCGTTGTCGCGG	$(GTAT)_{11}$	293	58	18	272 – 342
Ner-12 (AB0254152)	TGGAATGCACATGAATGCAC CACTAAACTCAATCGTGGACCC	$(ATGT)_{13}$	187	59	14	159 – 239
Ner-13 (AB0254152)	ATAGTACGGCATCATCGACAGA CAGCAGTGACAACAGCGAC	$(AT)_{12}$	101	58	13	93 – 118
Ner-14 (AB0254152)	GAGAACAAGGGCAACGACAG GAGGTTGGAGGGTTGGAGAT	$(CAA)_{17}$	118	61	12	87 – 121
Ner-15	TGGTCTACTTGTAAGCGAACCG	$(CAG)_{16}$	267	61	13	219 – 282

(AB0254152)	CTGCTGCTGCTCATCCTACTG					
Ner-18 (AB0254152)	GTCGGGTTAAGTCAGCATACCT CAACAGCCGTGAATAGATCAAG	$(GACCC)_{11}$	211	58	17	174 – 297
Ner-19 (AB0254152)	AGCAGTAGGACCGAATTTTCAT GGCTTATGTACGAAACCGTAGC	$(GA)_{14}$	103	61	8	91 – 105
Ner-20 (AB0254152)	TGGCAACGTAGTATCTCTGTGG TCTGACGAAATCAAGGTGAACA	$(AC)_{17}$	245	57	11	221 – 265

Locus name, primer sequence, motif repetition, clone size (bp), PCR annealing temperature (ºC), number of alleles found (*A)* and fragment size range (bp) for 3 populations of *N. leutkeana*.