

An Evaluation of Potential Genomic Applications in the Mining Industry

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Prepared for:

Genome British Columbia and the Ontario Genomics Institute



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Executive Summary

SRK Consulting (Canada) Inc. was hired by Genome British Columbia (Genome BC) and the Ontario Genomics Institute to identify ways in which the science of genomics could benefit the mining industry either economically or environmentally. This undertaking supports a broader mining and genomics related initiative led by Genome Canada and its regional partners, which include Genome BC and the Ontario Genomics Institute.

Genomics aims to decipher and understand the genetic information encoded in an organism's DNA and corresponding complements such as RNA, proteins, and metabolites. More broadly stated, the science of genomics seeks to better understand biological processes that underlie the interaction between organisms and their environment.

Many mining activities involve poorly understood biological processes. Using genomics to investigate these processes could create positive economic and environmental benefits while reducing risk and uncertainty within mining. To this end, SRK reviewed literature, assessed hypothetical case study applications, and interviewed key opinion leaders.

The results were positive. There appears to be as many potential applications for genomics within mining as there are biological processes associated with its activities, which range from exploration geology, baseline studies, and mineral extraction, to remediation and mine closure. It is difficult to envision how the potential benefits identified in this study could be realized without the use of genomics because of its ability to provide the biological information necessary for optimizing and fundamentally changing how mining projects operate.

SRK's analyses of three possible applications illustrated that significant economic benefits are attainable in areas of ore processing, water treatment, and mine closure. The magnitude of better financial performance or savings was found to be significant and is summarized in the following table.

Summary of mining and genomics cost benefit analysis.

Mining Process	Genomics Application	Economic Benefit	Potential Magnitude
Bioleaching	Metal recovery	Increase NPV	50%
Water treatment	Backfilled pits	Savings	\$100 M/facility
Covers	Develop biogeochemical reactions	Savings	\$20/facility

Source: Z:\01_SITES\GenomeBC\1CG026.000_Genomics and Mining Business\080_Deliverables\Report\020_Tables\Report_Tables_1CG016.000_CBK_REV00.xlsx]

The interviews with key opinion leaders within genomics and mining revealed many opportunities for genomics to help the industry, ranging from ore processing to environmental challenges. The ability of genomics to provide causal information underscores the benefits that the industry hopes to achieve from using genomics tools, whether to refine water quality predictions from mine waste or to optimize bioleaching processes. At the same time, one of the main concerns raised by those interviewed is the mining community's general lack of understanding of how genomic study results are presented and ultimately utilized.

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1 Introduction

SRK Consulting (Canada) Inc. was hired by Genome BC and the Ontario Genomics Institute (OGI) to identify ways the science of genomics could benefit the mining industry either economically or environmentally. This undertaking supports a broader mining and genomics related initiative led by Genome Canada and its regional partners, which include Genome BC and the Ontario Genomics Institute.

The scope of SRK's evaluation was provided in a work plan to Genome BC and the OGI dated August 19, 2014. This report summarizes the results of the work and is structured as follows:

- Background information and literature review
- Examples of how genomics might be used to address mining related biological processes
- Findings from interviews with key opinion leaders within genomics and mining

SRK understands the main use of this work will be to assist Genome BC and OGI in prioritizing funding efforts with its industry partners. The work may also serve as a basis for a workshop attended by personnel from key associations and innovation groups. The purpose of the workshop would be to further develop some of the ideas from this study into a strategic plan for effectively bringing genomic applications to the mining industry.

As defined on Genome BC's website (<http://www.genomebc.ca/>), genomics is a science that aims to decipher and understand the entirety of the genetic information encoded in an organism's DNA and corresponding complements such as RNA, proteins, and metabolites. Genomics is a powerful and essential tool for the investigation of biological processes, both in the laboratory and the field.

In general, the biological processes that take place in mining and mining-impacted environments are poorly characterized and understood. Using genomics to investigate these processes could create positive economic and environmental benefits while reducing risk and uncertainty within mining.

Genome BC and the OGI are two of the six regional genome centres that are a part of Genome Canada, which has developed a strategic vision for the application of genomics in mining (Genome Canada, 2013):

“Substantial improvement in the economic, environmental and societal performance of energy and mining sector operations in Canada and abroad is possible from application of genomics innovations.”

While this vision and related plan describe opportunities for genomics applications in mining, specific cost-benefit analyses are currently limited. In addition, although the vision statement was developed in association with opinion leaders in the mining industry, a better understanding of the barriers the industry faces for adopting genomics is needed. These two concerns provided the motivation for this study.

2 Literature Review

2.1 Overview

Using focused and pragmatic research efforts, SRK completed a literature review with the intent to identify opportunities to use genomics within mining activities. The basis and outcomes of the review are provided in this section and are grouped as follows:

- Search Criteria
- Genomics as a Tool for Mining Projects
- Bioleaching
- Bioremediation
- Future Opportunities

Bioleaching and bioremediation were identified in the literature and by participants of the industry consultations as two areas in mining with the greatest potential for enhancements through the use of genomics. Various other applications exist and are briefly discussed, but more thorough descriptions of bioleaching and bioremediation are provided. These form the basis for the cost benefit analysis (Section 3) and will likely be two subject areas that Genome BC and OGI need to evaluate for funding requests.

2.2 Search Criteria

One of main challenges in completing a literature review for genomics and mining is the two terms are rarely used together. As a result, advanced search criteria were developed to capture as many relevant publications as possible. The search terms used are provided in Table 2-1.

Table 2-1: Key search term combinations used for the literature review.

Genomics Terms	Mining Application Terms
genomics (including metagenomics, proteomics, metabolomics)	leaching and extraction
sequencing or profiling	waste rock and tailings
community or population	monitoring and assessment
DNA barcoding	remediation
microarray	acid rock drainage
various techniques (e.g. 16S rRNA gene, FISH, DGGE)	bioreactor

2.3 Genomics as a Tool for Mining Projects

Genomics has the potential to be applied in a wide range of mining environments, which are subject to the activity of multicellular (i.e. plants, fungi, and animals) and single celled organisms

(i.e. bacteria and archaea). Microbial communities are particularly relevant to overarching biological processes in mining environments. Bacteria have long been recognized as major agents of geochemical activity, catalyzing reactions to meet their metabolic needs. Microorganisms are at the root of global nutrient and biogeochemical cycles, influencing the release and attenuation of elements across the periodic table (Newman and Banfield, 2002). The direct or indirect products of microbial metabolism can increase reaction rates by orders of magnitude and drive reactions that are non-spontaneous under abiotic conditions (Singer and Stumm, 1970; Southam and Saunders, 2005). As a consequence, microbial communities can play antagonistic and advantageous roles in mining impacted environments. Microorganisms are known contributors to acid rock drainage, metal leaching at neutral pH, well souring during oil production, and corrosion of mining infrastructure. Conversely, microorganisms can be used to control leaching, souring, and corrosion, as well as enhance metal recovery and remediation of contaminated soil and water.

Despite their current importance and future potential, the microbial processes relevant to mining are often poorly understood or completely uncharacterized. This is due in part to technical and research challenges that have historically been faced by microbiologists. The study of microbial ecology has previously depended on the ability to culture microorganisms, >99% of which cannot be grown under laboratory conditions (Riesenfeld et al., 2004). Recent advances in molecular biology, including the advent of genomics, have allowed scientists to bypass culture-based analyses, building unbiased, semi-quantitative profiles of microbial populations using genetic information isolated directly from the environment.

Environmental DNA (eDNA) is nuclear or mitochondrial DNA that is released into the environment (USGS, 2013). Examples of eDNA include feces, exfoliation, mucus, urine, shed skin and hair. Through these processes, DNA can become suspended in an aquatic (habitat) medium, and it can then be collected and subsequently detected using quantitative Polymerase Chain Reaction (qPCR) genetic analysis techniques. The positive detection of a target taxon's DNA in the aquatic features used as habitat by the species can be used to establish species presence. A positive result from qPCR analysis suggests use, by the target taxa, of aquatic features at the sample site at, or shortly preceding (i.e. eDNA will only last for 7 to 21 days), the time of sample collection (USGS, 2013).

Another genomic technique known as transcriptomics focuses only on the subset of genes that are actively being expressed by organisms at the time of sampling through the isolation of RNA. In addition to reducing the complexity of the dataset to be analyzed, transcriptomics allows researchers to indirectly observe activity through transient expression profiles under given environmental conditions. This promotes the formulation of specific research questions about the relationship between organisms and their environment, facilitates the assignment of putative functions to ecologically important genes, and increases the likelihood of isolating genes that would otherwise be underrepresented or overlooked.

Genomics (irrespective of mining applications) first gained widespread public recognition in 2001 with the sequencing of the human genome. Since that time, rapid technological development has led to an exponential reduction in the cost of genomic analyses (Figure 2-1) and therefore they

have become a tool that can be used for a wider range of applications including mining. For example, at the end of 2014, genomic analysis costs from some providers are similar to that of water quality analyses (i.e. \$300–400 per sample) that all mine sites need to routinely perform.

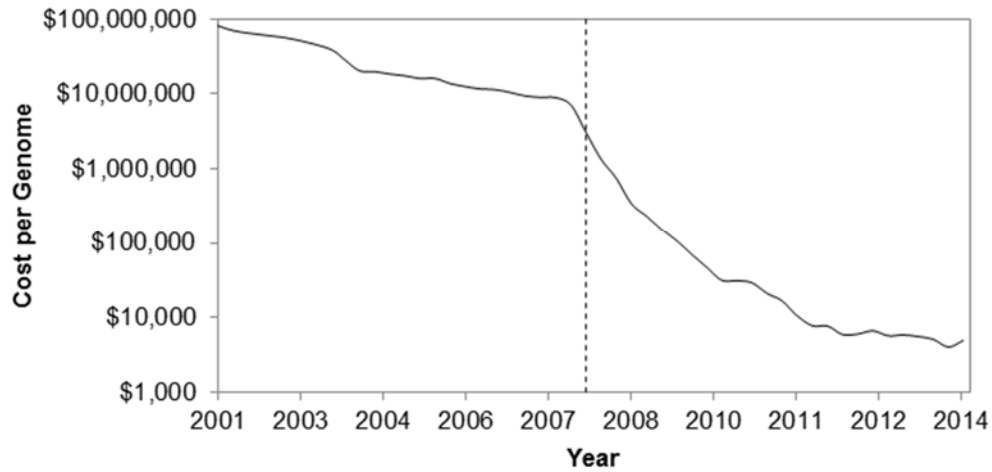


Figure 2-1: The reduction in cost per human genome sequenced over time (Wetterstrand, 2014).

Note: The vertical dashed line represents the period of transition from “first generation” to “second generation” DNA sequencing technologies.

Genomic techniques have been successfully applied to a variety of mining-related settings with different degrees of complexity, including soils (Vogel et al., 2009) and acid mine drainage sites (Tyson et al. 2004). The trend in lower genomic analysis costs is coupled with an increasing trend in the number of mining and genomic related publications with the last decade seeing more than double the number of publications in the field of mining and genomics (Figure 2-2).

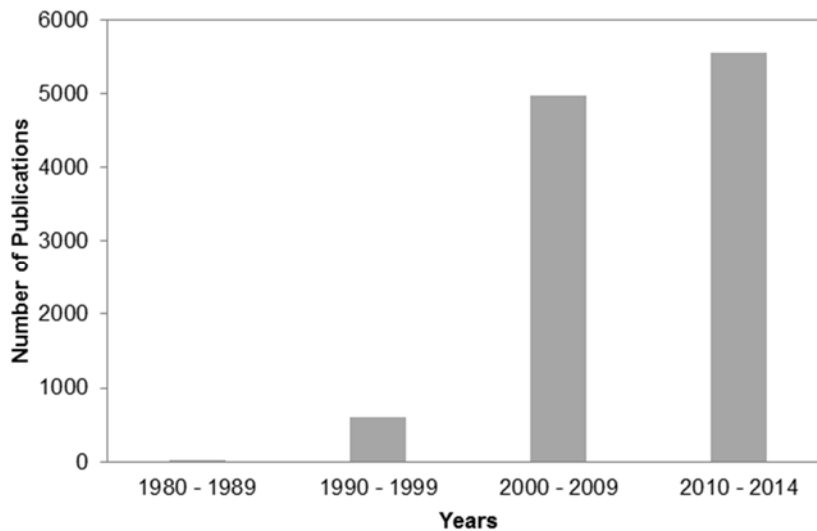


Figure 2-2: Peer reviewed published literature on genomics and mining studies over time

Two fields emerged from the literature review as the main focus of research and advancement: bioleaching and bioremediation. These two fields also form the basis of the cost-benefit analysis in Section 3 and as a result, are discussed more extensively in the following two sections.

2.4 Bioleaching

Conventional processing methods for sulphidic ores (i.e. gold, copper, nickel, zinc, etc.) typically provide high metal recoveries and certainty of consistent metallurgical performance, but the costs of production can also be relatively high. High production costs by conventional methods mean that many of the world's known deposits of sulphide associated metals remain uneconomic because the ore grades are very low.

Alternative bioleaching methods, in particular the large-scale dump or heap leaching methods, typically provide relatively low recoveries, with less certainty of consistent metallurgical performance, but the production costs per tonne of ore can be much lower than conventional methods. For many mineral deposits, the low metal recoveries and uncertainty of performance of biological methods make those projects financially unattractive because they are less profitable and have a higher risk of failure. Genomics has the potential to increase metal recoveries for a given production cost and improve the design and control of bioleaching processes to reduce the technical and financial risks.

The bioleaching process allows for metal recovery from ore (crushed rock) or tailings using the catalytic activity of ferrous iron- and sulfur-oxidizing chemolithotrophic bacteria (Norris et al., 2000). Heap bioleaching requires relatively simple equipment and operating procedures and has considerably lower capital costs than conventional froth flotation, smelting, and refining operations (Pradhan et al., 2008; Rawlings, 2004). Tank bioleaching can also offer less complex equipment and reduced costs. For example, there are at least 14 active gold projects using tank bio-oxidation as a means of enhancing metal recovery (Schippers et al., 2014), which was chosen instead of the more conventional and higher cost alternative of pressure oxidation. Table 2-2 shows examples of recent commercial projects using a range of bioleaching techniques and their average rates of metal recoveries.

Table 2-2: Examples of metal recovery rates from recent commercial projects using bioleaching.

Project and Location	Company	Bioleaching method	Recovery rate
Sotkamo, Finland	Talvivaara Mining	Heap bioleaching	Cu (3%), Co (14%), Zn (83%), Ni (94%) ¹
Sarcheshmeh, Iran	National Iranian Copper Industries Company	Heap bioleaching	Cu (60%) ²
Malanjkhand, India	Hindustan Copper Ltd.	Heap bioleaching	Cu (75%) ³
Carlin, Nevada	Newmont Mining	BIOPRO™ Process – heap oxidation	Au (78%) ⁴
Jinfeng, China	Eldorado Gold Corp.	BIOX™ Process – agitated tank oxidation	Au (87%) ⁵
Beaconsfield, Australia	BCD Resources	Bacox™ Process – tank oxidation	Au (95%) ⁶

¹(Gericke et al., 2009), ²(Pradhan et al., 2008), ³(Sukla et al., 2009), ⁴(Dunne et al.), ⁵(Lopez-Pacheco, 2014), ⁶(Neale et al., 2000)

For some bioleaching projects, metal recoveries are already relatively high, but a better understanding of the microbial communities that make bioleaching possible could significantly decrease processing time and thus capital and operating costs.

Although bioleaching has been successfully applied in the extraction of gold, copper, cobalt, nickel, zinc, and many other metals, certain minerals still present major challenges for processing on an industrial scale limiting the wider adoption of bioleaching techniques. Chalcopyrite, in particular, has been the subject of intense research activity, because of its tendency to form passivating layers of oxides on its surface, limiting copper recovery at temperatures and redox conditions suitable for microbial culturing (Gericke et al., 2009). Factors and parameters that affect bioleaching and metal recovery (Brandl, 2001) include:

- Physical and chemical parameters, such as temperature, pH, oxidation reduction potential, carbon dioxide and oxygen content, pulp density, and nutrient availability
- Biological factors, such as microbial diversity, microbial activity, population density, metal tolerance, ore particle attachment, and the properties of the inoculum
- Ore properties, such as composition, mineral type, acid consumption, grain size, mineral dissemination, surface area, porosity, hydrophobic galvanic interactions, and secondary mineral formation

Physical and chemical conditions are known to change dramatically over the course of the bioleaching process applying a strong selective force on microbial populations and activities. Understanding the structure and function of microbial communities responsible for metal recovery processes is critical to improving efficiency and expanding the role of bioleaching applications in the mineral industry. A variety of culture-independent methods have been employed to study the diversity of microorganisms in bioleaching environments, and some studies have attempted to link microbial community dynamics to changes in physicochemical conditions:

- Denaturing gradient gel electrophoresis
 - Change in microbial population structure over time in low grade copper sulfide heap under uncontrolled conditions (Demergasso et al., 2005; Schippers, 2007)
- 16s rRNA gene fragment sequencing
 - Comparison of microbial community structure in two different bioleaching systems (Xie et al., 2007)
 - Change in microbial population structure over time in low grade copper sulfide heap under uncontrolled conditions (Demergasso et al., 2010)
- Gene microarray
 - 50-mer oligonucleotide microarray based on most known genes associated with acidophiles in acid mine drainage and bioleaching systems, including 571 16S rRNA gene-related probes and 501 functional gene probes (Yin et al., 2007)

- Community genome array based on probes derived from 51 strains related to common microbial species found in acid mine drainage and bioleaching systems (Chen et al., 2009)
- Functional gene microarray monitoring *Leptospirillum ferrooxidans*' expression of energetic metabolism, electron transport, and ribosomal proteins over the course of bioleaching process (Remonsellez et al., 2009)
- Quantitative real-time PCR (qPCR)
 - qPCR of DNA microarray to monitor abundance of *Leptospirillum ferrooxidans* over the course of bioleaching process (Remonsellez et al., 2009)
 - qPCR of 16s rRNA gene to monitor microbial community composition as a function of pulp density (Wang et al., 2014)
 - Rapid detection of bacteria and archaea involved in bioleaching (Liu et al., 2006)
 - Monitoring of microbial community structure in mixed cultures (Zhang et al., 2009)

With the exception of the study conducted by Wang et al. (2014), a remaining limitation for the majority of genomic investigations in bioleaching is that DNA was isolated from liquid fractions of the environmental sample. This approach evaluates only the planktonic (free-floating) portion of the microbial community, when in fact microbial biomass and bioleaching activity occurs principally on the surface of mineral grains (Sand and Gehrke, 2006). Other reports suggest achieving maximum catalytic effects for metal recovery depends on the cooperative action between attached and planktonic microbes as their relationship works to oxidize mineral surfaces and then metabolize the intermediate products of oxidation in solution (Gautier et al., 2008; Sampson et al., 2000). Defining and understanding the interactions between microbial consortia members is key to improving the bioleaching process (Brierley and Brierley, 2013; Watling, 2006). There is also evidence that populations of heterotrophic microorganisms may be present during some periods of the bioleaching process, including reducing bacteria that may immobilize metal and reduce recovery (Pradhan et al., 2008). Currently, little is known of their role and interaction with other functional microbial groups in bioleaching systems.

Other notable gaps in the literature include:

- The effect of different chemical and physical conditions of microbial community structure and function
- The effect of leachate solution recycling on microbial community and bioleaching efficiency (Leaching liquor becomes increasingly toxic with repeated use, so microbial communities with adaptations for toxicity resistance would be an asset for continued operation.)
- The effect of different ore types on microbial community structure and function
- Optimal microbial community composition for maximum bioleaching rates
- Physicochemical conditions to encourage growth of optimal microbial community

- High-throughput 16S rRNA gene pyrosequencing and whole genome sequencing of bioleaching microbial communities

2.5 Bioremediation

Bioremediation is the process of sequestering or mitigating the release of certain chemical constituents that are considered environmental contaminants through the action of biological processes. Passive bioremediation (or natural attenuation) occurs through the activity of microorganisms and various forms of plant life found naturally in the contaminated environment, while active bioremediation refers to attempts to increase useful biological processes through the addition of organisms, nutrients, or chemicals. Bioremediation can in some cases offer a reduced cost and be more sustainable compared to conventional remediation techniques, often leading to complete contaminant removal when successful (Marco, 2010). Further, bioremediation may be the only practical option for remediating large, inaccessible areas such as subsurface environments (Chapelle et al., 2002).

Improving our understanding of bioremediation processes would help to assess and predict recovery of contaminated sites, increase the efficiency of contaminant degradation, and uncover novel microbial consortia and metabolic pathways—the majority of which are poorly characterized or unknown. Lear and Lewis (2012) suggest the success of individual bioremediation programs depends on understanding the following:

- Nature of the pollutant
- Physiochemical characteristics of the contaminated environment
- Structure and dynamics of in situ microbial communities
- Microbial community's phenotypic potential (e.g. biocatalytic capabilities)
- Microbial community's interactions with its environment

Due to its dependence on knowledge of active microbial communities, bioremediation studies are coupled with biomonitoring, an environmental assessment method based on detecting shifts in biological (predominantly the microbial) community structure and function in response to changing conditions. Since the vast majority of microorganisms cannot be cultured under laboratory conditions, genomic techniques offer the most complete characterization of microbial communities. A number of genomic options for biomonitoring have been successfully applied to investigate bioremediation processes in a variety environments (Desai et al., 2010). The following is a list of the most recent and advanced applications of genomics in mining-related bioremediation:

- High-throughput pyrosequencing of
 - 16S rRNA genes of microbial community in oil sands process water (OSPW) batch reactors (Choi and Liu, 2014)

- 16S rRNA genes to detect changes in microbial community in response to direct revegetation of Pb-Zn-Cu tailings (Li et al., 2014) (Results suggested further rehabilitation of rhizosphere communities was needed.)
- 16S rRNA genes of 90 microbial communities in a tailing impoundment, correlated with geochemistry (Liu et al., 2014) (The authors found that pH was primarily responsible for shaping community structure.)
- 16S rRNA genes for structure and function during acidification of Pb/Zn mine tailings (Chen et al., 2013), and
- 16S rRNA genes and metagenomics of microbial community and potential functional gene diversity for anaerobic hydrocarbon degradation and methanogenesis in oil sands tailings pond (An et al., 2013)
- Other low-throughput genomic methods
 - qPCR and DGGE (denaturing gradient gel electrophoresis) for oil sands process water cultures grown as a biofilm or planktonic suspension for the purpose of naphthenic acid degradation (Demeter et al., 2014)
 - Terminal restriction fragment length polymorphism analysis comparing fluid fine tailings bioreactors to tailings pond to determine community succession and whether laboratory populations are representative of whole field scale microbial communities (Fru et al., 2013)
 - Capillary electrophoresis single strand conformation polymorphism and DGGE to monitor microbial community remediating mine drainage (Hong et al., 2007)

2.6 Future Opportunities

Despite their advantages and broad applicability in the mining industry, there are many outstanding challenges to resolve before genomic techniques can be more widely adopted. Numerous laboratory studies have uncovered promising biocatalysts, but controlling key biological processes at full field scale has proven difficult, leading to the frequent failure of bioremediation in open ecosystems (Paerl and Steppe, 2003). More comparative research must be done to ensure effective scaling from bench to field. The majority of studies relevant to the mining industry have focused solely on the sequencing of 16S rRNA genes, for the purpose of taxonomic identification. Whole genome and whole community sequencing are useful for determining what genes are responsible for important processes, such as iron and sulfur cycling in bioleaching, acid mine drainage, and hydrocarbon methanogenesis (Galvão et al., 2005). The identification of functional genes is key to developing robust, low cost microarrays that can be used to efficiently monitor microbial communities and application progress (Bae and Park, 2006).

There is also a growing interest in a genomic method known as “DNA barcoding” in industrial settings requiring environmental monitoring and assessment. DNA barcoding utilizes gene segments as markers to identify particular species (Hebert et al., 2003), including those that are key indicators of ecosystem health. For example, the cytochrome c oxidase gene has been used for biomonitoring multiple taxonomic groups in rivers (Hajjibabaei et al., 2011). The relatively short

gene sequences required for identification and decreasing cost of sequencing services allows DNA barcoding to produce detailed and accurate reports over a broader area in a smaller time frame than traditional site sampling, which often requires months to years of analysis and risks generating outdated data with poor taxonomic precision (Baird and Hajibabaei, 2012).

Mixed communities of microbial species consistently show increased bioleaching and biodegradation efficiency and potential relative to monocultures (Demeter et al., 2014; García et al., 2001). Yet, virtually nothing is known of the interactions between different members of microbial consortia in these settings. Knowledge gained through genomics can be used to improve economically useful symbiotic relationships. For example, alder plants inoculated with *Frankia* species of microbes have been shown to increase soil quality, biodegradation, and revegetation rates in hydrocarbon contaminated soils (Lefrançois et al., 2010). Finally, genomic techniques have scarcely been applied to many aspects of mining operations that involve biological activity, such as the processes inherent to passive treatment systems, geosynthetic cover systems, and saturated rock fills.

3 Example Applications and Potential Benefits

3.1 Overview

This section presents example mining industry cases where genomics has the potential to add value. First, three example projects from SRK's recent experience are presented to illustrate the range of economic benefits associated with genomics inputs. The examples are genericized to avoid reference to particular sites, but the financial details are realistic. After the three examples, other possible applications are presented in less detail in Section 3.5. Note that all currency is provided in United States dollars (US\$).

3.2 Bioleaching Example

The first example looks at the potential value of applying genomics to ore processing. The specific application is bioleaching of refractory gold tailings, which was chosen because reprocessing low-grade tailings is often cited as a future opportunity for bioleaching and because several companies publicly report the operating performance of their gold bioleach processes. Also, in contrast to conventional processing of refractory ores, bioleaching can be relatively inefficient, leaving a lot of potential for improvement.

SRK developed a simplified economic model of an operation using froth flotation to pre-concentrate gold bearing sulphide minerals and biooxidation of the concentrate in stirred tank reactors, followed by solid-liquid separation, acid neutralization, carbon adsorption and desorption, electrowinning, and smelting. The resource used as input to the economic model is a hypothetical tailings deposit, but is based on SRK's experience evaluating tailings re-processing at existing sites. Other basic inputs and assumptions in the economic model included:

- Processing costs based on adjusted rates from Marsden and House (1992), CostMine (2013), and industry consensus market forecast for gold prices

- Ten-year life-of-mine (LOM) at a mining rate of 5,000 tonnes per day
- LOM average plant head-grade of 1.5 grams per tonne
- Base case LOM average gold recovery of 80%
- Mining by hydraulic methods and no requirement for crushing or primary grinding
- Facility construction time of 2.5 years
- Requirement for a new tailings facility and containing dam
- Discount rate of 5% for net present value (NPV) calculations

The economic model results for several cases with varying gold recoveries are summarized in Table 3-1. The base case economic model, assuming 80% recovery produced a positive NPV for the project of \$139 million. More important than the base case value of the example project is the sensitivity of that value to changes in the assumed gold recovery, which is shown in Figure 3-1. It indicates that if gold recovery were less than expected, say just 75%, the project would lose 25% of its NPV and may not provide adequate returns to investors. On the other hand, if the gold recovery could be increased from 80 to 85%, the value of the project would increase by 25% or 35 million. Looking to pressure oxidation techniques as a goal, recoveries are often greater than 90% and this would lead to an increase in the value of the project by 50%.

Table 3-1: Example project change in net present value with varying gold recovery.

Average gold recovery (LOM)		75%	80%*	85%	90%
Average gold price	US\$/oz	1,170	1,170	1,170	1,170
Undiscounted revenues and costs					
Gross revenues	US\$ M	740	789	839	888
Operating costs (total)	US\$ M	424	424	424	424
Capital costs (total)	US\$ M	148	148	148	148
Project net present value (NPV)	US\$ M	104	139	174	209

* base case

Source: Z:\01_SITES\GenomeBC\1CG026.000_Genomics and Mining Business\200_Evaluate Genomic Application to Mining\Economic Models\Tails_reprocess_1CG026.000_REV02_CBK_SRS.xlsx]

In the above example project, the achievement of consistently increased gold recoveries would most likely be achieved through faster rates of sulphide mineral oxidation. For a plant of a given size and cost, more complete oxidation of the mineral grains would allow more complete leaching of the contained gold with cyanide solution. Alternatively, process optimization could result in high recoveries for a smaller plant with lower capital and operating costs.

Genomics could provide the means to optimize and improve potential rate limiting steps of bacterial mineral oxidation, which is ultimately the controlling factor on recovery. Marsden and House (1992) state that the oxidation rate in stirred tank reactor circuits is directly related to the activity of the bacteria, which is determined, and driven by, the solution conditions. They list the primary conditions of interest as temperature, pH, pulp density, solution redox potential, and dissolved oxygen concentration. They also note the importance of bacterial adaptation to the inevitable changes in feed composition (in particular ore mineralogy) and the potentially toxic

effects of other chemical species in solution. Improved understanding of the relationships between the variable process conditions and the bacterial community genomics may be key to achieving consistently increased rates of oxidation.

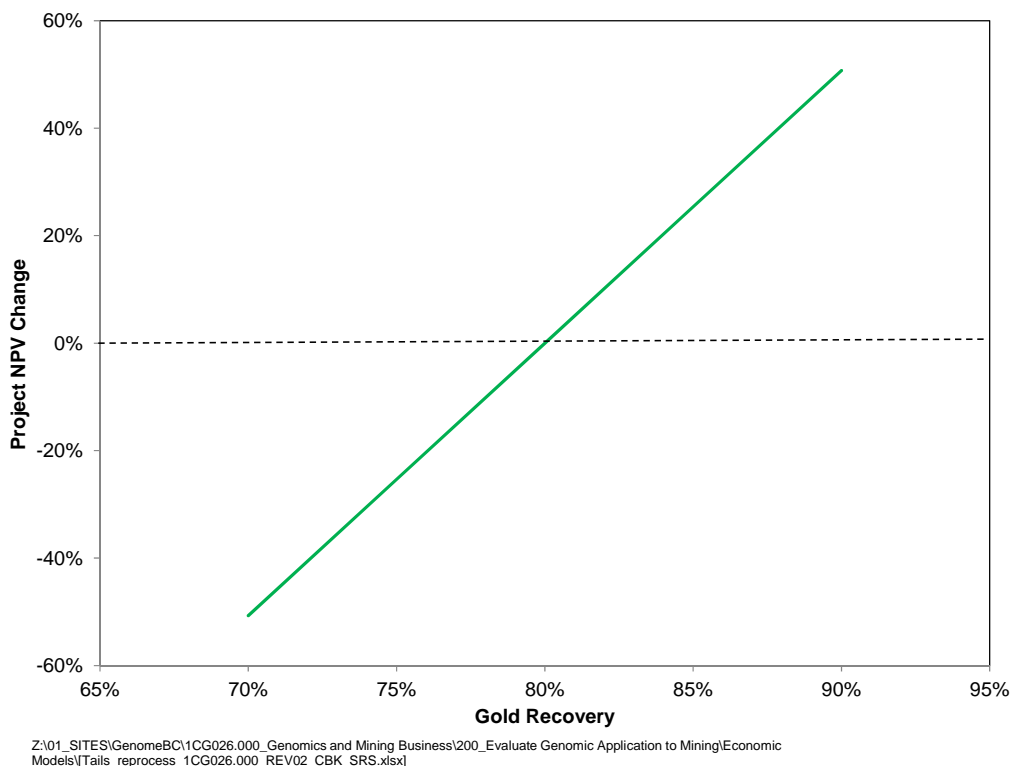


Figure 3-1: Example project net present value sensitivity to gold recovery.

The ability of genomics to improve the understanding of the fundamental processes of bioleaching to the extent metal recovery can be better controlled or improved, remains to be proven. However, this example shows the clear potential for value to be added. Many other examples in SRK’s experience would show similar results; metal recovery is typically one of the most significant risks in mining projects, and better control of metal recovery reduces risk and improves project economics.

3.3 Passive Water Treatment Example

The second example looks at the potential savings associated with the use of genomics to develop new water treatment methods. Construction and operation of water treatment plants is becoming a significant cost at many mines, and opportunities to create semi-passive treatment systems in mined-out voids are of growing interest. Most of the semi-passive treatment systems in operation or in research rely on poorly understood microbiological processes and therefore represent potential applications for genomics.

The example examined here is a treatment process that is currently in research and development (Bianchin et al., 2013; Teck, 2014; Kennedy et al., 2015). It sequesters selenium in backfilled pits by microbial reduction of selenate to the much less mobile selenite and elemental forms.

Investigations to date that support this model have included the use of metagenomics and microbial culturing (Kennedy et al., 2015).

Active water treatment processes to remove selenium to low levels are also in a state of rapid development, but currently available processes are costly. Assuming a treatment rate of 20,000 cubic metres per day treated using a fluidized bed reactor estimates presented in a recent MEND report indicate a capital cost of \$46 million and operating costs in the range of \$12 million per year (Hatch, 2014).

If the microbial processes active in FBR treatment can instead be implemented in a backfilled pit, most of the capital cost could be saved. Even assuming a cost of say \$10 million for injection, monitoring and withdrawals wells, the capital cost savings of using a backfilled pit would be \$36 million. Operating costs would also be reduced. Hatch (2104) does not provide a detailed breakdown of operating cost components, but a typical range would be roughly 1/3 for staff, 1/3 for reagents, and 1/3 for power. Assuming the semi-passive system allows both staff and power costs to be reduced by half, the savings would be roughly \$4 million per year. For a 20-year operation and using a discount rate of 5%, this equates to a NPV savings of \$50 million. The total of the capital and NPV operating cost savings associated with using the semi-passive system rather than active FRB treatment is \$86 million. Input parameters are calculated costs savings are provided in Table 3-2.

Table 3-2: Summary of potential water treatment cost savings using backfilled pits.

Treatment Method	CAPEX (M)	OPEX (M)	NPV (M)
Fluidized bed reactor	\$46	\$12	\$198
Backfilled pit	\$10	\$8	\$112
Savings	\$36	\$4	\$86

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This example illustrates the range of savings that are available to operating mines considering semi-passive water treatment methods. The assumptions used in the example are quite speculative, and Hatch (2014) places several caveats on their estimates, but SRK has looked at many other examples where semi-passive water treatment would result in a similar magnitude of savings. However, it should be recognized that many of these semi-passive treatment systems are several steps away from full scale implementation. The contribution of genomics in these case would be to advancing the research and development process, rather than to an immediate cost savings.

3.4 Reclamation and Closure Example

The third example looks at the potential contribution of genomics to mine closure and reclamation. The example considers the use of soil covers on an acid generating tailings deposit, and how the use of microbial processes below the soil cover could alter the selection of the cover design and the total cost of the closure plan. The example is loosely based on soil cover studies that SRK carried out over the last 15 years for closure of several abandoned mines in Yukon and

the Northwest Territories, although the use of microbial reactions was not considered at the time of those studies.

To eliminate the risk of acid generation, sulphide oxidation must be stopped, which is often achieved through limiting gas diffusion and is the primary role of the cover in this instance. Currently, the microbial reactions occurring below various types of covers are poorly understood and genomics would provide the tool to better understand the processes occurring and ultimately construct conditions that would promote the right kind of microbial community to achieve in situ inhibition of sulphide oxidation. While the example uses a tailings deposit that may generate acid, element leaching under neutral pH conditions is also a significant challenge to the mining industry and the same mechanisms and opportunities described herein could also lead to in situ sequestration of contaminants irrespective of acidic conditions.

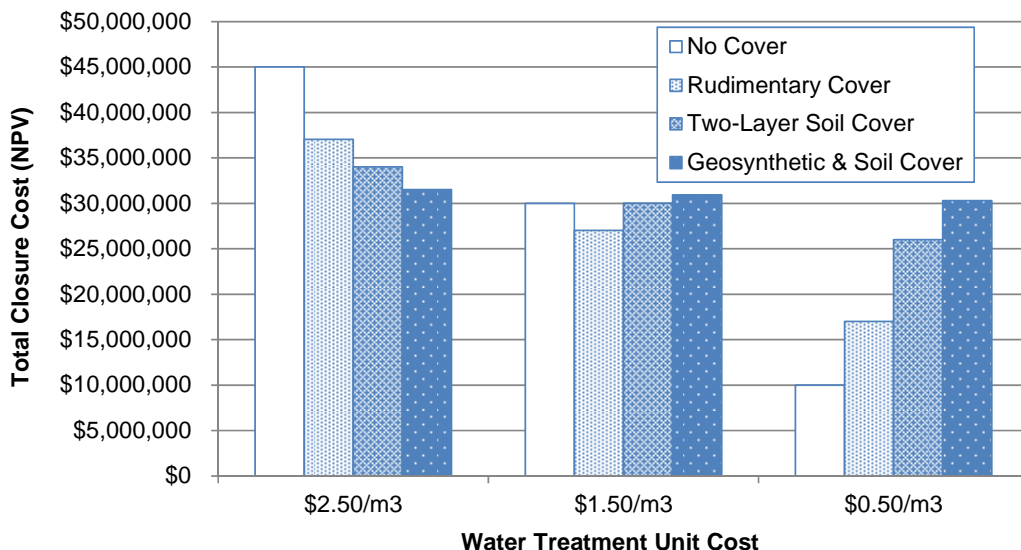
The tailings area is assumed to be 150 hectares in plan area, and the mean annual precipitation (MAP) is assumed to be 800 millimetres. If the tailings are not covered, it is assumed that 50% of MAP will infiltrate into the tailings and require water treatment. Soil covers of various designs would reduce the proportion of the MAP that would reach the tailings, so the key step in the design process is balancing of the cost of a soil cover against the savings in water treatment costs.

Key assumptions about the cover systems are as follows:

- A rudimentary soil cover consisting of one layer of reclamation material could be constructed at a cost of \$80,000 per hectare and would allow only 25% of MAP to infiltrate.
- A two layer cover consisting of a compacted lower layer and a reclamation layer could be constructed at a cost of \$160,000 per hectare and would allow only 10% of MAP to infiltrate.
- A geosynthetic and soil cover, consisting of a plastic or bituminous liner and a covering layer of reclamation material could be constructed at a cost of \$300,000 per hectare and would allow only 1.5% of MAP to infiltrate.

The water treatment process is assumed to have a base case operating cost of \$2.50 per cubic metre of water treated. The use of microbial reactions to consume oxygen or plug off oxygen diffusion pathways below the covers is assumed to reduce the contaminant loadings in the contact water so that treatment cost would be reduced either to \$1.50 per cubic metre or, more optimistically, to \$0.50 per cubic metre. In all cases the water treatment is assumed to be required for 200 years and NPV is calculated assuming a discount rate of 3%.

Figure 3-2 shows the resulting estimates of the total closure cost, including both the cost of the cover and the NPV cost of water treatment. Two points are noteworthy. First the cost of the “no cover” scenario drops from \$45 to \$10 million when the water treatment cost drops. This is the same pattern as in the second example where the use of microbial reaction in situ could lead to significantly reduced water treatment costs. Of more interest, and probably more realistic, are the patterns in the scenarios with covers, where the preferred cover option goes from geosynthetics and soil in the base case with \$2.50 per cubic metre water treatment to roughly equivalent in the \$1.50 per cubic metre case to rudimentary cover in the \$0.50 per cubic metre case.



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Figure 3-2: Tailings closure cost sensitivity to cover type and water treatment cost

This above example is simplified in many respects, but nonetheless illustrates the potential for “two-factor interactions” between conventional closure and reclamation methods and microbial assisted methods. When beneficial two-factor interactions like this can be demonstrated using simple examples, it is an indication that a range of combinations is worthy of investigation. While it is unlikely that a mine waste facility could ever be left uncovered in the future, the potential savings that could be realized going from a geosynthetic cover with water treatment requirements to a rudimentary cover designed to optimize microbial communities and therefore not require water treatment is \$20 million (Table 3-3). This is per waste facility and therefore the savings could be magnified significantly when the potential number of facilities needing covers is considered.

Table 3-3: Potential savings from cover selection.

Cover Type	CAPEX (M)	OPEX (M)	Total (M)
Geosynthetic Cover	\$30	\$2	\$32
Rudimentary Cover	\$12	\$0	\$12
Savings	\$18	\$2	\$20

Source: Z:\01_SITES\GenomeBC\1CG026.000_Genomics and Mining Business\200_Evaluate Genomic Application to Mining\Cover_costs\{Genomics_CoverWaterTreatmentNPVExample.xlsx}

The clear opportunity for genomics is to contribute to understanding and control of the microbial processes that would work in concert with the soil covers to reduce the impact of any oxygen that penetrates the cover system. Without genomics, it is difficult to image which other tools could provide the necessary information to develop cover systems that could achieve the estimated cost savings.

3.5 Other Applications

The potential uses of genomics as a tool for the mining industry are likely as diverse as the range of biological processes that interact with a mine operation. The examples in the above sections indicate the scale of economic impact, but many other opportunities exist. Based on SRK's experience, other areas should also be a priority for the application of genomics.

3.5.1 Reductive Dissolution for Metal Recovery

Reductive dissolution for metal recovery is the opposite of bio-oxidation discussed in the first example, but may hold a great deal of promise for deposits like nickel laterites where the metal is bound up in an oxidized mineral phase. While there are no nickel laterites in Canada, this is still a significant resource for Canadian mining companies with upwards of 70% of the global nickel resource in laterites. Bacteria would catalyze the reductive dissolution of iron oxides and release the nickel. To date, SRK is only aware of this possibility being investigated at UBC (by Professor Edouard Asselin) and genomics would likely be an extremely helpful tool to better understand the rate limiting steps to the reaction and how to optimize the microbial community.

3.5.2 Exploration Geology

Typically, geochemical signatures in water and sediments have been used for exploration geology, but this likely only provides a small snapshot of weathering processing reflected in the sample. A genetic profile from a water sample or sediment would likely be more sensitive to the history of weathering and not likely suffer from dilution and other inputs that render some geochemical results difficult to interpret.

3.5.3 Pit Lakes

Pit lakes are used as semi-passive water management systems. Their biogeochemical processes involve single-celled and multi-cellular organisms and are so diverse and complicated that they are a scientific discipline on their own. Genomics has the potential to help optimize their use for water management or to simply understand the long-term impact of water quality in the pit lake and surrounding ecosystem.

3.5.4 Constructed Wetlands

Constructed wetlands are used as a semi-passive water management systems. They are often incorporated into mine site design. When they are operating as intended, they are very effective at helping manage water quality, but often suffer from failure somewhat abruptly. Genomics could likely help with early identification of stress responses in the biological community so that changes could be made before failure occurs.

3.5.5 Biological Water Treatment Plants

Active biological treatment systems also rely on bacteria that are conditioned to specific applications, but they are currently monitored by physical and chemical parameters. Genomics could help better define the thresholds of operating parameters for acceptable plant performance and help lower costs and/or make the risk of failure much lower. The causes of water treatment

plant disruptions or failure could also be better understood and would benefit from a tool such as genomics.

3.5.6 Groundwater Plumes

The water that percolates through a waste rock dump or tailings deposit can emerge on surface as a seep, or continue to move as groundwater, in varying proportions. The biogeochemical processes that take place once in the subsurface may be amenable to management in such a way that a microbial community could passively treat leached contaminants. Genomics is a tool that could help better understand the biogeochemical reactions occurring and how to optimize passive treatment.

3.5.7 Baseline Studies

Baseline studies are the means of determining the characteristics of an ecosystem before it may be impacted by mining. These can be difficult studies to effectively complete and a tool like genomics could provide a higher resolution over a broader reach than current sampling and visual taxonomic identification. The use eDNA is already showing great promise for this task with Hemmera estimating completion of a survey for the Rocky Mountain tailed frog taking one-tenth the time and with much greater accuracy than typical approaches (J. Dobbs, personal communication).

3.5.8 Naphthenic Acid Degradation

Naphthenic acid degradation is one of the main constituents of interest in effluents from oil sands mining operations. Natural degradation by microbial communities has been demonstrated, but it is slow (i.e. decades). Recent work by Demeter et al (2014) found that stimulating a diverse community with multiple carbon sources resulted in the best community to degrade naphthenic acids over more useful timeframes for mine operations. Genomics could be used to help optimize the microbial community to changes in composition and understand what the rate limiting steps are in the degradation process.

4 Industry Consultation

4.1 Objectives and Approach

The main objective of the industry consultation process was to assess the current state of genomic understanding in the mining community and to identify areas of potential research to help guide Genome BC and the OGI when evaluating future funding requests.

Industry consultation was completed through interviews with 20 individuals, including mining executives, consultants, regulatory agencies, and academics all considered key opinion leaders in their field (participation list is provided in Appendix A). A series of questions were asked of each interviewee that focused on mining and biology and mining and genomics. At the end of the questions, each interviewee was also given a “carte blanche” opportunity to provide their opinions if something was not touched on during the interview. Notes were taken during each interview.

4.2 Findings

4.2.1 Overview

The range of experience in the participant list was well reflected in the responses to the interview questions. Several themes were identified and have been grouped as follows:

- Understanding the relationship between mining and biology
- Current and potential utility of genomics in mining
- Challenges for implementation

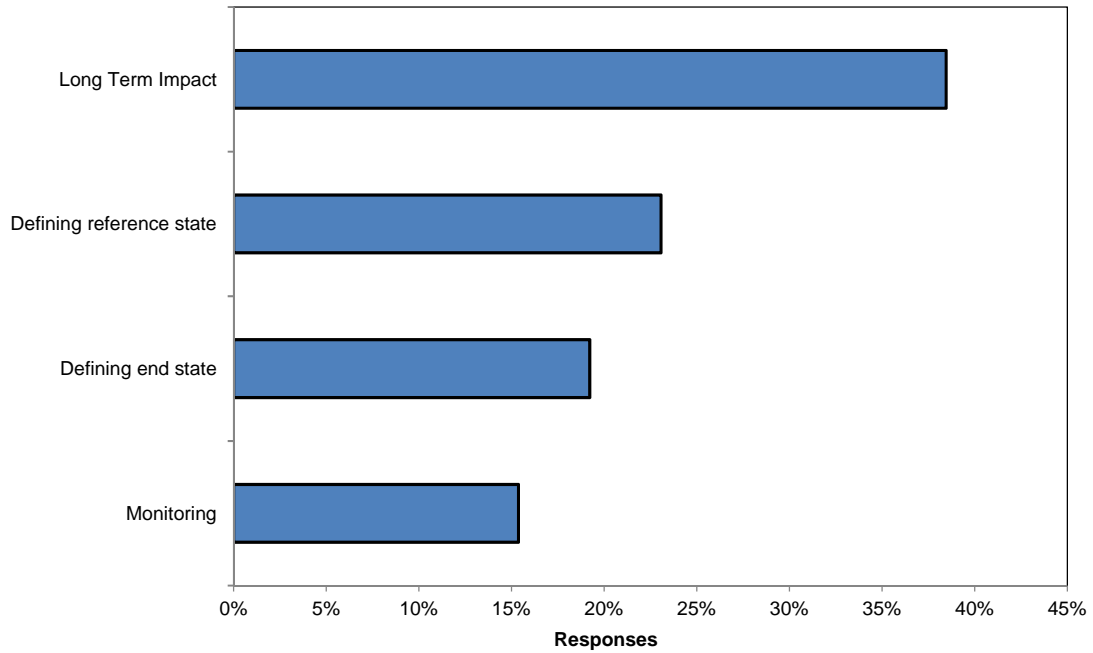
Participant consensus and discussion of each of the themes as they relate to the potential application of genomics in mining is provided in the following sections.

4.2.2 Understanding the Relationship Between Mining and Biology

The biological component of a mining process, whether for metals extraction or water treatment, is often referred to as a “black box”. Specifically in this study, the term “black box” was used by nearly 50% of the participants and better understanding the biological component was identified as something needing more work by all participants.

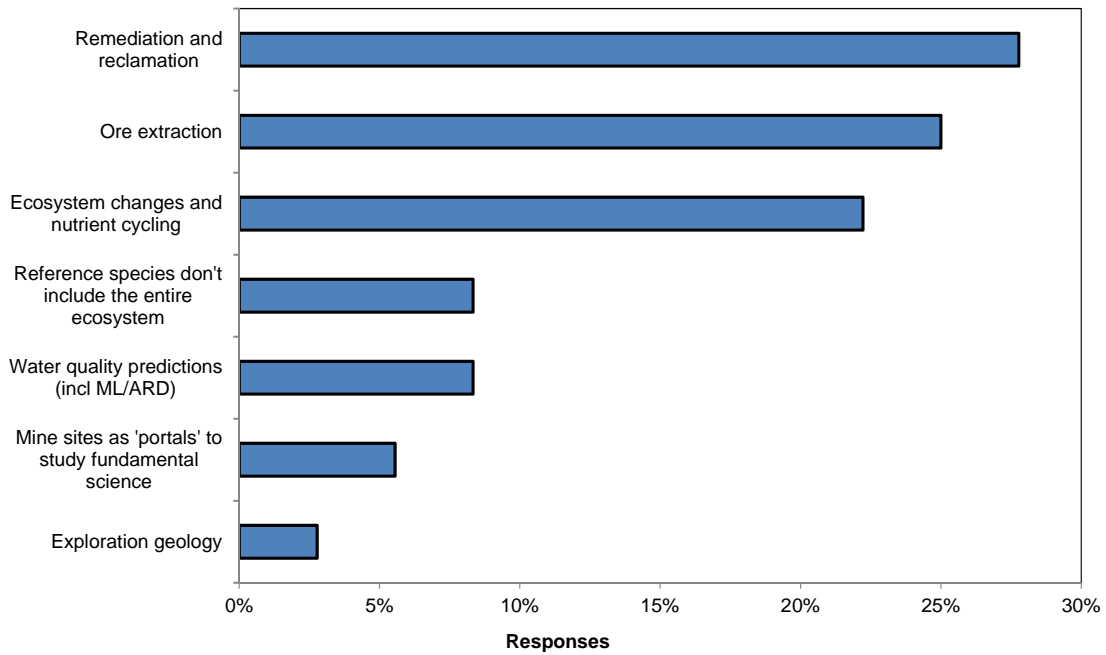
The most challenging aspect to understanding mining impacts on the receiving environment was identified by participants as predicting long term impact (Figure 4-1). Defining what the reference state is, or was, for most mining projects is also very challenging, which is often the objective of baseline studies. Many long-lived mining operations do not have any records of the reference state, which also makes defining the goal of conditions after operations (i.e. end state) uncertain. A common sub-theme was the high level of uncertainty in any study to better understand mining impacts on the environment, which can include monitoring challenges, to the length of time and cost to produce baseline studies, often with only a small fraction of an ecosystem understood.

All participants agreed there is a need to better understand the ways mining impacts biological processes in the receiving environment and also how biology impacts mining processes. The most common need identified was remediation and reclamation, although ore extraction through bioleaching and bio-oxidation was also prevalent (Figure 4-2). Other notable responses are also included in Figure 4-2, with a generalized theme being uncertainty in terms of how the entire ecosystem changes, not just pre-identified marker species like fish.



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Figure 4-1: Most challenging aspects to understanding mining impacts.



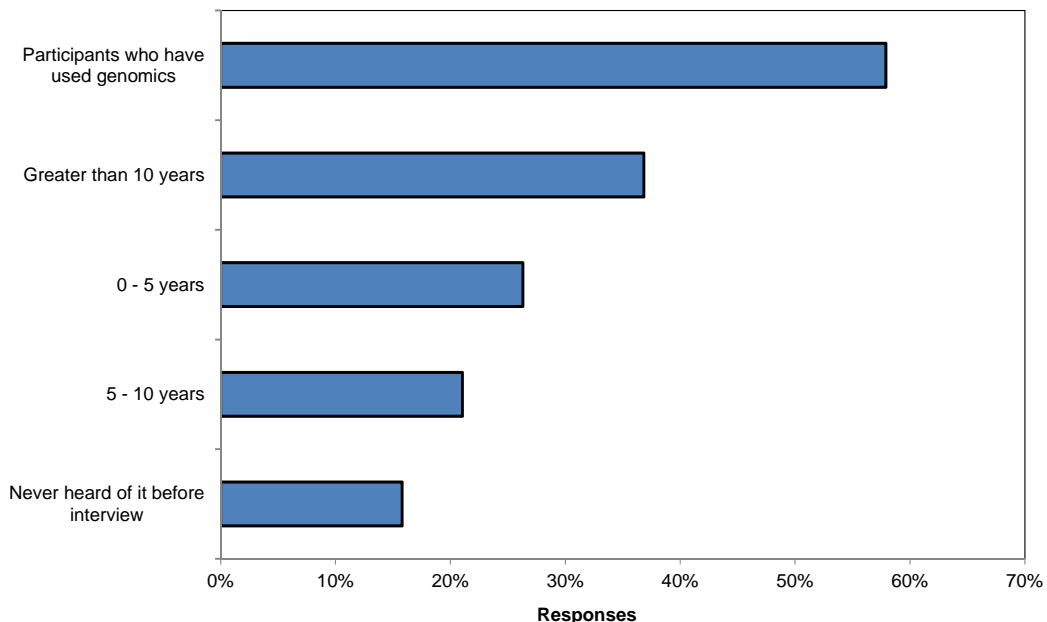
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Figure 4-2: Why the interaction between biology and mining needs to be better understood.

Despite the many reasons why the mining industry needs to do better, there is a sense of optimism that the scale of potential improvement is large, with participants indicating orders of magnitude improvements. As with all engineering design, improvements will likely need to be incremental, although in some instances, improvements cannot really be measured because certain processes are like a light switch and either “on or off” if biology can be better understood. Improvements were although thought possible on the physical side of mining (e.g. comminution), but optimized biological processes could also help lead to better design of a mine site with lower footprint and less impact on the receiving environment. So while the question asked participants where the greatest potential for mining processes to improve existed, the two should not necessarily be kept separate from one another.

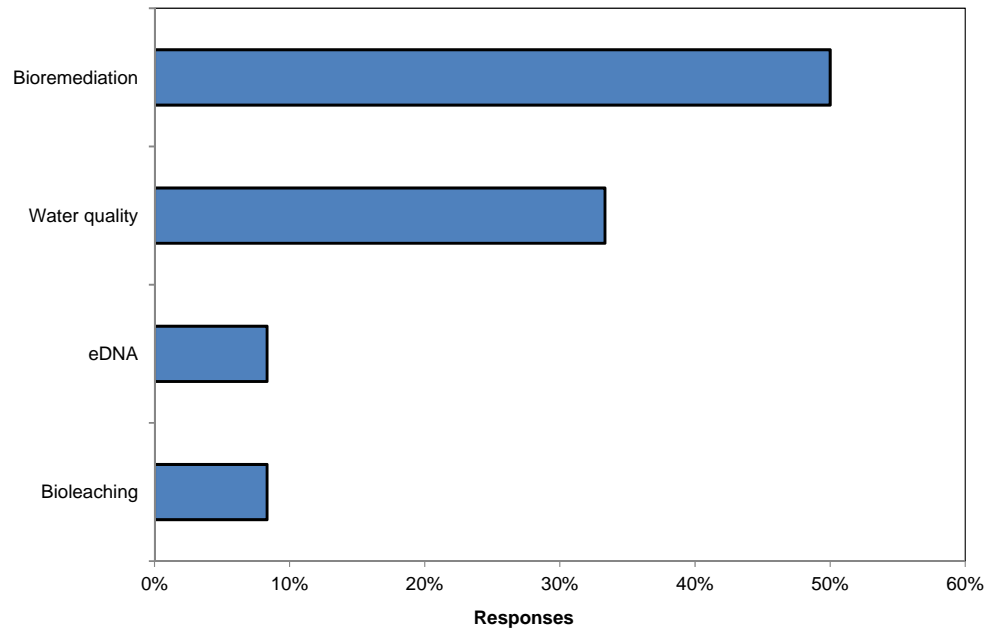
4.2.3 Current and Potential Use of Genomics in Mining

Nearly all of the participants had some knowledge of genomics (Figure 4-3), with approximately 60% using genomics as part of investigations to better understand mining processes. The most common type of genomics application for mining projects was in bioremediation (Figure 4-4), although water quality in terms of its prediction and impacts on the receiving environment was also prevalent. The use of eDNA to identify multi-cellular species for baseline studies and other related impact studies before, during or after operations was low on the list, although the technique potentially holds a great deal of promise for better understanding ecosystem composition compared to traditional approaches like visual taxonomy. Bioleaching was of great interest to the participants, although none working in this subject area had used genomic methods in their work.



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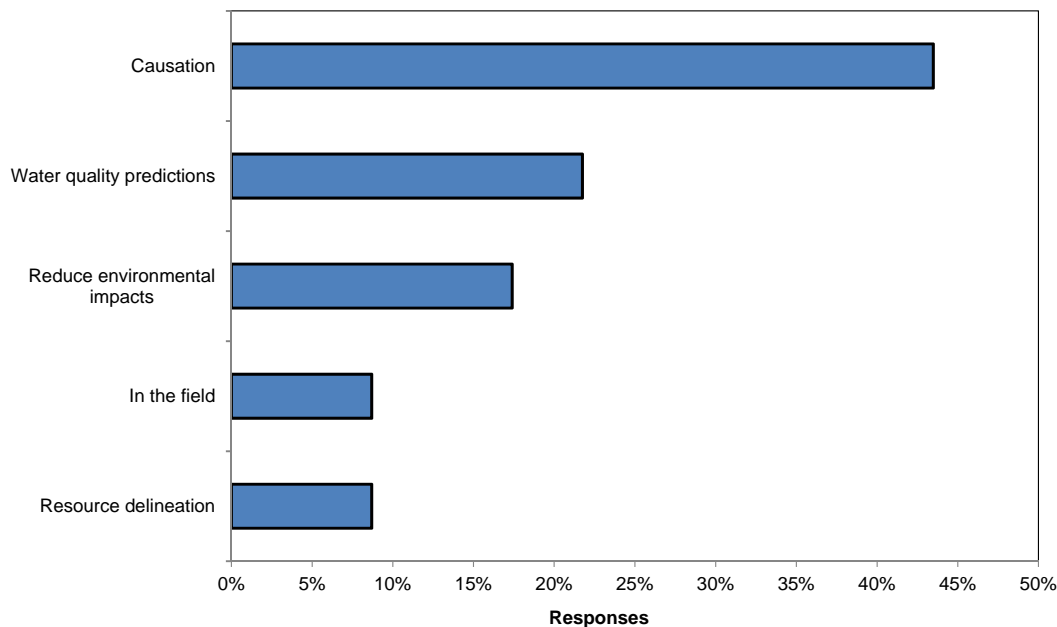
Figure 4-3: Participants experience with genomics.



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Figure 4-4: Most common types of genomic applications in mining projects.

Looking to the future, the participants predominantly want to use genomics as a tool to better understand causation relationships (Figure 4-5). Better understanding the biological communities that are present is important, but what appears to be needed is the ability to see how biological systems change in response to changes in mining processes and therefore inputs, to the biological system. Causation was referenced in relation to a number of subject areas, ranging from bioleaching for metal recovery to predicting and control of metal leaching and acid rock drainage to the stress response of the biological community in a passive treatment system.



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Figure 4-5: How participants want to use genomics.

Some other notable input from participants with regards to future use of genomics included water quality and exploration geology. Biology is often considered an expression of chemistry and therefore characterizing the genetic profile of the biology in a water sample using genomic methods may provide far more useful and complete information than inorganic water quality analyses (e.g. methods like inductively coupled plasma – mass spectrometry). Costs for a genomic analysis are now less than typical water quality analyses and therefore routinely obtaining the biological expression in a mine impacted water sample is becoming economically feasible.

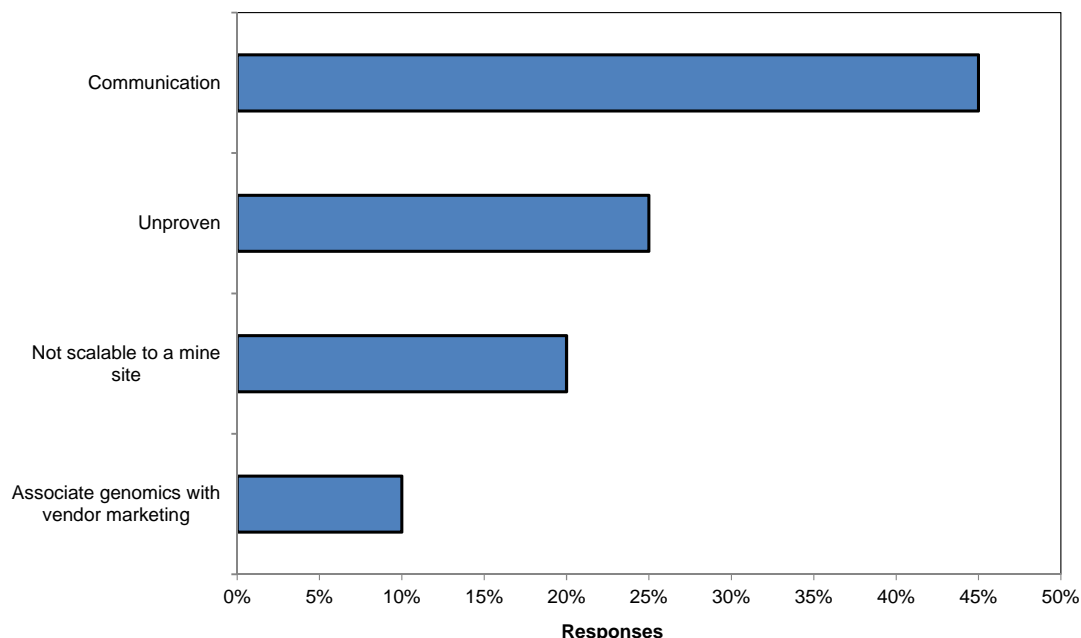
Genomic profiling of a water sample likely holds the potential to provide far more useful information for management and mitigation than current industry standard approaches. For example, one industry approach to understand water quality impact on the receiving environment usually involves testing lethal doses on selected aquatic species (i.e. a specific species of fish) and then setting guidelines based on that one species response. Of course the receiving environment is made up of a great many species, and therefore any tool that can provide a far more detailed understanding of impacts over a much broader spectrum of the receiving environment will certainly allow mine operators to better understand why and how they need to manage their impacts.

Rock outcrops have been leaching trace elements long before humans began mining and certain receiving environments will be better adapted to certain trace elements than others. Imposing the same stringent criteria for all receiving environments regardless of adaptation is certainly a situation that can be improved upon, and genomics can play a central role in this.

The use of genomics for exploration geology is somewhat like the example above for water quality. If biology is the expression of chemical inputs, then it is possible that the genetic profile of a water sample from a stream or other water body may provide more accurate clues as to where mineralized bedrock (i.e. potential ore) may exist. Typically geochemical signatures in water and sediments have been used for this purpose, but water quality likely only provides a small snapshot of weathering processing reflected in the sample, whereas a genetic profile may be more sensitive to the history of weathering and not likely suffer from dilution and other inputs that render some geochemical results difficult to interpret. This is also a possibility for soils as there is even evidence of microbial communities being different in areas of kimberlite pipes in organic sediments (Donkervoort and Southam, 2009), which most would dismiss as having a low probability of success compared to more oxidized gossan type outcrops.

4.2.4 Challenges for Implementation

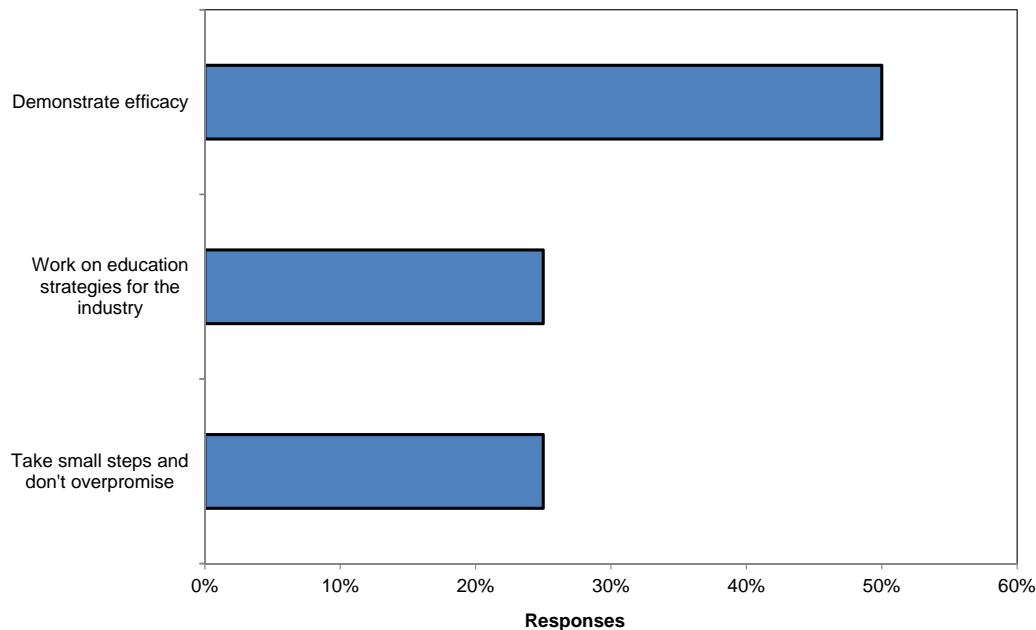
Regardless of the industry, all new technologies or tools face headwinds and genomics is no exception based on the input from participants (Figure 4-6). Communication was the main challenge identified, which encompasses many aspects from explaining what genomics even is to how it can be applied to mining projects. Genomics was also associated with genetic modification (“genetic engineering”), which is not necessarily how it may ever be applied for mining.



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Figure 4-6: Mining industry challenges for acceptance of genomics.

The other most prevalent challenges that are impeding acceptance of genomics are that genomics is an unproven technology, not scalable to a mine site, and associated with vendor marketing (i.e. “bug sellers”). Vendor marketing is in reference to mining companies being approached by groups that promote the use of a “special” microbial cocktail that can be applied to fix any number of environmental problems.



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Figure 4-7: Participant suggestions for implementing the use of genomics in mining.

Implementation suggestions were provided by most participants in the final open-ended question of the survey (Figure 4-7). Of those who provided implementation suggestions, 50% suggested that efficacy of the tool needed to be demonstrated. Many of the participants also indicated that this is a very critical time for genomics in mining, as the wrong research and industry projects could really hurt the reputation and broader scale acceptance of the tool.

Education outreach was also noted to help with implementation, which includes mining operators, consultants, stakeholders, and regulators. A mining project that utilizes genomic tools to support a change in management will have a very difficult time getting the approach accepted if the information is new and not easily understood. Lastly, taking small steps is good advice for any initiative and not unique to genomics, but some participants have seen too many new technologies that promised far greater than what was realized.

5 Conclusions

The potential role of genomic tools to better understand mining processes seems limited only by the number of scenarios in which biology and mining interact. Genomics has many possible applications in all phases of the mining life cycle, including exploration geology, baseline studies, mineral extraction, remediation, and mine closure.

Genomics has the potential to make significant improvements to many aspects of mining projects. For example, extraction NPVs could be increased by up to 50%, while remediation and closure management requirements could save tens of millions of dollars per waste facility. When the potential cost savings are multiplied across multiple facilities and mine sites, there is a possibility for significant financial upside. However, economic benefits should not overshadow the potential

that genomics has for lowering environmental risks and improving stakeholder acceptance. If a project is unable to proceed because it is unable to meet regulatory and stakeholder requirements, NPV calculations become irrelevant.

Without the use of genomics, it is difficult to envision how the potential benefits identified by this study could be realized. No other tool currently exists that has the promise of providing the necessary biological information needed to optimize and fundamentally change how mining projects operate.

The interviews with key opinion leaders within genomics and mining showed the following:

- Many see opportunities for genomics to help the industry manage environmental and ore processing challenges.
- The ability of genomics to provide causal information underscores the benefits the industry hopes to achieve from using genomics tools, whether to refine water quality predictions from mine waste or to optimize bioleaching processes.
- At the same time, one of the main concerns raised by those interviewed is the mining community's general lack of understanding of how genomic study results are presented and ultimately utilized.

With so many potential opportunities and applications of genomic tools in the mining industry, a pragmatic approach is needed to strategize where future funding efforts should be focused. A strength-weakness-opportunities-threats (SWOT) or similar strategic analysis with selected industry representatives would help Genome BC and the OGI further define the potential uses of genomics within the mining industry.

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Appendix A

Name	Affiliation	Role with Organization
Clara Qualizza	Teck Resources Ltd.	Manager of applied R&D at Teck, specifically Elk Valley selenium investigations
Rob Klein	Teck Resources Ltd.	Field Program Lead for R&D, specifically Elk Valley selenium investigations
Scott Weston	Hemmera	Director, including experience with genomic tools for improving passive mitigation of mine drainage
Brent Peyton	Montana State University	Professor of Chemical and Biological Engineering
Christopher Wend	CH2M Hill Inc.	Water treatment engineer - microbial selenium removal
Patrick Littlejohn	BioteQ Environmental Technologies	Senior Technology Specialist
Paul Miller	Sulphide Resource Processing Pty	Bioleaching expert
Monique Haakensen	Contango Strategies Ltd.	Specialist in mine passive treatment systems
Chris Bryan	University of Exeter, UK	Professor in sustainable mining and minerals resourcing, with a focus on microbial ecology in mine environments
Paul West-Sells	Casino Mining Corporation	President and CEO
Sue Baldwin	University of British Columbia	Professor developing genomic tools for monitoring and improving passive mitigation of mine drainage
Stephane Brienne	Teck Resources Ltd. – Applied Research and Technology	Section Leader - Environmental Technology
Gilles Tremblay	CANMET	Acting Director, Green Mining Initiative and part of genomics in mining working group
Bill Price	Natural Resources Canada (NRCan)	Federal reviewer for mining projects, specializing in metal leaching and acid rock drainage (ML/ARD)
Elizabeth Edwards	University of Toronto	Professor of Engineering with experience in bioleaching
Jean Vavrek	Canadian Institute of Mining (CIM)	Executive Director and founder of genomics in mining working group
James Higgins	Environmental Technologies Development Corp. (ETDC) Engineered Bioreactor Systems	President of ETDC and expert in wetland engineering, bioremediation
Chris Twigge-Molecey	Canada Mining Innovation Council (CMIC)	Director of CMIC, senior advisor at Hatch and past president of CIM and MetSoc
Lisa Kirk	Montana State University/Enviromin Inc.	Adjunct professor and consultant with specialization in selenium microbial ecology
André Sobolewski	Clear Coast Consulting	Water treatment specialist

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