- **Environmental factors associated with invasion: modeling occurrence data from a**
- **coordinated sampling programme for Pacific oysters**
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Abstract

 Documenting establishment and spread of invasive species requires extensive co- ordinated sampling programmes. Identifying the factors promoting or inhibiting local establishment of an invasive species can improve capacity to predict further spread and underpin strategies to limit spread. Here, a structured sampling programme was used to assess the current distribution of feral populations of Pacific oysters, *Crassostrea gigas*, in Ireland. Sixty-nine sites were sampled using a standardised protocol combining semi- quantitative and quantitative approaches. Sites were chosen to represent variation in proximity to aquaculture and a range of environmental variables. Oyster populations were found at 18 locations, with densities ranging from single individuals to nine 27 individuals per m^2 . The broad size range of oysters found is indicative of more than one recruitment event. Logistic regression indicated that feral oysters were positively associated with the presence of hard substrata or biogenic reef, long residence times of embayments and large intertidal areas. There was also a tendency for oysters to occur disproportionately in bays with aquaculture, but > 500 m from it. Small-scale analysis within sites showed that oysters were almost exclusively attached to hard substrata and mussels. The approach taken here provides a rigorous repeatable methodology for future monitoring and a detailed basis for the prediction of further spread.

Keywords: logistic regression, environmental variables, *Crassostrea gigas*, aquaculture

Introduction

 Improving our knowledge of distributions of non-native species assists predictions of spread and allows strategic targeting of management actions for their control (Anderson et al. 2003; Gormley et al. 2011; Simberloff and Rejmánek 2011). Species' distributions are not easy to predict because they are controlled by many factors acting upon different life stages, e.g. hydrodynamics and tides can influence the delivery of spat (Roughgarden et al. 1988; Gaines and Bertness 1992; Dunstan and Bax 2007) whereas habitat availability is important for settlement (Travis and Dytham 1999; Kinlan and Gaines 2003) and post-settlement mortality can strongly affect recruitment (Minchinton and Scheibling 1993; Hunt and Scheibling 1997; Jenkins et al. 2009). Furthermore, propagule pressure plays a major role in the early stages of an invasion (Lockwood et al. 2005; Johnston et al. 2009).

 Distributions of invasive species are often documented in a rather fragmented and descriptive way and data are often collated from a number of sources and can be of mixed quality and resolution (Ruiz et al. 2000; Zaniewski et al. 2002; Elith et al. 2006; Hulme and Weser 2011). Interpreting such data requires synthesis and meta-analysis and does not yield unequivocal tests of hypotheses about factors associated with colonisation by the species. It is recommended to use well-designed survey data and analyse functionally relevant predictors (Elith and Leathwick 2009; J Elith unpublished). Thus, extensive coordinated surveys and monitoring and assessment programmes using carefully standardised protocols and well thought-out designs are preferable as they avoid survey bias and result in balanced comprehensive datasets. When a set of sites has been surveyed and presence/absence or abundance has been recorded, generalised linear models encompassing logistic regression are especially useful as additive combinations of predictors and manually selected interaction terms representing interactions between predictors can be included (Elith and Leathwick 2009; Franklin 2009).

 Species distribution models (SDM) estimate the relationship between species and spatial and/or environmental characteristics and are widely used to estimate current and potential distributions of species (Elith et al. 2006; Franklin 2009). They have been widely used in terrestrial ecosystems but applications for distribution of species in marine habitats are sparse (Kelly et al. 2001; Garza-Pérez et al. 2004; Beger and Possingham 2008; Robinson et al. 2011). Additionally, including measures of introduction effort is important for assessing on-going biological invasions or for identifying areas that are susceptible to invasion (Herborg et al. 2007; Therriault and Herborg 2008).

 Since the 1980's, world aquaculture production has grown steadily by an average of 9% per year (FAO 2012a). It now produces almost half of the fish and shellfish consumed by humans and will continue to expand in the future (Duarte et al. 2009; FAO 2012a). The expansion of aquaculture also brings with it an increased risk of establishment of wild populations of non-indigenous species.

 The Pacific oyster (*Crassostrea gigas*, Thunberg 1793) has been introduced for aquaculture to many parts of the world and has become one of the world's main aquaculture species (FAO 2012b). In many locations, wild oyster populations became established soon after oyster farming had commenced (Diederich et al. 2005; Brandt et al. 2008; Melo et al. 2010; Troost 2010), often in shallow, enclosed bays, where larval retention might be high. Invasive populations can now be found worldwide in a range of habitats, from coastal sheltered soft-sediment environments to exposed rocky shores

 (Reise 1998; Diederich 2005; Ruesink et al. 2005; Nehls et al. 2006; Troost 2010). They can have substantial impacts, including saturation of the carrying capacity of estuaries, alterations of habitats and changes in benthic and pelagic communities, food webs and ecosystem processes (Ruesink et al. 2005; Cognie et al. 2006; Troost 2010; Eschweiler and Christensen 2011; Green et al. 2012). Given its rate of spread, there is an urgent need to characterise its pattern of establishment at an early stage and determine which factors are associated with its presence or absence and spread.

 Increasing temperatures have been associated with the spread of Pacific oysters in Europe (Diederich et al. 2005). The northern boundaries of its distribution are expanding, with populations becoming established in England and Wales (Couzens 2006), Northern Ireland (Guy and Roberts 2010) and Scandinavia (Wrange et al. 2010). There have also been reports of individuals in the wild in Ireland, where Pacific oysters are extensively farmed around the north, the west and south coasts (Browne et al. 2007), however, the size and distribution of these populations is not yet known.

 In this study, a coordinated national sampling programme was undertaken using a cost- effective, but rigorous and repeatable sampling protocol. It was used at selected sites to firstly, document the current distribution and abundance of Pacific oysters in Ireland and, secondly, build a model using the factors that might be asscociated with their settlement in the wild. Factors considered here were: embayment residence time, habitat type, wave exposure, distance from aquaculture, latitude and intertidal area. The approach undertaken here might not only improve prediction of the future spread of Pacific oysters but will be broadly applicable to other benthic marine invaders with planktonic larval dispersal.

Methods

Sampling programme

 A sampling programme was undertaken from May until September 2009 at 69 sites around the coast of Ireland (coordinates provided in Online Resource 1). The sites were selected to represent variation in distance from aquaculture, latitude, wave exposure, embayment residence time, intertidal area (shore width) and habitat type (Table 1 and 122 Online Resource 1). Sites ranged in area between approximately 3500 m^2 (narrow rocky 123 shores) and 40000 m² (mussel beds) and salinities ranged between 22.5 and 35 psu.

 Sites were visited and sampled during spring low tides. The sampling methodology was designed to be flexible, repeatable and efficient. *Phase 1* of the methodology involved a timed semi-quantitative sample of oysters at each site and a simple characterisation of the habitats available at that site. It could be completed within 40-45 min maximising the number of sites it was possible to visit in the available time. *Phase 2* was only used at sites where oysters were found. It involved a more detailed quantitative survey of the area of greatest density of oysters to enable comparisons among sites and between present and future surveys. In addition, it also provided the basis for analyses of small- scale associations between oysters and features of the biotic and abiotic environment. Further details of these phases are provided below.

 Phase 1: At each site the first 40-45 min were spent identifying the habitat types in the lower intertidal, searching for Pacific oysters within those areas and assessing their abundance using the SACFOR scale (Connor et al. 2004). The abundance categories used 139 were: Superabundant (100-999/m²), Abundant (10-99/m²), Common (1-9/m²), 140 Frequent (0.1-0.9/m²), Occasional (0.01-0.09/m²), Rare (< 0.009/m²) and Absent. After the timed search, each location was classified using a modified EUNIS framework of

 habitat types (Connor et al. 2004) to better describe the types of substratum encountered in the habitats studied here. The modified categories were: bedrock; boulders (25.6 cm – 102.4 cm); cobbles and pebbles (25.6 cm – 1.6 cm); gravel (1.6 cm – 0.4 cm); sand (0.063 mm – 4 mm); mud (< 0.063 mm); mixed sediment; biogenic reef (mussel beds, *Sabellaria* reefs); and macroalgae-dominated sediment (from here onwards referred to as 'macroalgae'). More than one habitat was noted for a site if the type of substratum changed significantly (visual estimation) (see Online Resource 1). Coverage by different types of substratum was expressed in % of the area by visual estimate, generally in increments of 10%, except in a few cases where increments of 5% were used.

 Aquaculture was categorised as absent, close (trestles with Pacific oysters were encountered during the timed search) and far (known to be present in the embayment, but generally > 500 m from the study site) based on licensing information from Bord Iascaigh Mhara, the Irish Sea Fisheries Board. Wave fetch was used as an index of wave exposure; it was defined as the closest distance to the land in 16 angular sectors (average in km), and calculated after the method developed by Burrows et al. (2008). Residence time was determined using the formula developed by Hartnett et al. (2011): 160 TPR is the tidal prism ratio, which

161 was derived from the volume of water between low water and high water $[m³]$ divided 162 by the volume of the embayment at high water $[m^3]$; B₀ is the width of the mouth of the embayment [km]; and L is the length of the embayment along the longitudinal axis [km]**.** 164 Each site's intertidal width was categorized into $1 = 0.50$ m, $2 = 51.100$ m, $3 = 101$. 150 m, 4 = > 151 m, based upon measurements from high water line to the lowest water line. Each site was classified according to each of the variables described above with up to three habitats per site (see Table 1 and Online Resource 1 for details).

 Phase 2: When oysters were present at overall densities greater than 0.1 individuals/m² (i.e. abundance category Frequent or above), two transects of 30 m x 1 m were randomly placed in the habitat of greatest oyster density. In each transect, the numbers of oysters, the sizes of oysters to the nearest mm (Vernier callipers) and substrata to which they were attached were recorded. If more than 100 oysters were found in the first transect, only counts and attachments to substrata but no further size measurements were recorded in the second transect. On mussel beds, 17 random quadrats of 1 m x 1 m were taken in each transect as densities were too high to account for every single oyster within a transect line. Conversely, in the Shannon Estuary, extended transects were run on two rocky shores to ensure that sufficient length measurements were collected for size frequency analysis.

 To estimate substratum availability, substrata were recorded quantitatively along two 10 m tapes placed haphazardly in the habitat where oysters occurred. The distances along the tape at which the substratum changed from one type to another were recorded, and these distances were converted into estimates of the percentage area covered by different substrata. These data were used in conjunction with the data collected on oysters and the substratum they were attached to. This enabled tests of small-scale associations between oysters and biotic and abiotic features of habitat.

 Teams of researchers from the different institutions were trained in the use of the protocols by the coordinator of the project, who also accompanied each team on its first sampling trip to ensure consistency of methodology. Each team was assigned a number of specific sites to survey in a sequence that ensured minimal temporal and observer bias with respect to the site variables described above. Each team surveyed a maximum

 of two sites on each day, with pairs of sites selected to be in close proximity to each other. Each site visit was timed such that the low shore could be visited within 20 minutes of a spring low tide. In any given day, a *Phase 1* survey was initiated one hour before predicted low water, with the timed search gradually progressing down the shore in step with the receding tide. If oysters were found at that site, the *Phase 2* survey was completed during the incoming tide. If no oysters were found, the team moved on to the second site for the day and completed a *Phase 1* survey during the incoming tide.

Data Analysis

 Logistic regression allows multiple explanatory variables, and their interactions to be included in a single model (Vittinghoff et al. 2005). Here, logistic regression was used to find a set of environmental variables that could be used to predict oyster presence/absence. In the 69 sites visited during the sampling programme, 127 habitats were identified (*Phase 1*) and classified for presence/absence of oysters and the environmental conditions encountered, including proximity of aquaculture (see Online Resource 1). Our model was based on this set of 127 observations.

 Prior to running the model, Spearman rank correlations (ρ) were calculated among all pairs of environmental variables. When a Spearman rank correlation exceeded an absolute value of 0.35, one of the pair of variables was omitted from the model to avoid 214 co-linearity (Dormann et al. 2012). The following pairs of variables had $|\rho| > 0.35$: 215 Macroalgae with Rest ($\rho = -0.63$), Latitude with Residence ($\rho = 0.46$), Rest with Width 216 (ρ = 0.46) and Macroalgae with Hardreef (ρ = -0.35), where 'Rest' refers to the EUNIS categories sand, gravel, mixed sediment and mud, 'Hardreef' refers to bedrock, cobble, pebble and biogenic reef, 'Residence' refers to residence time and 'Width' refers to shore width. Latitude, Rest and Macroalgae were therefore omitted from the model. The

 variables used in the full model were % cover of bedrock, cobble, pebble and biogenic reef (called Hardreef), proximity to aquaculture (called Aquaculture with levels: absent, far and close), residence time (called Residence), wave fetch (called Fetch) and shore 223 width (called Width with levels $\lt 50$ m and ≥ 50 m)(see also Table 1).

The full logistic model used a logit link function and a model equation

Oysters~1+Width+Fetch+Aquaculture+Residence+Hardreef+Hardreef:(Fetch+Width+

Residence+Aquaculture)+Fetch:Width

 The variable Oysters is 1 if oysters are present and zero otherwise, the other variables 230 are explained in Table 1 and ':' indicates an interaction between two variables. All interactions between Hardreef and the other variables are included in this full model because oysters attach almost exclusively on hard substrata. Additionally, an interaction between Fetch and Width was included because the extent of the shore is not considered in the calculation of wave fetch and can be important when shores are wider than 100 m (see Burrows 2008). Starting from this full model, backward stepwise selection was used with Akaike's Information Criterion (Akaike 1974) to arrive at a 'best fit' model. The performance of the 'best fit' model to correctly classify oyster presence/absence at a habitat unit was quantified using ROC curves and their AUC values (Fielding and Bell 1997). Additionally, we selected a probability threshold that gave a classifier that weighed omission errors (false negatives, where oysters are incorrectly predicted to be absent) more than commission errors (false positives, where oysters are incorrectly predicted to be present) as this type of classifier is mostly desirable for invasive species (Gormley et al. 2011).

245 γ^2 analysis (goodness-of-fit test) was used to test hypotheses about small-scale

 associations between oysters and different types of substratum (using data obtained during *Phase 2*).

 Logistic model calculations were performed with R, using the MASS and pROC packages (R Development Core Team 2011). For calculations of residence time and wave fetch, detailed descriptions can be found in the original papers (Burrows et al. 2008; Hartnett et al. 2011).

Results

Distribution, densities and sizes of feral Pacific oysters

 Pacific oysters occurred at 18 of the 69 sites (Figure 1). No oysters were found at sites in the south. Most oysters were found in the large estuaries of Lough Swilly, Lough Foyle and the Shannon, with many sites scored Common or Frequent for the abundance of oysters. Oysters were Occasional or Rare at five sites in Galway Bay and single individuals of oysters were found at one site in Tralee Bay and another site in Ballynakill Harbour, which therefore scored Rare on the SACFOR scale.

263 Oyster densities in the different habitats varied from single individuals to 8.5 ind./ $m²$ (Table 2). Sites in Lough Swilly and Lough Foyle had the highest densities whereas sites in the Shannon Estuary, Galway Bay, Tralee Bay and Ballynakill Harbour oysters were found in lower densities (Table 2). Pacific oysters were mostly found in the lower intertidal. During an exceptionally low spring tide, a subtidal mussel bed could be 268 accessed at Rathmelton in Lough Swilly, where densities were estimated at 12.5 ind./m².

270 At all of the sites with oysters > 0.1 ind./m², the range of sizes of oysters found exceeded 120 mm (Figure 2). In Lough Swilly, oyster sizes ranged from 13.8 mm – 125.7 mm on a

272 mussel bed (n = 147) and from 25.3 mm $-$ 135.0 mm on a rocky shore (n = 182). Similar sizes of oysters from 23.0 mm – 135.5 mm (n = 182) were also measured on a mussel bed in Lough Foyle. In the Shannon Estuary slightly larger oysters were found, with the smallest and largest oyster measuring 43.4 mm and 146.2 mm (n = 125) respectively at 276 Loghill. At Glin, oyster sizes ranged from 40.4 mm $- 123.0$ mm $(n = 101)$.

Associations between oysters and environmental variables at the scale of sites (Phase 1)

 127 different habitats were identified at the 69 sites of which there were 27 with oysters present and 100 where no oysters were found (Figure 3). Four variables (Aquaculture, Width, Hardreef and Residence) and no interactions were retained in the best-fit logistic regression model (Table 3). Comparing the best-fit model's predictions against the oyster presence/absence data gave an AUC of 0.9. Applying a classification probability threshold of 0.1 to this model (corresponding to the threshold that maximised the sum of specificity and sensitivity) gave 25 true positives, 71 true negatives, 29 false positives and two false negatives for our oyster presence/absence data. Another approach to estimate model performance is Cohen's kappa (Cohen 1960). Cohen's kappa is maximised for our model at a threshold of 0.48. However, classification performance with this threshold had less true positives and more false negatives and was therefore not considered as the best classifier. Oyster presence was positively associated with Hardreef (bedrock, boulders, cobbles, pebbles or biogenic reef), Residence and Width \geq 50 m. 'Aquaculture far' was also positively associated with oyster presence ($p = 0.035$,

 Table 3). Removing 'Aquaculture absent' from the model did not affect the other coefficients, indicated by a high standard error on the regression coefficient (Table 3). It is important to note that Latitude, Rest and Macroalgae, which were omitted from the full model due to co-linearity, could equally well underlie the same associations as the

 terms that were left in the model in their place (i.e. Residence, Width and Hardreef respectively). Thus, Latitude might equally be positively associated with oyster presence whereas Macroalgae or a low % cover of Rest might be negatively associated with oyster presence. Fetch was in the full model but was not kept in the best-fit model owing to its low explanatory power.

Small-scale associations between oysters and habitat within sites (Phase 2)

 Oysters were disproportionately associated with hard substrata (boulders, cobbles, pebbles and mussels) given their availability relative to that of macroalgae, sand, *Sabellaria* tubes and mud (Table 4). Oysters were never found attached to macroalgae (with one single exception (J Kochmann, pers. obs.).

Discussion

 The structured framework and sampling protocol here was used in cooperation with relevant state agencies in Ireland and allowed rigorous analysis of the extent of spread and factors influencing the distribution of Pacific oysters. Its cost-effectiveness and repeatability make it valuable and widely applicable for future assessments and also relevant for other marine benthic species with similar life-history traits.

 Unlike the situation in many other European countries, no dense intertidal reefs of Pacific oysters are established yet in Ireland, despite extensive aquaculture. Pacific oysters were 318 found at 18 of 69 sites. Densities at those sites ranged from single individuals to 8.5 ind./m² in the intertidal; they were also observed at higher densities in the shallow subtidal in Lough Swilly (J Kochmann, pers. obs.) and are known to occur in subtidal areas in Loughs Foyle and Swilly (McGonigle et al. 2011; Marine Institute and BIM 2012). Comparably low densities of 0.01-42.44 ind./m2 were found, e.g. in Sweden and Denmark (Wrange et al. 2010), the

 Wadden Sea (Reise 1998; Wehrmann et al. 2000; Diederich et al. 2005) or Argentina (Orensanz et al. 2002) in the early stages of invasion. Guy and Roberts (2010) found 325 densities of one individual per m^2 in Northern Ireland with the largest oysters reaching lengths of 155 mm. Based on their analysis of age-size relationships in Strangford Lough (Northern Ireland), we would estimate that the largest oysters found in our study were approximately 6 years old. However, age-size relationships of *C. gigas* can vary among sites (references in Diederich 2006), so this inference is tentative. In the Wadden Sea, Pacific oysters usually reach 20-50 mm in the first year and 30-80 mm in the second year on mussel beds (Reise 1998; Schmidt et al. 2008; Fey et al. 2010) which are the lower size ranges also found in this study. Little evidence of recruitment was found in 2008 at the sites where transects were sampled, with few individuals found < 50 mm. New recruitment (oysters < 15 mm length) has since been observed in the intertidal in 2011 (J Kochmann, pers. obs). The range in sizes observed at individual sites (> 100 mm in four of the sites sampled, e.g. from 25.3 mm to 135.0 mm mm at Lough Swilly) is greater than would have arisen in a single cohort and is indicative of successful recruitment of Pacific oysters in more than one year in several bays in Ireland.

 Colonization of sessile benthic invertebrates often starts with a few individuals settling onto pieces of hard substratum and is widely known for oysters (Reise 1998; Escapa et al. 2004; Diederich 2005; Nehls et al. 2006). Similarly, in the current study oysters were always found attached to bare boulders, cobbles, pebbles or biogenic reef (live or dead material) and were very rarely found under macroalgae. Due to the co-linearity of Macroalgae and Hardreef, the positive association of Hardreef with oyster presence could also be a negative association with the % cover of macroalgae. However, when both factors were kept in the full model, Hardreef was kept in the 'best-fit' model indicating it as a better predictor than Macroalgae. Field studies with barnacle larvae

 have shown that algal fronds can inhibit settlement on their surfaces by exuding metabolites (Brock et al. 2007) and that macrophyte canopies could prevent larvae from settling on rocks underneath them because they sweep the surface and limit access to the substratum (Jenkins et al. 1999). These effects might also play a role in the settlement patterns of oysters affecting recruitment and mortality (Thomsen and McGlathery 2006) and interfering with filter-feeding apparatus (Cadée 2004). The positive correlation of Width with Rest might be an indication of the characteristics of the larger intertidal areas surveyed; they were often extensive intertidal mud- or sandflats. Consequently, as intertidal shore width (> 50 m) was positively associated with oyster presence, the model also captured the likelihood of oysters being found on extensive, intertidal sedimentary shores.

 For marine species with planktonic life-stages, the duration of the larval stage determines the length of time that the larvae are subject to movement by currents and exposed to sources of mortality (Pechenik 1999; Pineda et al. 2007). High reproductive rates, spawning in multiple seasons or years and short development times can facilitate retention (Byers and Pringle 2006). Even if larvae do not necessarily behave as passive particles (e.g. Knights et al. 2006), flushing characteristics of coastal waterbodies such as residence times can help in the identification of areas likely to retain larvae (see Dyer and Orth 1994). Indeed, limitations in larval supply resulting from the interactions between spawning location and local hydrodynamics may impede the proliferation of introduced species (Dunstan and Bax 2007; Brandt et al. 2008; Rigal et al. 2010). The dynamics of retention will not only differ between bays but also between species and will influence their range expansion. For example, the larval duration of the invasive seastar *Asterias amurensis* (Lütken, 1871) can take 120 days (Dunstan and Bax 2007), whereas spores of the Asian kelp *Undaria pinnatifida* (Harvey) Suringar might last only

 several hours in the watercolumn (Hay and Luckens 1987). The planktonic larvae of Pacific oyster can spend three to four weeks in the water column before they reach competence to settle (Quayle 1988). Thus, enhanced oyster settlement could be expected to occur in bays exceeding the residence time of 21 days as larvae may be entrained for the duration of their planktonic phase. Except for two bays, Ballynakill and Tralee Bay, where single individuals of oysters were found, oysters were present in bays with residence times of more than 21 days.

 Although not explicitly considered here, temperature also plays and important role for the timing and magnitude of population growth through its influence on reproduction, survival of planktonic stages and on dispersal distances (Gillooly et al. 2002; O'Connor et al. 2007). It is widely assumed that large recruitment events of introduced species have been favoured by increasing summer temperatures and led to an increase in population growth, e.g. in the Australian barnacle *Austrominius modestus* (Darwin, 1854) (Witte et al. 2010) and the slipper limpet *Crepidula fornicata* (Linnaeus, 1785) (Thieltges et al. 2003). Similarly, there is considerable evidence in support of this contention for Pacific oysters (Diederich et al. 2005) and temperature has been used to predict its potential geographic range (Carrasco and Barón 2010). If latitude were considered a broad proxy for temperature, our finding of greater densities of feral Pacific oysters in northern sites than southern sites might be considered surprising. In fact, local temperatures and biogeographic patterns cannot simply be predicted by latitude (Helmuth et al. 2002; Dutertre et al. 2010) and temperature data from the Irish Environmental Protection Agency (EPA), which was available for some bays, suggests that averages of maximum summer temperatures cannot be simply characterized by latitude but vary between bays. Thus, the high correlation of residence time and latitude suggests that any influence of latitude in the current study might be more related to bay features than to

 temperature. Certainly, bay features can also be related to temperature and part of the reason for a positive association between residence time and oyster occurrence in the current study may be that extensive shallow bays tend to be warmer at certain times than smaller deeper ones. Generally, even if temperature regimes might be favourable and spawning could be initiated, planktonic larvae might be carried away before they attain competence to settle. Thus, residence time, which takes different bay features into account, should be considered more relevant as a predictor for the presence of benthic species with planktonic larval stages than average depth of a bay or a physiological temperature threshold only.

 Another hydrodynamic factor that can influence intertidal communities and abundance patterns of introduced species is exposure to wave action (e.g. Andrew and Viejo 1998; Branch et al. 2008). Although abundance patterns of Pacific oysters on rocky shorelines can differ between sites of different exposure (Ruesink 2007), in this study, wave exposure (quantified by wave fetch) played no role in our selected model of oyster presence. It could be argued that wave exposure indices based on wave fetch alone might not prove to be as powerful as including other aspects of wave climate, e.g. variations due to wind climate (Davies and Johnson 2006). However, this would involve more complex physical models and until those can be widely applied, wave fetch indices remain useful for ecologists (Burrows et al. 2008). As shown by Burrows et al. (2008), the extent of the shore is not considered in the calculation of wave fetch and can be important when shores extend > 100 m. This might be especially important when extensive intertidal areas offer some kind of hard substratum for attachment. Thus, intertidal width was additionally used as a proxy for settlement area and the model 425 selection showed that intertidal width was a better predictor of oyster presence than wave fetch with a shore width smaller than 50 m being negatively associated with oyster

presence.

 Although aquaculture provides considerable economic and social benefit, the use of non- native species in aquaculture increases the risk of unintentional escapes into ecosystems (Carlton 1996; Naylor et al. 2001). A wide range of non-indigenous species are already cultivated (FAO 2012a) and many additional species are being trialled for aquaculture in countries outside their native range (see review Cook et al. 2008). Improved understanding of the risks of escapes from aquaculture is clearly needed. Although more oysters were expected in close proximity to oyster racks and aquaculture sites, a tendency of oysters to be present more frequently far from aquaculture was found (*p* = 0.035, Table 3). Cognie et al. (2006) suggested that farmers' upkeep activities might explain the low biomass of oysters on used racks and might have also played a role in our observations with a negative association of close proximity to aquaculture and oyster presence. In this study, most of the sites visited (62 of 69) were located in bays where aquaculture of Pacific oysters was present and only one single individual of Pacific oyster was found in a bay without aquaculture. It will be important to sample more bays where aquaculture is absent to draw more detailed and robust conclusions about associations of aquaculture and Pacific oysters in the wild. However, the fate of established non-native populations may not depend on reproduction success of farmed counterparts (e.g. Kochmann et al. 2012); the overall significance of aquaculture might be high in the initial establishment phase but less in subsequent spread. Therefore, monitoring environmental factors that are related to recruitment success and incorporating distances to sites where establishment has occurred might be more important to follow spread than focusing only on potential initial introduction sources.

Recently, surface seawater and atmospheric temperature records were used to predict

 the potential geographic range of the Pacific oyster in South America (Carrasco and Barón 2010). However, the authors averaged monthly near-coast temperatures over several years and acknowledged that in some locations, especially in estuaries and tidal flats, their predictions of oyster occurrence did not match the real situation, most likely because of a mismatch between local and near-coastal temperature regimes. Predictor variables such as embayment characteristics and habitat availability might increase the effectiveness for spatial predictions, particularly to discriminate among sites with similar temperature regimes. On the basis of the current study, we would anticipate that the sites most likely to develop populations of oysters would (a) be in embayments with aquaculture and with temperature regimes allowing for oyster spawning and larval development and with long residence times, (b) have hard substrata, e.g. mussel beds and rocky shores, (c) not have extensive cover of macroalgae and d) be intertidal areas > 50 m wide. The predictive performance of the model could be tested easily elsewhere as oyster populations have been found in places worldwide outside their native range for at least 40 years (Ruesink et al. 2005; Carrasco and Barón 2010).

 Our sampling methodology differs from other approaches in marine bioinvasions, such as passive sampling methods that use settlement plates, or rapid assessments that record only presence or absence and do not quantify densities (see Campbell et al. 2007). Furthermore, when species-environment relationships are studied the scale of analysis should match the scale of a species' response to its environment (De Knegt et al. 2009). Our methodology incorporated factors that correspond to the spatial scale relevant for the different life-stages of invertebrates, such as larval supply, settlement and recruitment. Rather than using only fixed levels of environmental factors, our approach also allowed inclusion of continuous covariates (substratum, wave fetch and residence time). This resulted in more degrees of freedom in the model as only the slope

 for a continuous variable and not a coefficient for each level had to be calculated. The AUC of 0.9 and also the individual classification threshold indicate a high discriminatory ability of our model (Fielding and Bell 1997). However, the same data were used to fit the model and to calculate model performance, which is not an independent validation of the model. Several sites were sampled within individual embayments, and several habitats were sometimes sampled within sites, thus, sampling locations were spatially clustered and could lack independence. This might have led to spatial autocorrelation, which can cause Type I error. However, initial results from mixed-model logistic regression that correct for spatial autocorrelation with a random effect of site on the intercept did not change results, i.e. estimated coefficients remained qualitatively the same as in the logistic model, which justified the use of a non-spatial model. Seeing the same qualitative outcome in the mixed-model suggests that oyster presence is affected by local differences in habitat (within site), and makes sampling of more than one habitat per site important.

 The presence of non-native species and also their abundances at sites cannot be explained exclusively by single factors. Beside sources of introduction, a comprehension of the early stages of spread requires a broad understanding of abiotic and biotic factors. Large-scale dynamics affect pelagic larvae and benthic juveniles, and biological, small scale interactions affect their survival and recruitment to the benthos. Statistical and process-based models are valuable tools for estimating the relative importance of multiple factors and combining them into 505 future invasion scenario predictions. Foremost, investigations of population dynamics at an early stage of marine bioinvasion are extremely valuable to allow early action to reduce the risk of invasion (Simberloff et

 al. 2013). Carefully designed sampling programmes using cost-effective methodologies and coordinated over large areas to encompass variation in a range of predictor variables, could make valuable contributions to such investigations. Furthermore, these programmes should provide for robust outputs that can be easily communicated to stakeholders and managers so that any subsequent management measures that target relevant risk factors are suitably informed and justified.

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777 **Table1** Categories of environmental variables and aquaculture. The number of habitats with oysters 778 present and absent is only shown for categorical variables. Note that categories for Width with the same 778 present and absent is only shown for categorical variables. Note that categories for Width with the same
779 superscript letters were combined for the logistic regression. Latitude was not included in the model and 779 superscript letters were combined for the logistic regression. Latitude was not included in the model and
780 Hardreef was the only Substratum cover used in the full model. More details of the variables are provided 780 Hardreef was the only Substratum cover used in the full model. More details of the variables are provided in the text

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Table2 Density of Pacific oysters estimated by transects (2 x 30 m²) or random quadrats (2 x 17 x 1 m² on 785 mussel beds) in intertidal areas with the highest density of oysters at each site at which oysters were 785 mussel beds) in intertidal areas with the highest density of oysters at each site at which oysters were
786 found. The locations of sites can be seen in Figure 1. At sites scored rare or occasional on the SACFOR scale 786 found. The locations of sites can be seen in Figure 1. At sites scored rare or occasional on the SACFOR scale
787 (see methods), no transects were used as densities were too low. In those cases, the SACFOR values are

787 (see methods), no transects were used as densities were too low. In those cases, the SACFOR values are given in the table as Occasional = 0.01 - $0.09/m^2$ or Rare = < $0.009/m^2$ given in the table as Occasional = 0.01 -0.09/m² or Rare = < $0.009/m^2$

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Table3 Coefficients, Standard Errors and p-values from the 'best fit' logistic regression model. The

810 intercept corresponds to Width ≥ 50 m, Aquaculture close, Residence = 0, Hardreef = 0

823 **Table4** Observed and expected numbers of oysters depending on availability of substrata at sites where 824 transects or quadrats were sampled (*Phase 2* of the protocol). Chi² goodness-of-fit test was used and p-823 Table4 Observed and expected numbers of oysters depending on
824 transects or quadrats were sampled (*Phase 2* of the protocol). C
825 values were simulated when expected values were smaller than 5

 $\frac{825}{826}$

828 **Figures**

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830 830 **Fig.1** Sampling sites and abundance of feral Pacific oysters in Ireland in 2009. Sites are categorised on the 831 SACFOR scale on the basis of timed searches (see methods) by symbols. Open circle: Absent; grey triangl 831 SACFOR scale on the basis of timed searches (see methods) by symbols. Open circle: Absent; grey triangle: 832 Rare; black triangle: Occasional; black circle: Frequent; grey circle: Common. Names of embayment where 832 Rare; black triangle: Occasional; black circle: Frequent; grey circle: Common. Names of embayment where
833 oysters were found are given oysters were found are given

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835 835 **Fig.2** Size-frequencies of Pacific oysters in 5 mm size intervals at different locations, a Lough Swilly, 836 Rathmelton, rocky shore, b Lough Swilly, Rathmelton, mussel bed, c Shannon Estuary, Loghill, d Shannon B37 Estuary, Glin, e Lough Foyle, Muff, mussel bed. Measurements were taken from transects (see methods), 837 Estuary, Glin, e Lough Foyle, Muff, mussel bed. Measurements were taken from transects (see methods), n = number of oysters n = number of oysters

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840 **Fig.3** Visualized results of estimated types of substratum from all collected habitats with and without 841 oysters. The number of habitats with and without by sterming brackets oysters. The number of habitats with and without oysters is given in brackets

Figure 2.

Figure 3. 848
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