



## Opinion paper

# A primer for use of genetic tools in selecting and testing the suitability of set-aside sites protected from deep-sea seafloor massive sulfide mining activities



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## ARTICLE INFO

### Article history:

Received 3 July 2015

Received in revised form

13 January 2016

Accepted 17 January 2016

Available online 25 January 2016

### Keywords:

Hydrothermal vent

Population genetics

Connectivity

Management

Mining activity

## ABSTRACT

Seafloor massive sulfide (SMS) mining will likely occur at hydrothermal systems in the near future. Alongside their mineral wealth, SMS deposits also have considerable biological value. Active SMS deposits host endemic hydrothermal vent communities, whilst inactive deposits support communities of deep water corals and other suspension feeders. Mining activities are expected to remove all large organisms and suitable habitat in the immediate area, making vent endemic organisms particularly at risk from habitat loss and localised extinction. As part of environmental management strategies designed to mitigate the effects of mining, areas of seabed need to be protected to preserve biodiversity that is lost at the mine site and to preserve communities that support connectivity among populations of vent animals in the surrounding region. These “set-aside” areas need to be biologically similar to the mine site and be suitably connected, mostly by transport of larvae, to neighbouring sites to ensure exchange of genetic material among remaining populations. Establishing suitable set-asides can be a formidable task for environmental managers, however the application of genetic approaches can aid set-aside identification, suitability assessment and monitoring. There are many genetic tools available, including analysis of mitochondrial DNA (mtDNA) sequences (e.g. *COI* or other suitable mtDNA genes) and appropriate nuclear DNA markers (e.g. microsatellites, single nucleotide polymorphisms), environmental DNA (eDNA) techniques and microbial metagenomics. When used in concert with traditional biological survey techniques, these tools can help to identify species, assess the genetic connectivity among populations and assess the diversity of communities. How these techniques can be applied to set-aside decision making is discussed and recommendations are made for the genetic characteristics of set-aside sites. A checklist for environmental regulators forms a guide to aid decision making on the suitability of set-aside design and assessment using genetic tools. This non-technical primer document represents the views of participants in the VentBase 2014 workshop.

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## 1. Introduction

Deep-sea mining is rapidly becoming a reality, with deposits of

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seafloor massive sulfides (SMS), polymetallic nodules and cobalt-rich crusts currently of commercial interest. In the case of SMS mining, exploitation is expected to occur in the southwest Pacific before 2020 (Baker and Beaudoin, 2013). SMS deposits are formed through the rapid precipitation of minerals as hot, sulfide-rich hydrothermal fluids are cooled by ambient seawater at seafloor vents, often creating chimney structures on the seafloor. The resulting deposits are often rich in gold, silver, and base metals, such as lead, copper and zinc (Krasnov et al., 1995). Globally there are 165 recorded SMS deposits (Hannington et al., 2011) that exist across a range of depths and geographical locations (reviewed by Boschen et al., 2013).

The hydrothermal environment that forms deposits also supports unique chemosynthetic communities that are reliant on the hydrothermal activity at these deposits to survive (reviewed by Van Dover, 2000). Where hydrothermal activity has ceased, relict (inactive) deposits are colonised by diverse communities characterised by slow growing sessile suspension-feeders (Galkin, 1997; Collins et al., 2012; Boschen et al., 2015a). The communities inhabiting both inactive and active deposits are vulnerable to disturbance, with mining activities expected to remove all large organisms and their habitat in the immediate exploitation area (Van Dover, 2011). One of the mitigation strategies is to preserve genetic diversity within the region by providing “set-aside” areas with similar physical and biological characteristics to the mine site that are designated as no-impact zones (Coffey Natural Systems, 2008; International Seabed Authority, 2010, Collins et al., 2012). To be effective, these set-aside sites need to support communities with taxonomic composition, abundance and diversity similar to the mine site. The populations of species at the set-aside site also need to have genetic properties similar to those found at the mine site and to be connected to other populations in the region as part of a coherent network, with high connectivity among sites (International Seabed Authority, 2011; Van Dover et al., 2012). With mining cessation, it is possible that the altered habitat may also sustain some recolonization from these set-aside areas, although this will depend upon the scale and nature of habitat regeneration.

However, assessing the suitability of a set-aside site or the connectivity within a network of sites is a considerable challenge to environmental managers. To assist this assessment, there are a number of techniques available, of which genetic tools are a subset. These tools can be used to assess the diversity of communities at sites and use the natural genetic variability of individuals and populations to assess the genetic structure of, and the connectivity among, neighbouring populations. This information can be used to determine if potential set-asides have similar biodiversity to the mine site, to identify populations that are potentially more vulnerable to mining disturbance and to identify populations that are sufficiently diverse and well connected to help maintain regional genetic diversity or to facilitate the recovery of mined sites. As such, genetic tools can be used to help identify suitable set-aside sites and assess the connectivity among sites within a network. An example of such an approach was developed to support the proposal for a network of areas of particular environmental interest set aside in the Clarion-Clipperton polymetallic nodule region in the north Pacific (Smith et al., 2008).

The aim of this document is to provide best practice recommendations for using current genetic tools to select and assess the suitability of either individual or a network of set-aside sites in the context of potential future mining of SMS deposits. The document includes a brief overview of communities inhabiting SMS deposits and the distribution of hydrothermal vent fauna; introduces the concept of population and genetic connectivity within vent systems; discusses the concept of the set-aside; provides an overview of the genetic tools currently available for set-aside assessment;

and outlines how genetic tools can be used during the stages of set-aside selection, assessment and long term monitoring. We also provide a checklist for regulators and environmental managers regarding the suitability of a proposed set-aside in terms of genetic connectivity. This document stems from discussions at the VentBase 2014 meeting at the National Institute of Water and Atmospheric Research, New Zealand. This workshop followed on from VentBase 2012, which produced a similar guideline document on Environmental Impact Assessment development for SMS mining (Collins et al., 2013a). VentBase was established as a forum where academic, commercial, governmental and non-governmental stakeholders can develop a consensus regarding the management of exploitation in the deep-sea, specifically the mining of SMS deposits. A primary goal of VentBase is the production of best-practice documents that can inform stakeholders and highlight the most up-to-date science in order to underpin effective management (Collins et al., 2013b; <http://www.indeep-project.org/ventbase>).

## 2. Biology of SMS deposits and the distribution of vent fauna

Biological communities of macrofauna (animals < 2 and > 0.5 cm) at SMS deposits fall into three broad categories: (1) vent endemic hydrothermal communities dependent on a chemosynthetic food web associated with active venting of hydrothermal fluids; (2) a halo/peripheral community usually at a short distance from active venting; and (3) the fauna of inactive SMS deposits, where venting has ceased. In the last two habitats, opportunistic ‘background’ fauna that typically characterize other deep-sea habitats may congregate to take advantage of additional food, such as bacterial mat dislodged from the vents (Erickson et al., 2009).

Biological communities associated with hydrothermally inactive SMS deposits harbour many taxa similar to those encrusting hard substrata in the deep sea (Galkin, 1997; Collins et al., 2012), although there are a limited number of studies. Levels of endemism among taxa on these deposits are poorly described but a specialised fauna adapted to the weathered sulfide environment (Van Dover, 2007, 2011) may exist, and a recent study identified faunal assemblages that appear to be unique to inactive SMS deposits (Boschen et al., 2015a). These organisms are typically sessile, slow-growing suspension feeders (Galkin, 1997; Collins et al., 2012; Boschen et al., 2015a) and would likely take decades to recover from mining disturbance, if they recover at all (Van Dover, 2011; Boschen et al., 2013).

The vent fauna inhabiting hydrothermally active areas exists in close proximity to hydrothermal flow, because it is reliant on the primary production of chemosynthetic bacteria that use reduced substances in the vent fluids for energy (reviewed by Van Dover, 2000). Vent communities typically contain relatively few species but individual abundance and overall biomass can be large (Grassle, 1985). Vent animals typically have rapid growth rates, enabling them to mature rapidly and to colonise new vent habitat via larval dispersal (Lutz et al., 1994). Although vent communities undergo natural disturbance, such as habitat loss through changes in hydrothermal or volcanic activity (Lutz et al., 1994; Tunnicliffe et al., 1997), perturbation from mining activities could pose an additional stressor, with the potential for cumulative impacts to negatively affect vent species (Van Dover, 2011). As the vast majority of vent species cannot survive away from hydrothermal activity, vent communities should be considered to be at high risk from anthropogenic activities, such as deep-sea mining and drilling, which are expected to remove hydrothermal habitat and to change remaining areas (Van Dover, 2011, 2014; Nakajima et al., 2015).

On a global scale, vent communities differ across oceans and regions, known as biogeographic provinces. There are many

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