Chapter 4.

Biotechnology and biomass sustainability

This chapter focuses on biotechnology in food production and the future roles of marine biotechnology. Given the extensive discourse on competing uses of biomass in food and industry, this is an important area for policy makers. If land extensification possibilities are limited, and agricultural productivity is declining, the industrial use of biomass would also be limited. Even as other forms of biomass are being sought as biorefinery feedstocks, agricultural productivity and sustainability need to be improved. The yield increase of the so-called green revolution in modern agriculture from the 1950s is flattening out. In addition, agricultural practices with higher inputs, such as pesticides and fertilisers to ensure high yields, are not considered environmentally sustainable. Therefore, the contributions of biotechnology to land extensification and intensification will be crucial in future. In addition, the marine environment remains a virtually untapped resource.

Introduction

Biotechnology, whether through genetic modification or not, is already making a huge impact on the sustainability of food production. This will continue to rise in importance as the human population increases and fossil dependence decreases. Despite apparent progress, the surface has merely been scratched. Biotechnology in agriculture can still make a huge impact.

Marine biotechnology and the sustainable exploitation of the marine environment are in their infancy. Whether exploiting its biomass or genetic potential, the marine environment will play a major role in a sustainable bioeconomy. It will reduce pressure on land and relieve fears about the competing use of terrestrial biomass for food and industry. Nevertheless, the oceans also have to be exploited sustainably.

Although powerful, genomics does not necessarily involve genetic modification (GM) or synthetic biology. Consequently, the negative societal issues that have haunted GM in many applications can be avoided. Rather, -omics technologies can be applied to animal and plant breeding to make selection of traits much more efficient. This is especially important for trees given the long timescales needed for growth and trait expression.

To exploit its full potential, genomics information needs to be linked to phenotypic characteristics. The availability of well-defined linkage maps and the extent of genetic studies conducted on them vary among different crops. This, in turn, influences the feasibility of any activity related to marker-assisted selection (MAS).[1] MAS can reduce the breeding cycle time significantly (e.g. for cassava from five to two years) and is much more accurate (Ly et al., 2013).

Genomics and biotechnology in food production

Increasing incomes in developing economies have contributed to a large increase in meat and milk consumption. From the beginning of the 1970s to the mid-1990s, the increase in meat consumption in developing countries was almost triple the increase in developed countries. Similarly, the increase in milk consumption was more than twice the increase in developed countries (Delgado, 2003). Naturally, this creates strains on a bioeconomy as less biomass can be devoted to industrial uses. Clearly, new ways are needed to increase food production efficiency in these areas.

Chinese Taipei offers a good example of the shift in diet that occurs with development. In the 30 years from 1959-89, per capita consumption of rice halved, while fish consumption doubled, meat consumption (chicken, beef and pork) quadrupled and fruit consumption quintupled (Huang and Bouis, 1996). Similar patterns were seen in Japan and Korea as household incomes increased.

From a bioeconomy point of view, this trend is negative. Large amounts of crops are produced to feed animals; ruminant production has notoriously high greenhouse gas (GHG) emissions (Table 4.1) and water consumption.

Beef production

The Australian beef industry today sees “unprecedented demand from the entire Asia Pacific, as well as the Middle East” (Kondo, 2014). Previously, demand was mostly from Japan, and then later the People’s Republic of China (hereafter “China”). But beef

production is resource-intensive in terms of land, feed and water, and also creates large GHG emissions. Policy makers are seeking measures to improve efficiency of beef production, and genomics offers some solutions.

Table 4.1. **GHG emissions associated with various meat production systems**

Product	CO_2 (eq./kg)
Beef	44.80
Idaho and Nebraska beef (average)	33.50
Idaho lamb	44.96
Swedish pork	3.3-4.4
Michigan pork	10.16
Chicken	2.0-4.6
Poultry (US)	1.4
Cod	3.2
Farmed salmon (sea-based, UK)	3.6
Farmed salmon (sea-based, Canada)	4.2
Farmed salmon (sea-based, Norway)	3.0
Farmed trout	4.5
Capture fish (global average)	1.7

Source: Jiménez-Sánchez, G. and J.C. Philp (2016), "The bioeconomy, genomics and society".

Genomics has been propagated as a "paradigm shifting" innovation in livestock production over the last decade. The possibility of predicting breeding values using genomic information has exerted major changes within the dairy cattle industry. This technology is now being used in beef cattle, but the diversity of breeds presents a challenge to develop genomic tools.

There is large scope for the development of novel applications in the livestock sector. These include selection tools for new traits (meat quality, disease resistance, feed efficiency, heat tolerance), animal traceability and parentage verification (e.g. McClure et al., 2013). Scientists are sequencing important animals in the global beef industry to identify variants and to associate those variants with the genetic variation observed across beef populations.

Selecting beef cattle for protein production requires appropriate emphasis on economically relevant traits (ERTs). Most ERTs are quantitative, such as early life growth and carcass quality attributes. These traits are output ERTs that impact revenue. Many ERTs are left out of breeding objectives for several reasons. In some cases, the capacity to collect data in the field does not exist. In other cases, the cost of collecting enough data for a national evaluation programme is too high. Many of these ERTs affect input costs of production such as animal health, feed efficiency and adaptability. These traits are fertile ground for the application of genomics technology. There is also great scope for increased international collaboration in all livestock species (Pollak et al., 2012).

In the near future, artificial reproductive technologies (ART), such as artificial insemination, embryo transfer and in-vitro fertilisation, combined with genomic evaluation (GE) approaches, may fine-tune cattle breeding. On the one hand, GE-improved methods will identify the exact gene alleles desired for a given type of animal. On the other, ART will enable checking for the presence of these favourable alleles in early stage in-vitro produced embryos, making the whole selection and breeding process much more accurate.

Development of specific "genomic-audited" lineages will also likely carry specific and interconnected alleles selected inside the traditional breeds. This will offer better chances

to the livestock industry to produce the animal required for each type of application, fostering quantity and quality parameters.

The Department of Agriculture, Food and the Marine of the Irish government has a Beef Data and Genomics Programme (BDGP) for 2015-20 (BDGP, n.d.). The EUR 300 million programme is addressing the widely acknowledged weaknesses in the maternal genetics of the Irish suckler herd. It will make a positive contribution to farmer profitability and reduce the greenhouse gas intensity of Ireland's beef production. As one objective, the programme will place Ireland at the forefront of climate-friendly agriculture. It will also further the positive environmental image of Irish beef production, which is considered to add value to Irish beef in high-value markets around the world.

Milk production

Genomics studies of milk have varied goals, underlining its significance as a human food. Topics include the capacity of milk to manipulate the gut microbiota; manipulation of bovine milk fat; genetic selection for economically important traits; and diagnostics. Genomics has revolutionised the dairy industry (see Hayes et al., 2009). Genetic tests are used to select every bull that sires milk-producing cows. Traditionally, after breeding the bull with a cow, the breeder would wait nine months for calves to be born. It would then take another three years until the calves begin lactating to know whether the bull produces higher milk-yielding offspring. Genetic testing doubles the speed of achieving those same milk production gains (Darcé, 2010).

Molecular mechanisms that create variations in milk components are important processes for human nutrition. As such, they require further investigation. Protein content, for example, is an important economic trait. In dairy cattle, the heritability of milk protein yield has been estimated at 23%. Identifying the polymorphisms contributing to milk traits could enable breeding programmes to increase milk protein yields, with obvious economic and societal benefits. Furthermore, identification of the gene pathways involved would contribute to understanding of the mechanisms that regulate lactation. This could also lead to new approaches to improve milk production.

Raven et al. (2013) produced evidence supporting a role for the RNASE5 pathway in milk production, specifically milk protein percent (and not other traits such as fat content or fertility). The evidence indicated that polymorphisms in or near these genes explain a proportion of the variation for this trait. Moreover, the gene set method applied to the RNASE5 pathway could be used to rapidly assess the role of other emerging pathways and functions with a genetic validation relevant *in vivo*.

Bacterial genomics can improve control of the microbiological safety and quality of food products, which is particularly relevant for milk. The process can keep milk free from pathogenic bacteria and ensure the concentration of spoilage microorganisms is as low as possible (Marco and Wells-Bennik, 2008). Human pathogens detected in raw milk include *Campylobacter jejuni*, enterohaemorrhagic *Escherichia coli*, *Salmonella* spp., *Listeria monocytogenes*, *Bacillus cereus* and *Yersinia enterocolitica*.

Non-pathogenic bacterial species determine milk quality and limit shelf-life by producing off-flavours, unwanted acidification and structure defects. Culture collection and model strains are instrumental for gaining knowledge on the behaviour of food-associated bacteria. However, the behaviour of "wild" strains in a dairy environment can differ significantly from the laboratory-adapted reference strains. Obtaining genome sequences of additional dairy isolates can help better understand their survival, persistence and pathogenic potential.

The International Milk Genomics Consortium aims to accelerate understanding of the biological processes underlying mammalian milk genomics (http://milkgenomics.org). It organises the annual International Milk Genomics and Human Health Symposium to promote advancement of milk genomics, proteomics, metabolomics and bioinformatics knowledge tools. The symposium facilitates communication between scientists, sponsors and others to accelerate progress and identify commercial opportunities.

Chicken as a food source in a bioeconomy

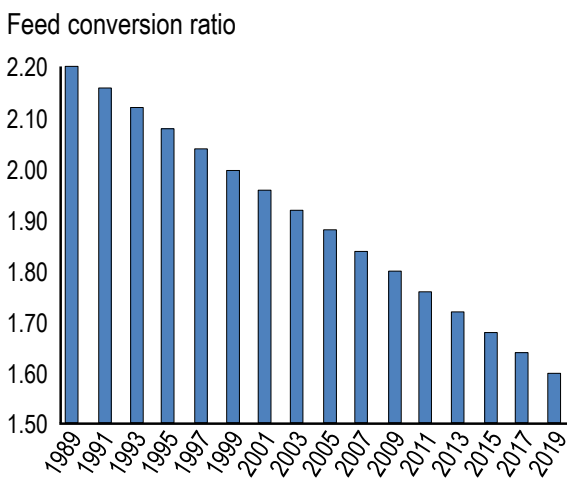
Chickens are a major source of protein in the world, with around 20 billion birds alive today. It was the first livestock species to be sequenced and so leads the way for others (Burt, 2005). As its production is relatively low in GHG emissions, chicken is an excellent food source in bioeconomy terms (Table 4.1). It is also cheaper to produce and less energy-intensive than rearing lamb, beef or pigs.

In parallel with the chicken genome sequencing project (Hillier et al., 2004), a consortium set about identifying single nucleotide polymorphisms (SNPs[2]). The availability of a standard set of 10 000 or more SNPs holds much promise towards identification of genes controlling quantitative trait loci (QTL), including those of economic interest.

During the past 80 years, modern selective breeding has made spectacular progress in both egg and meat production traits. These successes, however, have also generated undesirable traits that impose added costs on the industry. With increased requirement for food safety, there will be a need to reduce the use of chemicals and antibiotics and increase genetic resistance to pathogens. Further, the consumer wants high-quality products, such as increased egg shell strength; such new traits are difficult and costly to measure by conventional genetic selection. Developments in poultry genomics in the last few years promise new solutions to these problems. Therefore, genomics research may be expected to be directed at these "sustainability" criteria.

Figure 4.1. **Selective breeding of poultry for higher meat production and more efficient feed conversion**

(a) Feed conversion ratio over 30 years in meat-producing broilers at 42 days



(b) Broiler feed to produce a 2.5 kg chicken at 42 days

Source: Jiménez-Sanchez and Philp (2015), "Genomics and the bioeconomy: Opportunities to meet global challenges".

One key trait improved every year through selective breeding is feed efficiency (Figure 4.1) – the number of kilos of animal feed needed to produce a kilo of poultry meat (Technology Strategy Board, 2010). Genomic technologies are expected to enhance this trend. Since animal breeding is cumulative, even small enhancements to the rate of improvement can multiply into huge differences for commercial customers over time and have very large impacts. As a result, the same land resources can feed more people. Improved feed efficiency can also free up land as a resource such as to produce biomass for industrial use.

The Aviagen genomics project is concerned with identifying naturally occurring markers within the genome of elite birds (Aviagen, n.d.). It uses those markers to help breed stronger and more productive birds through the selective breeding programme, a completely natural process. Aviagen became the first company to include genomic information as a critical additional source of information in a research and development (R&D) breeding programme.

Fish and food security

Between 1998 and 2008, global exports of fish products doubled to a value of over USD 100 billion. It is estimated that more than 20 000 species of fish are used for food. Of more than 34 million global fishers (i.e. excluding aquaculture) in 2008, over 8.25 million were in China alone. Further, more than 2.25 million were in Indonesia compared to under 13 000 in Norway. Per capita consumption of fish continues to rise – from 10 kg to 19 kg between the 1960s and 2012 (FAO, 2014).

From the bioeconomy perspective, fish protein relieves pressure on land as the source of biomass for both agricultural and industrial uses. Given the health benefits and the lower GHG emissions associated with fish (Table 4.1), eating more fish would appear to be desirable for a future bioeconomy.

Overfishing has reduced some fish stocks to near extinction. Further, destructive fishery practices, such as bottom trawling, have damaged the habitat of the ocean floor. Coastal development and the resulting domestic and industrial wastes continue to perturb marine ecosystems and threaten coastal habitats in some areas. In extreme cases, agricultural pollution has resulted in hypoxia, which weakens established ocean ecosystems and sometimes leads to permanent “dead zones”.

About 90% of global wild fish stocks are already at capacity or are in precipitous decline (Tinline, 2015), with 60% of wild stocks fully fished and 30% overfished (FAO, 2014). Wild fisheries should therefore be regarded as “not necessarily renewable”. Well-reported universal difficulties associated with wild fisheries are related to identifying fish species. These include species with limited diagnostic morphological features, cryptic species, juvenile identification or unavailability of adequate drawings and descriptions.

Aquaculture has continued to grow in volumes and species as a consequence of deeply troubled wild fishing and increasing demand for fish. It produced 66.6 million tonnes in 2012 compared to 91.3 million tonnes for wild fish. However, the growth rate of aquaculture is more instructive. From 2007-12, the aquaculture industry grew by 33.5%, whereas capture fishing grew by a mere 0.6% (which is effectively static). Continuing future increases in demand are likely as the global middle class explodes in growth (D’Hondt et al., 2015). Most future growth in fish will likely have to come from aquaculture.

The benefits arising from the rapid growth in aquaculture have been accompanied by serious environmental, social and production challenges. For most countries, reliance on fish feeds remains an issue as they are often derived from scarce wild resources. Fish health, rearing and containment are also constant challenges. To grow and fulfil the promise of a

"blue revolution", aquaculture will need to balance its long-term environmental sustainability with its goal of growing large fish rapidly. Marine biotechnology offers some solutions.

Biotechnology in the capture fish and aquaculture industries

The increased availability of hardware, software and genetic information in the last decade has opened possibilities for biotechnology to contribute to both capture fishing and aquaculture. Many of these applications are not related to GM technologies and therefore are unlikely to cause public resistance.

Capture fishing: Traceability is becoming urgent

Almost 34% of the world's fisheries catch from 1950-2002 lacked species-level identification. The use of DNA barcodes for species delimitation, and the availability of a standardised and globally accessible database (BOLD, n.d.), facilitate numerous related applications. These include issues relating to traceability, eco-labelling, illegal fishing and fish fraud (Costa et al., 2012), and more fundamental information such as migration and dispersal behaviour (Box 4.1). A common fraudulent practice is species substitution. This can be unintentional or intentional to evade taxes, launder illegally caught fish or to sell one fish species for a higher-priced species. Illegal, unreported and unregulated (IUU) fishing remains a major threat to marine ecosystems (FAO, 2014). Traceability is becoming urgent (Waughray, 2017).

Box 4.1. **Atlantic herring identification through genomics**

Herring has been an important food source for hundreds of years over a very wide distribution. For many decades, it has been in dramatic decline. The Pacific herring, however, has sustained low abundances even after reductions of fishing pressure. Offered reasons include climate-induced ecological changes in distribution of predators and prey; disease; overfishing; and the rebound of marine mammal populations that prey on herring (McKechnie et al., 2014). A study of Atlantic herring on the Gulf of Maine–Georges Bank indicated that predation mortality rates were relatively low during the 1960s, when Atlantic herring were abundant. However, they increased in the late 1970s and early 1980s, when Atlantic herring declined. Predation mortality rates declined in the 1990s as Atlantic herring abundance increased. Sustainable fisheries management for herring is therefore extremely complicated. In addition, herring are generally highly migratory (Overholtz et al., 2008). This further complicates fish stock management, which requires precise and accurate data on the population identity of harvested fish. This allows managers to maximise long-term fisheries yield at minimal risk to population viability.

The risk associated with failure to identify individual populations in herring stock assessments is well known. Weak levels of differentiation among populations have prevented accurate assignment of individual fish to specific origins. Genomic resources, especially single nucleotide polymorphisms (SNPs), heralded the identification of Atlantic herring to unprecedented levels of geo-localisation in this weakly structured fish.

Bekkevold et al. (2015) extended the utility of genetic techniques for herring, demonstrating the applicability of Genetic Stock Identification (GSI). They showed this approach can be used as an adaptive tool to address biodiversity indicators applicable to natural resource management, and also to address illegal fishing and mis-labelling.

The practical advantages of DNA-based identification include the ability to use a range of fresh, preserved or highly processed material. This allows non-experts to collect samples with relatively little cost and effort. The method is also transferrable across laboratories and SNP genotyping platforms. It can be readily extended for additional populations and (or) genetic markers.

About 70% of the global tuna fish catch is taken from the Pacific. Most of the 23 tuna stocks are either over-exploited or depleted. Bluefin tuna are unrivalled in popularity, especially in sushi, and the economic value per fish is unmatched by any other species. However, its over-exploitation seriously threatens its future. Some advocate that consumers should avoid eating bluefin tuna altogether. Moreover, prices of yellowfin tuna and Pacific bluefin tuna are drastically different. But if they are used in cooking, it is difficult even for experts to distinguish between them. DNA barcoding therefore holds out promise for various policy goals: to reduce fraud, to play a role in cultivating conscientious consumerism (by helping conserve threatened species) and to regulate by eliminating market ambiguity effectively (Lowenstein et al., 2009).

To date, no one technique can identify species at the molecular level perfectly. However, DNA barcoding analysis is a significant advancement upon previous DNA techniques because it is based on a universal methodology (Hanner et al., 2011). Linking DNA barcoding to a universally accessible, expert-authenticated database of species identification data would arguably address many problems that plague the system of species authentication (Clark, 2015).

Aquaculture and genomics

Aquaculture production has continued to grow annually at around 6-8%. Today, farmed seafood production (around 60 million tonnes) exceeds that of wild fisheries and has significant potential for future growth. World aquaculture is heavily dominated by the Asia-Pacific region, which accounts for roughly 90% of production, mainly due to China. In 2008, 85.5% of fishers and fish farmers were in Asia, compared to 1.4% in Europe and 0.7% in North America (FAO and WHO, 2010). However, much work remains to improve productivity in Asia: fish farmers' average annual production in Norway is 172 tonnes per person; in China, it is 6 tonnes and in India only 2 tonnes.

High priority traits for farmed fish are the development of single sex populations and improving disease resistance. Production of mono-sex female stocks is desirable in most commercial production since females grow faster and mature later than males. Understanding the sex determination mechanism and developing sex-associated markers will shorten the time for the development of mono-sex female production, thus decreasing the costs of farming.

Tilapia

Nile Tilapia is one of the most important farmed species with a production exceeding 2.8 million metric tonnes in 2010. Tilapia farming is increasingly important in Asia, with (at least) Bangladesh, China, Indonesia, Malaysia, Myanmar, the Philippines, Thailand and Viet Nam all producing significant tonnages. Most Asian countries do not export significant amounts of Tilapia, demonstrating its role in food security.

Tilapia is unusual in that intensive commercial production generally requires all-male stocks. This is because males grow faster, but also to avoid uncontrolled reproduction before harvest. A restriction-associated DNA (RAD) sequencing study by Palaiokostas et al. (2013) identified a reduced candidate region for the sex-determining gene(s) and a set of tightly sex-linked SNP markers. Although they could not identify the causative gene(s), no female was mis-assigned using their sex-associated SNPs. This means those SNPs could be of high practical value towards the production of all-male stocks for the Tilapia aquaculture industry.

Salmon genomics

Salmonids, in particular Atlantic salmon, are among the most important aquaculture species. In 2010, farms worldwide produced approximately 1.5 million tonnes of Atlantic salmon, corresponding to a value of just over USD 7.8 billion (FAO, 2010). It is an important bioeconomy species due to the low GHG emissions associated with farming salmon. Outstanding challenges to the industry include reducing unsustainable fish losses, and controlling or eradicating sea lice and salmon Rickettsia septicaemia. These cost the industry hundreds of millions of dollars in lost production.

Genomic resources for Atlantic salmon are among the most extensive of all aquaculture species. They include several genetic maps, a physical map, an extensive Expressed Sequence Tags database of approximately 500 000 tags and several microarrays (Gonen et al., 2014). In June 2014, the International Cooperation to Sequence the Atlantic Salmon Genome (ICSASG) announced completion of a fully mapped and openly accessible salmon genome, which is housed at its own website (ICISB, n.d.). Some expected outcomes of this research are understanding the attacks by viruses and pathogens on salmon and producing new vaccines to reduce losses through disease; applications for food security and traceability and brood-stock selection for commercially important traits; and better understanding of interactions of farmed salmon with wild counterparts.

Selective, marker-assisted breeding of salmon, made possible due to access to the genome, will be more targeted and efficient. This could, for example, select for individuals that are more resistant to disease and parasites. It could also select fish that grow more quickly while being adapted to new feed types. In the longer term, genomic knowledge should help streamline the aquaculture industry, while providing consumers with healthier farmed salmon that are produced with as little environmental impact as possible.

The power of marker-assisted breeding is illustrated by the success in breeding salmon resistant to sea lice infection (University of Glasgow, 2015) or Infectious Pancreatic Necrosis (IPN) virus (World Fishing & Aquaculture, 2014). Not only can the use of pesticides and antibiotics be omitted, but losses are also greatly decreased. Survival rates of salmon in aquaculture of just a few per cent higher translate into major earnings for the Norwegian aquaculture industry, where the annual turnover is NOK 45 billion (approximately EUR 5.6 billion, or USD 7.6 billion) (Science Daily, 2014).

In the case of salmon, then, the power of relatively small public research funding of genomics to transform an industry is clear. In this case, a single tool can address many industry problems, which makes genomics unique as a solution provider.

Vaccines and the end of the antibiotic era

Marine biotechnology, in the form of new vaccines and molecular-based diagnostics, has already helped increase production, reduce the use of antibiotics and improve fish welfare (Sommerset et al., 2005). In many places, the use of antibiotics has plummeted; Norway produces 99% of farmed salmon without antibiotics. In other countries, however, especially developing countries without access to molecular-based tools and technologies, use of antibiotics remains widespread (Cabello, 2006). Genomic and related technologies have also been used to create new DNA-based vaccines for economically important diseases (e.g. Apex-IHN, Novartis, for the treatment of infectious hematopoietic necrosis in farmed salmon) and highly sensitive specific tools for disease detection (Cunningham, 2002).

Molecular aquaculture

The application of new genomic knowledge and technologies to the practice of aquaculture is termed "molecular aquaculture". This helps distinguish it from the more production-oriented activities in aquaculture such as improved feeding systems, cage design and husbandry. Molecular aquaculture is characterised by the incorporation of new omics knowledge, high-throughput genomics technologies and recombinant DNA technology. These technologies have facilitated selective breeding for economically important traits such as body shape or disease resistance.

Molecular aquaculture holds great potential for increasing sustainable food production. This can help meet anticipated increases in global demand through the culture of species such as salmon, Tilapia, shrimp and oysters. However, molecular aquaculture is developing and diffusing at different rates in different countries, potentially limiting the productivity gains and sustainability of the endeavour.

Hybrid technologies for aquaculture/agriculture

Building solar-powered desalination plants for aquaculture in hot, sunny climates is a possibility (Palenzuela et al., 2015). A hybrid system combining solar-powered desalination with a "floating farm" has been described in concept (Moustafa, 2016). This concept envisages growing crops that need freshwater rather than seawater. Construction of such a system (a "bluehouse" rather than greenhouse) offshore would relieve pressure on land. In other words, it is about moving terrestrial crop production offshore.

Genetic modification in aquaculture

Much more controversial than genomics and traditional vaccine development, GM technology has already been applied to salmon breeding. GM technology varies widely in its acceptability in different countries. In the United States, the Food and Drug Administration (FDA) has approved the first GM salmon. It contains a growth hormone gene from a related species that allows the salmon to grow to market size in 16-18 months rather than over three years. As a result, this salmon consumes at least 25% less feed over its lifetime than conventionally farmed salmon. It thus saves money, which could mean lower prices for the consumer if it reaches the market.

The US FDA began its review of this technology (AquaBounty, n.d.) in 1993. In 2012, it concluded that AquAdvantage was safe for human consumption and unlikely to damage the environment. A lengthy public consultation ensued (Baehr, 2014), during which the salmon was not available to consumers. Finally, on 19 November 2015 it became the first genetically engineered animal to be approved for human consumption in the United States (Ledford, 2015).

Feeding the fish that feed humans

Well-described benefits of eating oily fish come from the long-chain polyunsaturated fatty acids (LC-PUFA) commonly referred to as omega-3 fatty acids. They are, however, not synthesised by the fish themselves; rather, the synthesis is done by single-celled algae and the molecules then pass up the food chain to small, herbivorous fish and thence to large, carnivorous ones (The Economist, 2015).

Paradoxically, farmed fish such as salmon are fed fish meal, made from wild-caught oceanic species such as anchovies that are not in great demand as human food. This helps boost their levels of the two critical omega-3 fatty acids, docosahexaenoic acid (DHA) and eicosapentaenoic acid (EPA). The aquaculture industry needs to find new fish food

sources, particularly to replace or supplement these high-quality inputs from fishmeal and oil; lack of new fish food is increasingly seen as a limitation for future growth in aquaculture production (McAndrew and Napier, 2011).

More than one strategy to find new fish food sources is being investigated. First, it is possible to genetically engineer plants to modify seed oil composition[3] to include omega-3 PUFAs; the collective data available (e.g. Usher et al., 2015) confirm the promise of transgenic plants. However, while levels of EPA achieved are equivalent to marine sources, DHA still represents a challenge.

Rather more controversial would be to engineer the fish to make omega-3 fatty acids directly. In one study, zebrafish were transformed with a salmon desaturase, leading to modestly increased tissue levels of EPA and DHA (Alimuddin et al., 2005). While zebrafish is a model organism, Tilapia is an aquaculture species. The Institute of Cellular and Organismic Biology in Chinese Taipei is examining how metabolic engineering in Tilapia could express high levels of omega-3 PUFA biosynthesis genes in the liver.

Crop genomics and precision crops

Feeding the 9 billion people on the planet by 2050 is a major food security issue. Moreover, the demand for biomass for bio-based production of fuels, chemicals and plastics will further stress land availability and productivity. The effects of climate change will exacerbate difficulties facing conventional agriculture. Although seldom acknowledged in discussions of agricultural genetic resources, soils are the critical life-support surface on which all terrestrial biodiversity depends. Meanwhile, the world is losing soil at a rate 13-80 times faster than soil is being formed. In October 2017, the environment secretary of the UK government warned that the United Kingdom is 30-40 years away from "the fundamental eradication of soil fertility" (van der Zee, 2017). In the face of soil destruction, more crops will have to be grown more efficiently. At the same time, methods are needed to halt or limit soil destruction.

Many applications of genomics to crop production will be used in the future bioeconomy e.g. pest resistance, more "efficient" plants that use less water, resistance to environmental stresses and the development of crops that can fix nitrogen to replace synthetic fertilisers. Heat and drought stress are used as examples of applying genomics to agriculture. On the other hand, too much water in the case of rice can also destroy crops.

Heat and drought stress: An increasingly important problem associated with global warming

Improvement of dual stress tolerance to heat and drought in crop plants has become a top priority for the development of agricultural biotechnology for both food and bioenergy markets. Performance Plants, a Canadian company, has identified and completed functional studies of a subset of target genes that constitute a novel regulatory cascade that controls plant responses to the combined stress. In laboratory conditions, *Arabidopsis* and canola plants with missense expression of these regulatory genes could tolerate independent higher temperature or drought treatment. More importantly, when both stresses were applied simultaneously, these plants produced higher seed yield compared to their controls. Charge-scale, multiple season and location field trials further confirmed the dual stress tolerance and yield enhancement properties of the transgenic plants. These results represent a significant breakthrough in crop improvement. Technologies derived from this research could enable farmers around the world to maintain higher yield and productivity over variable and adverse environmental conditions.

Sunflower is mainly grown for edible oil, but is also used for biodiesel, biogas, wood and charcoal, with its use likely to expand. Drought is the main threat to sunflower production, and genomics is taking its place to select new varieties for future crops. It is already rather drought-resistant and the mining of the genome of extremophile variants holds promise for improved drought resistance and increased oil yield (Badouin et al., 2017).

Oil palm genomics

Oil palm illustrates a classic bioeconomy dilemma. It is the most productive oil-bearing crop, accounting for 33% of all vegetable oil and 45% of edible oil worldwide. Although it is planted on only 5% of the total world vegetable oil acreage, increased cultivation competes with dwindling rainforest reserves. Global production of palm oil more than doubled between 2000 and 2012 (FAO, 2013). Thus, the competing imperatives of a bioeconomy are clear to see: creating economic growth while reining in detrimental environmental effects to create a future economy that is sustainable.

Palm oil production is central to the economy of Malaysia, employing close to half a million people. Historical statistics indicate that Malaysian palm oil yields have typically appreciated over time. In 2009, however, an unexpected break in the long-term national growth pattern occurred, which has persisted. Explanations for the abrupt change are varied, which include a combination of adverse weather, ageing trees and plant disease (USDA Foreign Agriculture Service, 2012).

Data indicate the vast majority of trees has already reached or passed through its peak yielding years. A small but growing problem is a lethal fungal disease. *Ganoderma* has the capacity to cause significant yield losses well before it has killed an oil palm. Once it has been introduced, its spores can spread to ever increasing areas of a plantation. Therefore, increasing oil yield and disease resistance would be obvious targets for genomics applications. With growing needs for edible and biofuel uses, increasing yield for oil palm would reduce its rainforest footprint.

The oil palm genome and oil yield

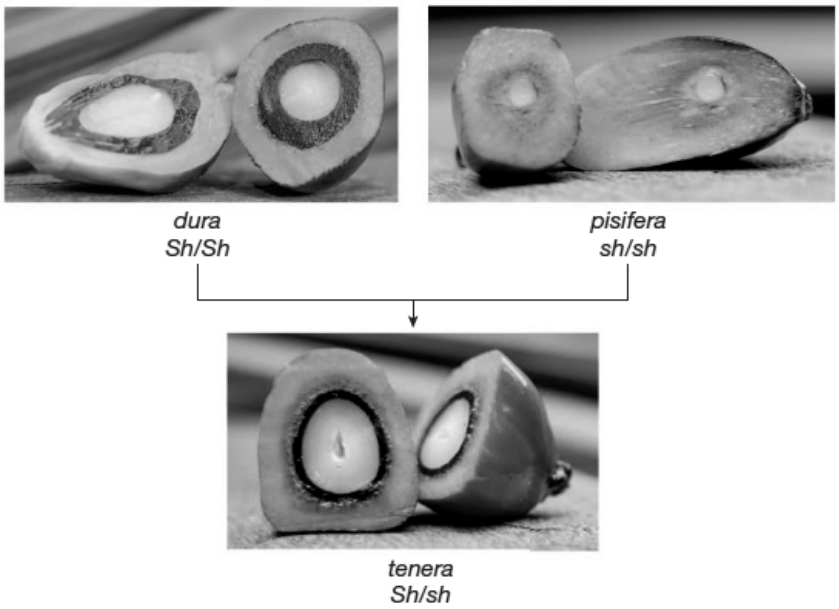
Many of the economic, social and environmental concerns surrounding the bioeconomy are present with oil palm. This puts the crop at the front line of issues around its sustainability. An incident in 2015 exemplifies the seriousness of the concerns. In August 2015, four large groups of Asian companies were excluded from the Norwegian sovereign wealth fund over instances of deforestation in Indonesia (Milne, 2015).

Singh et al. (2013b) published the oil palm genome sequence, which enables the discovery of genes for important traits, as well as alterations that restrict the use of clones in commercial plantings. The oil palm, largely undomesticated, is an ideal candidate for genomic-based tools to harness the potential of this remarkably productive crop. The authors claim that the dense representation of sequenced scaffolds on the genetic map will help identify genes responsible for important yield and quality traits.

The modern oil palm tree *Elaeis guineensis* has three fruit forms: *dura* (thick-shelled); *pisifera* (shell-less); and *tenera* (thin-shelled) (Figure 4.2). The *tenera* palm yields far more oil than *dura*, and is the basis for commercial palm oil production in all Southeast Asia. In 2013, a remarkable discovery was made. The *Shell* gene has proven extremely challenging to identify in oil palm, given the large genome, long generation times and difficulty of phenotyping in experimental populations. Singh et al. (2013a) identified the gene and determined its central role in controlling oil yield. Regulation of the *Shell* gene

will enable breeders to boost palm oil yields by nearly one-third. This is excellent news for the industry, the rainforest and its champions worldwide, and also for bioeconomy policy makers.

Figure 4.2. **Oil palm tree fruit forms**



Note: The *Shell* gene is responsible for the oil palm's three known shell forms: *dura* (thick); *pisifera* (shell-less); and *tenera* (thin), a hybrid of *dura* and *pisifera* palms. *Tenera* palms contain one mutant and one normal version, or allele, of *Shell,* an optimum combination that results in 30% more oil per land area than *dura* palms.

Source: Singh et al. (2013a), "Oil palm genome sequence reveals divergence of inter-fertile species in old and new worlds".

Seed producers can now use the genetic marker for the *Shell* gene to distinguish the three fruit forms in the nursery long before they are field-planted. Previously, it could take six years to identify whether an oil palm plantlet was a high-yielding palm. Even with selective breeding, 10-15% of plants are the low-yielding *dura* form due to uncontrollable wind and insect pollination, particularly in plantations without stringent quality control (Tarr, 2013).

Such accurate genotyping has a critical implication for a bioeconomy. Enhanced oil yields will optimise and ultimately reduce the acreage devoted to oil palm plantations. This provides an opportunity for conservation and restoration of dwindling rainforest reserves (Danielsen et al., 2009).

Decoupling agriculture from fossil fuels

Nitrogenous compounds in fertilisers are major contributors to waterway eutrophication and GHG emissions. The Haber-Bosch process for making fertilisers is energy-intensive, consuming 3-5% of the world's natural gas production and releasing large quantities of CO_2 to the atmosphere (Licht et al., 2014). By January 2013, the price of Brent crude oil per barrel rose from around USD 50 to about USD 110. Over the same period, prices for ammonia in Western Europe and the mid-western corn belt in the United States roughly tripled (Chen, 2013).

Several efforts are ongoing in a tantalising research area – creating crop plants that make their own fertiliser. A collaborative project between UK and US scientists aims to design and build a synthetic biological module that could work inside a cell. The project aims to re-engineer the cyanobacterial machinery to fix nitrogen using solar energy as a first step towards transferring the machinery into plants themselves. This has the potential to revolutionise agriculture, and significantly decouple it from the fossil fuels industry. Using synthetic biology, full nitrogen fixation in cereals may be about a decade away (Keasling, 2015). However, partial nitrogen fixation may be available before then (Stokstad, 2016).

Gene editing could usher in a paradigm shift in agricultural biotechnology

As of early 2015, the European Union had granted its member state governments greater power in deciding whether to plant GM crops (BBC News, 2013), which are highly restricted in Europe. The new directive may have split the EU policy landscape, with some states clearly opposed and others in favour (Rabesandratana, 2015). This has come at a time when precision crops are becoming easier to produce through advances in gene editing techniques such as CRISPR/Cas9. Such gene editing techniques are being hailed as low-cost and simple to perform. They are also applicable across all breeding programmes, from large-scale row crops to local and minor species (Von Essen, 2016).

A regulatory shift may bring the application of gene editing techniques to crop production under less scrutiny. Regulators often classify these crops as the product of "new breeding techniques" (NBTs) that are sometimes distinct from classical GM varieties (Nature, 2016). Some mutations edited into the genome already exist in wild plant relatives in nature. The argument then becomes whether the regulator should treat crops produced in this way differently (less stringently) from GM crops.[4] Both the United States and Europe are examining the implications.

More controversial still could be the use of gene editing in domesticated animals. Scientists in Korea and China have created experimental "double-muscled" pigs by editing a single gene, a change that is much less dramatic than those made in conventional, transgenic genetic modification (Cyranoski, 2015). The pigs reportedly provide many of the benefits of the double-muscled cow, such as the Belgian Blue. These include leaner meat and a higher yield of meat per animal – important targets for food security in a bioeconomy. Government agencies may view this more leniently than conventional forms of genetic modification; no "new" DNA has been inserted.

China may be the first to adopt this technology in animals, and this pig could be among the first genetically engineered animals to be approved for human consumption. However, the technique has also been proven to work experimentally in creating double-muscled cows and sheep (Proudfoot et al., 2015).

Policy implications

- A biotechnology revolution in food production has already begun. Production of virtually all animals and crops can benefit from genomics. This includes some critical economic considerations, such as feed efficiency and disease resistance that benefit food security now and into the future. But the benefits are also environmental, although this is even more in its infancy. This message is not well understood at the political level, and the benefits of biotechnology in food production are under-valued and under-reported.

- Governments could better see the advantages of genomics in agriculture, and could more efficiently steer research programmes, by sponsoring programmes that train farmers in genomics. The Irish Beef Data and Genomics Programme is a good example. Gathering relevant field data has been a past limitation, but providing incentives to farmers could help.
- Genomics speeds up breeding, making it more efficient without genetic modification. Campaigns that make this clear could remove public resistance.
- The costs of genomic studies have tumbled through the revolution in next-generation sequencing. Bringing genomics testing to the farms will increase the range of applications as these are clearer to farmers than to researchers. Education and information programmes throughout the agricultural production chain would demystify genomics in agriculture.
- Genetic modification and gene editing have many other applications to offer, but the level of public resistance is greater. However, the United States has cleared GM salmon for human consumption. Its performance in the market may influence consumers in positive or negative ways. Governments could promote the benefits of such GM foods after their safety is guaranteed.

Notes

1. Marker-assisted selection or marker-aided selection (MAS) is a process whereby a marker (morphological, biochemical or one based on DNA/RNA variation) is used for indirect selection of a genetic determinant or determinants of a trait of interest (e.g. productivity, disease resistance, abiotic stress tolerance and quality).
2. An SNP represents a difference in a single DNA building block, called a nucleotide: http://ghr.nlm.nih.gov/handbook/genomicresearch/snp.
3. Over 400 different fatty acids have been identified in seed oils although, remarkably, none have been found to contain the very long chain omega-3 fatty acids.
4. The common white button mushroom (*Agaricus bisporus*) has been modified to resist browning using CRISPR/Cas9, and can be cultivated and sold without further oversight in the United States. The USDA will not regulate a mushroom modified with the gene-editing tool CRISPR/Cas9. The decision means that the mushroom is the first CRISPR-edited organism to be approved by the US government (Waltz, 2016).

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Part II.

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