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Review Article

Challenges for genetic improvement of livestock and aquatic animals

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Abstract-This article reviews the challenges for genetic improvement of livestock and aquatic animals to produce sufficient qualities and quantities of food supplies for the increasing world population. Both sectors are threatened by various factors, and genetic improvement is a promising way to achieve the goals. For livestock genetic improvement, it is crucial to enhance contributions to small scale farmers, probably through on-farm genetic improvement programs, while minimizing the impact on extinction of local breeds. Genetic improvement can mitigate climate change by improving traits that indirectly result in less emissions of greenhouse gases (GHG) throughout the production period. It also provides adaptation measures by improving animals with adaptability (e.g., heat tolerance, disease resistance, etc.) traits. Genetic improvement for stress tolerance and other related traits would cope with issues on animal welfare while disease resistant traits would partially solve problems enhanced by globalization (e.g., trans-boundary animal translocation). While in the aquaculture sector, genetic improvement also has high potential to overcome the upcoming limitations and threats, particularly climate change (e.g., improving salt tolerance traits to cope with saline water intrusion, stress tolerance traits to withstand extreme environments, etc.), concern about animal welfare (e.g., improving stress tolerant traits), and globalization (e.g., improving disease resistant traits). However, due to a large number of species to work with and short history of development, there are more limitations to tackle on the aquaculture side. To attain a successful genetic improvement program, the studies on the following issues are at priori, characterization of gene pools, development of efficient breeding techniques, development of cost effective tagging techniques, and characterization of target traits for genetic improvement.

Keywords: Genetic improvement, food security, climate change, animal welfare

1. Introduction

World food security is jeopardized because of the enormous increases in food demand while the food production potential is declining. FAO forecasts that the world population will reach 9 billion in 2050, and thus will demand an increase in food production by 70% (FAO, 2009). Livestock and fisheries products comprise at least 50% of total agriculture products, for which the demands are apparently increased. This is not only to cope with the demand from the hungers but also the expanding population. The rapid expansion of urbanization and increasing per capita income have triggered people to change the type of food they consume to more animal protein (FAO, 2009).

There are many constraints towards increasing agricultural products. For instance, agricultural land is gradually diminishing due to various factors. Lambin and Meyfroidt, (2011) predicted that within the next 30 years urbanization will result in the loss of agriculture land by 1.6 – 3.3 million hectare (Mha)/year while 1-2.9 Mha/year will not be suitable for agriculture due to land degradation. Moreover, at present, as a result of diminishing resources of fossil-base fuels, there is a tendency that there will be strong competition for land between food crops and energy crops (Lambin and Meyfroidt, 2011).

A shortage of water supply is one major limitation for enhancement of agricultural products. Agriculture is the biggest sector (70%) utilizing world water resources (FAO, 2013a). It is estimated that about 1 m^3 of water is required to produce 1 kg of cereal grains, while production of 1 kg of beef needs about 13.5 m^3 water (Rijberman, 2006). While demand for water is increased, water available for agriculture and human consumption is dramatically decreased (Ayibotele, 1992). At present many areas of the world have faced water scarcity, but the situation will be worse in the future due to many reasons, for example, population growth, pollution, land reclamation, and reduced precipitation (FAO, 2009).

Lastly, global warming is another important factor that hampers enhancement of livestock and fisheries products, probably through increased temperature and changing amount of precipitation, which will both directly affect the animals and indirectly trigger expansion of diseases and parasites to new areas (De Silva and Soto, 2009).

To achieve the goal of producing enough food for the rapidly expanding world population within the limited resources, using genetic improved animals would be a promising strategy. Genetic improvement has been proven to be the most effective approach to increase the yield of

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livestock (see Hume *et al*., 2011). For example, from the 1960's to 2005, the number of pigs weaned/sow/year has increased by 50%, while the increment rates have been 30% for the number of eggs produced by a laying hen/day, 67% for kilograms of milk/cow/lactation, and the reduction of days until 2 kg of broiler by 60% (reduced from 100 to 40 days) (Hume *et al*., 2011). Although the genetic improvement programs for aquatic animals are relatively young compared to those of livestock (Gjerdrem, 2012), the genetically improved strains have tremendously enhanced world production of some aquatic species, e.g., Atlantic salmon, Nile tilapia, and Pacific white shrimp (Thodesen and Gjedrem, 2006; Gjedrem, 2012). For example, the achievement of the GIFT (Genetically Improved Farmed Tilapia) strain of Nile tilapia (*Oreochromis niloticus*) was accepted as a major factor for the expansion of world production (ADB, 2005; Ponzoni *et al*., 2010), e.g., from 970,756 MT in 2000 to 3,436,526 MT in 2013 (FAO, 2015). The Taura syndrome resistant strain of Pacific white shrimp (*Litopenaeus vannamei*) (Gjerdrem, 2012) has triggered an expansion of the culture area of this species around the world and the production has been increased and reached 3,314,447 MT in 2013 (FAO, 2015). Interspecific hybridization between Thai walking catfish (*Clarias macrocephalus*) and African sharp-tooth catfish (*C. gariepinus*) (Nukwan *et al*., 1990) has caused a rapid increase in Thailand's annual production by nine fold within 14 years (Na-Nakorn, 2013).

2. Challenges for genetic improvement of livestock

Despite the enormous past achievements, genetic improvement of livestock in the new era cannot focus on only enhancing production. Rather, the program must be designed to cope with the concerns on various issues, such as, enhancing contributions to small-households, sustainability of the local breeds, climate change, animal welfare, and globalization.

2.1 Enhancing contributions of the genetic improvement program to small-households: It has been shown that the genetic improvement programs in the past have benefited the intensive commercial farms but had less contribution to small-households (Rege *et al*., 2011). Although the intensive commercial system produces a majority of livestock products (55% pork, 68% eggs, 74% poultry and meat), the small household system of production involves a large number of smallholders and pastoralists. Thus, it supports livelihood and rural food security.

In general, the characteristic of livestock/poultry genetic improvement in the tropics is crossbreeding and upgrading of local breeds with improved breeds/lines/strains from the temperate region. For example, Holstein (Black and White cattle; *Bos taurus*) has been used to upgrade crossbreds or native cattle for the improvement of milk production (Tadesse and Dessie, 2003; Haile *et al*., 2009; Koonawootrittriron *et al*., 2009); Charolais (French creamy cattle; *Bos taurus*) has been used to cross with Brahman, crossbreds, or native cattle for the improvement of meat production (Long, 1980). These practices benefit the intensive commercial livestock production worldwide and have contributed to the rapid increment of the world production. However, the contribution to the small holders is less due to many reasons. For instance, farmers could not exploit benefits from genetic improvement programs to the maximum potential because a small number of animals prevents fair or unbiased comparison and selection for genetic improvement. Moreover, a lack of good genetic management has caused inbreeding and loss of genetic variation which eventually results in deterioration of the breeds (Oltenacu and Broom, 2010). In addition, education background or understanding (selection and mating) of the farmers could also cause uncontrolled genetic variation and then slow genetic progress e.g., a case of dairy cattle, Holsteinxother breeds multibreed dairy population in Central Thailand which showed almost zero genetic trend (Koonawootrittriron *et al*., 2009; Sarakul *et al*., 2011)

2.2 Minimizing the adverse impacts of livestock genetic improvement on extinction of local breeds:
Although local breeds may be perceived as having low economic value, they are an invaluable source of useful traits, for example, tolerance to harsh conditions, tolerance to parasitic and infectious diseases, drought, and poor quality feed. FAO predicted that at present there are 4,500 major breeds from at least 40 animal species having a contribution to livestock production. However, it was predicted that six breeds are dying out every month and 30 percent of the world's breeds are almost extinct (FAO, 2013b). The scientific evidence was revealed using molecular markers in the Vietnamese Black H'mong pig breed from Ha Giang province that comprised of various degrees of genetic admixture from the exotic breeds (Landrace and Yorkshire) and it was predicted that after 60 generations, 100% of Black private alleles will be lost (Berthouly-Salazar *et al*., 2012).

Despite the risk of losing the local breeds, the lesson learnt from genetic improvement of small ruminants in sub-Saharan regions suggested that the cross between local and exotic breeds is an effective way to improve production of livestock (e.g. goat improvement in Africa, Peacock, 2008; Peacock *et al*., 2011; Mohlatlole *et al*., 2015). However, the program should be operated on-farm rather than working solely in a breeding nucleus and that the program should be incorporated into the production system, under close supervision of the experts.

2.3 Coping with climate change: Livestock plays a role as a contributor to the green-house gases (GHG), while this sector is impacted by climate change. Genetic improvement is an effective tool for handling both problems. There are scientific evidences showing that the emission of greenhouse gases by livestock could be indirectly reduced by genetic improvement, e.g., improvements in growth rate and fertility in pigs and dairy cattle in the United Kingdom resulted in a 0.8% annual reduction in GHG emission while improving the feed conversion ratio in broilers and layers reduced the emission of GHG by 1.2 and 1.3 %, respectively (Jones *et al*., 2008); genetic gain in milk performance has considerably reduced the environmental impact of diary production in the USA (Capper *et al*., 2009).

On the opposite corner, it is well understood that livestock is impacted by climate change but it is hard to predict the effect. However, there is a trend that temperature is increasing, e.g. increase of 0.7°C in the past decade (IPCC, 2007), thus environmental adaptability (e.g., heat tolerance) traits will be one of the important desired traits. Projections suggest that further selection for breeds with effective thermoregulatory control will be needed. This calls for the inclusion of traits associated with environmental adaptability in breeding indices, and more consideration of Genotype-by-Environment interactions (GxE) to identify animals most adapted to specific conditions (Gebryohannes *et al*., 2015).

Climate change may result in the spreading of diseases and parasites due to the contact between domesticated and wild species that changes their distribution because of climate change. This may trigger the transmission of pathogens or parasites from one species to another. For examples, a case of lungworm that is a common parasite of Dall's sheep and has never been found in *Musk oxen* is currently observed in *Musk oxen* (Kutz *et al*., 2004). Moreover, climate change may expand the habitats for insects that spread diseases. For example, the bluetongue disease, which is an insect-borne disease infecting ruminants, has spread from Southern to Northern Europe. Scientists suggested that this may relate with the rising temperature that may enable the vector to spread to higher latitudes or the rising temperature may enable the virus to use other species of *Culicoides* as a vector (Carpenter *et al*., 2009).

The best adaptation to these problems would be through genetic improvement. Therefore, it is urgent to search for the desired traits, for example, traits that lead to heat tolerance and disease resistance, which potentially exist in local breeds. For example, several Latin American cattle breeds with a very short, sleek hair coat were observed to maintain lower rectal temperatures. This is an example of a useful genepool for genetic improvement for heat tolerance. At present, research in the major "slick hair" gene which is dominant in inheritance and located on Bovine Chromosome 20 is ongoing (Olson *et al*., 2003; Dikmen *et al*., 2008). However, genetic correlation between the desired traits and other economic traits should be taken into consideration, e.g., the desired heat tolerance has a negative correlation with milk yield and reproduction of cattle. Thus heat tolerant dairy cow may not be possible, whereas beef cattle may be improved for heat tolerance (Prayaga and Henshall, 2005).

2.4 Enhance animal welfare: Currently the issues on animal welfare are taken more seriously in livestock production. Animal welfare acts were issued in several countries to protect animals from inhumane treatments. While environments and management are improved to provide livestock with unstressed conditions throughout their lifespan, genetic improvement is also helpful in this regard.

In fact, genetic improvement can either compromise or enhance animal welfare. On the dark side, genetic improvement can have adverse effects that compromise animal welfare. Over selection for a single trait may result in adverse or unexpected effects on other traits. For example, the genetic selection for both rapid growth and high, lean meat yield may relate with the appearance of highly excitable and difficult to handle animals (Grandin, 1994). The increased incidence of the "weaver" condition in Holsteins is possibly related to increased selection for high milk production; while, broiler chickens have reduced cardiopulmonary capacity in relation to their muscle mass and cannot withstand much physical exertion (Broom, 1987; 1993a; Julian, 1993; Julian *et al*., 1986).

On the contrary, genetic improvement can promote animal welfare. For example, seven generations of selection in laying hens resulted in a strain that shows much less feather pecking and cannibalism than a control strain which increased aggressiveness and social dominance during adolescence, with no decrease in productivity. Therefore, this strain does not require beak trimming and hence will enjoy a higher level of welfare in cages (Muir and Craig, 1998).

In order to employ genetic improvement programs for this purpose, the traits under selection must be precisely identified. These include at least three possible broad categories to consider: behavior, physiology, and production traits.

2.5 Adaptation to globalization: In the past pathogens were mostly spread to new areas by the introduction of improved breeds and semen for artificial insemination. For example, emergence of porcine reproductive and respiratory syndrome (PRRS) (Thanawongnuwech *et al*.,2004a, b) and porcine circovirus–associated diseases (PCVAD) (Tantilertcharoen *et al*., 1999) in Asian countries. In addition, the movement of livestock can cause the emergence of new diseases or re-emergence of fully controlled diseases. For example, the epidemic of foot and mouth disease (FMD) in the United Kingdom in 2001 (Green *et al*., 2006) and the outbreak of FMD in South East Asia (Nuntawan Na Ayudhya *et al*., 2012), were caused by the movement of livestock. There is a concern that the uniting of different economic zones may enhance movement of livestock between countries and eventually may trigger the emergence or re-emergence of diseases, e.g., Wongsathapornchai *et al*. (2008); Cai (2012). Several measures have been established to control these diseases, and have cost huge amounts of money (e.g. US $ 820 million for global strategy against FMD, FAO, 2012). Genetic improvement, which shows potential to improve disease resistance of livestock (Stear *et al*., 2001), may be an additional measure to ease the problems.

3. Challenges for genetic improvement in aquaculture

The culture of aquatic animals, or aquaculture, is following livestock footsteps in that the availability of genetically improved strains becomes a prerequisite of success, as has been shown for species like Atlantic salmon, Nile tilapia, and Pacific white shrimp. Similar concerns have been raised for aquaculture, however with some diversification. Due to the different nature of aquatic species and livestock, and shorter history of genetic improvement of aquatic animals, more challenges will be faced by scientists who work on aquatic animals. There are many limitations towards genetic improvement of aquatic species, for example, lack of well characterized gene-pools, lack of efficient breeding (producing offspring) techniques in some species, lack of efficient tagging techniques, and lack of well characterized targeted traits.

3.1 Lack of well characterized gene-pools: Aquaculture is young when compare to livestock production and it covers a large number of species. Only a few species are domesticated, among which some species have been domesticated regardless of genetic principles. As such, the well characterized gene-pools are lacking. Genetic improvement always started with pooling of genetic variation from wild and farm stocks without knowing performances (e.g. genetic improvement programs for Pacific white shrimp, Argue *et al*., 2002; Rohu, *Labeo rohita* in India, Mahapatra *et al*., 2006; Atlantic salmon in Norway, Thodesen and Gjedrem, 2006) with some exceptions (e.g., the GIFT Nile tilapia, Eknath and Acosta, 1998, and common carp in Hungary, Bakos *et al*., 2006). Thus a chance of including populations with undesired traits is possible.

3.2 Lack of efficient breeding techniques: A lack of efficient breeding techniques prevented the species from benefiting from good genetic improvement. Breeding of aquatic animals requires diverse techniques from natural spawning to artificial breeding. The rearing of larvae and fry also requires knowledge, specific to each species in some cases. Due to the large number of species involved in aquaculture (FAO, 2015), it is understandable that certain species still do not have efficient breeding and rearing technologies. This can easily lead to unnoticed mis-management of broodstock. For example, despite the large number of brooders kept by farmers, only a few pairs contribute to the next generation due to limited success of breeding techniques, and thus it causes a loss of genetic variation and eventually results in inbreeding. Similarly, communal spawning practiced in some species, e.g. sea bream (Brown *et al*., 2005) and groupers (Wachirachaikarn *et al*., 2011), has led to a reduction in the effective population size.

3.3 Lack of efficient tagging techniques: A lack of efficient tagging techniques has caused difficulty in employing efficient genetic improvement methods. For example, to select based on family performance, single families must be separately reared, which requires unaffordable infrastructure in most cases. However, with the assistance of molecular markers and parentage assignment computer software, families can be communally reared and identification is performed at measurement (e.g. Norris *et al*., 2000; Sekino and Hara, 2007; Karaket *et al*., 2011; Lafarga-de la Cruz). This surely requires a high cost.

3.4 Lack of well characterized targeted traits: Genetic improvement of aquatic animals mostly focused on a few traits, such as growth and disease resistance, for which a majority of selection programs emphasized simple traits, such as growth rate, survival rates, or time to death after disease challenging (e.g. Na-Nakorn *et al*., 1994; Henryon *et al*., 2005; Mahapatra *et al*., 2008). In fact, there are many physiological traits that relate to growth, disease resistance, and other desired traits. These physiological traits may have different levels of heritabilities, and thus, would allow scientists to improve low heritability traits by selecting for the traits with high heritabilities, which positively correlate with the targeted traits.

4. Genetic improvement as a tool for adaptation to future threats

Aquaculture also faces threats emerging from similar factors as those faced by livestock, for instance, climate change, globalization, and animal welfare, etc. To utilize a genetic improvement approach to cope with those threats, suitable traits should be characterized and genetic parameters regarding those traits should be intensively studied.

4.1 Adaptation to climate change by genetic improvement in fish: The impacts of climate change to aquatic fauna are not conclusive. However, the impact may be similar to that of livestock to some degree, such as the increase in water temperature (Poff *et al*. 2002; De Silva and Soto, 2009) may expand culture areas for warm water species to cold climates and may consequently enhance the spreading of disease and parasites to the cold water areas. In particular, due to a rising of sea level, invasion of saline water to inland water is predicted (Rahel and Olden, 2008; De Silva and Soto, 2009). Genetic improvement can help in this regards by improving strains to increased salinity tolerance. For example, a salt tolerant strain of tilapia was developed by interspecific hybridization, e.g., hybridization between the genetically improved strain of Nile tilapia, *O. niloticus* with a salt-tolerant species, *O. mossambicus* (Villegas 1990; Garcia-Ulloa *et al*., 2001) or *O. spilurus* (Ridha, 2012).

Climate change potentially enhances eutrophication in tropical inland waters and also triggers extreme climate conditions (De Silva and Soto, 2009). As such, genetic improvement for stress tolerance may lead to fish strains that can withstand fluctuating/extreme culture conditions. The potential of this purpose is discussed in the later section on “Genetic improvement to enhance animal welfare”.

4.2 Genetic improvement to cope with transboundary translocation of aquatic animals: Globalization obviously enhances intensive translocation of aquatic animals for commercial culture. Although this practice benefits aquaculture industries, it also possesses severe threats to local biodiversity and also on the aquaculture of native species through disease transfer. For example, the outbreak of herpes virus in fancy carp (*Cyprinus carpio*) and other native cyprinid fishes was caused by the introduction of fancy carp from Japan (Chansu and Tangtrongphairot, 2005); the outbreak of Taura syndrome virus in tiger prawn in 2004 was a result of the introduction of Pacific white shrimp (*L. vannamei*) which is native to South America (Limsuwan and Chucherd, 2007); and the outbreak of Noda and Extrasmall viruses in giant freshwater prawn (*Macrobrachium rosenbergii*) in Thailand was caused by the introduction of conspecific exotic stocks for genetic improvement (Chucherd *et al*., 2007). Measures have been established to prevent these unwanted circumstances, however, other approaches should also be considered. For example, genetic improvement has high potential to increase resistance to diseases as indicated by moderate to high heritability (Ødegård *et al*., 2011). However, more parameters that closely relate to resistance must be identified and employed in the selection program, e.g., immune related traits. In addition, selection based on molecular genetic information is a new approach that can enhance the efficiency of the selection program (Ødegård *et al*., 2011).

4.3 Genetic improvement to enhance animal welfare: Although the issue on animal welfare is not yet strongly addressed in aquatic animals, in the near future this issue will surely affect aquaculture, especially the species involved in international trade. Actually the traits related to welfare also affect production, for example, stress response. Stress in aquaculture occurs from transportation, handling, harvesting, water quality change, crowding, and diseases, etc. Even though there was limited information on selection potential of physiological traits, there was a concrete evidence that supported the genetic improvement potential of these traits, e.g., significant heritability of primary (cortisol) and secondary (glucose, osmolality, and haematocrit) stress responses (mean heritability, h^2= 0.60±0.20 for plasma cortisol; 0.61±0.20 for plasma glucose) of brook charr, *Salvelinus fontinalis,* suggesting strong potential for genetic improvement in the stress response to transport (Crespel *et al*., 2011).

5. Conclusions and recommendation

While the demand for animal protein is dramatically increasing, livestock and aquaculture sectors are facing several limitations and threats. One promising adaptation and mitigation measure is genetic improvement. Despite the great contribution from livestock genetic improvement programs, their adverse impacts, e.g. less contribution to small scale farmers and enhancement of local breed extinction, etc., have been recognized and become challenges for scientists in this field. The additional challenges are to efficiently employ genetic improvement to cope with the problems of animal welfare, emissions of GHG, and adaptation to adverse impacts of globalization. While in the aquaculture sector, genetic improvement was proven to enhance global production of some aquatic species. It also has high potential to overcome the upcoming limitations and threats, particularly climate change, concern for animal welfare, and globalization. However, due to the large number of species to work with and short history of development, there are more limitations to tackle on the aquaculture side. To attain a successful genetic improvement program, the studies on the following issues are at priori, characterization of gene pools, development of efficient breeding techniques, development of cost effective tagging techniques, and characterization of target traits for genetic improvement.

It is quite clear that the scientists who have been working on livestock and aquatic animal genetic improvement are challenged with similar problems. Thus, they should combine their efforts and exchange experiences so that genetic improvement of aquatic animals, which has a much shorter history, can be progressed without repeating the mistakes from livestock. At the same time, assistance from people of different areas of expertise, especially in the field of physiology and behavioral science, is crucially needed to enhance the precise identification of target traits and data collection for genetic improvement programs.

References

ADB. 2005. An Impact Evaluation of the Development of Genetically Improved Farmed Tilapia and Their Dissemination in Selected Countries. The Asian Development Bank, Manila, Philippines, pp. 137.

Argue, B. J., Arce, S. M., Lotz, J. M. and Moss, S. M. 2002. Selective breeding of Pacific white shrimp (*Litopenaeus vannamei*) for growth and resistance to Taura Syndrome Virus. Aquaculture 204, 447-460.

Ayibotele, N. B. 1992. The World's Water. Keynote paper, International Conference on Water and the Environment, Dublin, Ireland, 26-31 January 1992, pp. 26.

Bakos, J., Varadi, L., Gorda, S. and Jeney, Z. 2006. Lessons from the breeding program on common carp in Hungary. In: Ponzoni, R.W., Acosta, B.O. and Ponniah A.G. (Eds.), Development of Aquatic Animal Genetic Improvement and Dissemination Programs: Current Status and Action Plans, WorldFish Center Conference Proceedings 73, pp. 27-33.

Berthouly-Salazar, C., The´venon, S., Van, T. N., Nguyen, B.T., Pham, L. D., Chi, C.V. and Maillard, J. 2012. Uncontrolled admixture and loss of genetic diversity in a local Vietnamese pig breed. Ecology and Evolution 2(5), 962–975. doi: 10.1002/ece3.229

Broom, D. M. 1987. Applications of neurobiological studies to farm animal welfare. Current Topics in Veterinary Medicine and Animal Science 42, 101-110.

Brown, R. C., Woolliams, J. A. and McAndrew, B. J. 2005. Factors influencing effective population size in commercial populations of gilthead seabream, *Sparus auratus*. Aquaculture 247, 219-225.

Cai, C. 2012.The risk of foot and mouth disease entering China through the movement of animals from Upper Mekong region countries. Ph.D. thesis, Murdoch University. Available on web http://researchre pository.murdoch.edu.au/13598/

Capper, J. L., Cady, R. A. and Bauman, D. E. 2009. The environmental impact of dairy production: 1944 compared with 2007. Journal of Animal Science 87, 2160-2167.

Carpenter, S, Wilson, A. and Mellor, P. S. 2009. Culicoides and the emergence of bluetongue virus in northern Europe. Trends in Microbiology 17(4), 172-178.

Chansu, N. and Tangtrongphairot. C. 2005. Survey Koi Herpes Virus (KHV) disease of fancy carp (*Cyprinus carpio* Linn.) in Bangkok and perimeter in March - June 2005. Thai Veterinary Medical Association 56 (3), 13-21.

Chucherd, N., Limsuwan, C., Sriwongpuk, S. and Flegel, T.W. 2007. Study of *Macrobrachium rosenbergii* Nodavirus (MrNV) and Extrasmall virus (XSV) infection in intensive farm-reared giant freshwater prawn (*Macrobrachium rosenbergii* de Man) in Thailand. Journal of The National Research Council of Thailand (Sci) 39(1), 65-81.

Crespel, A., Bernatchez, L. and Audet, C. 2011. Quantitative genetic analysis of the physiological stress response in three strains of brook charr *Salvelinus fontinalis* and their hybrids. Journal of Fish Biology 79, 2019–2033.

De Silva, S. S. and Soto, D. 2009. Climate change and aquaculture: potential impacts, adaptation and mitigation. In: Cochrane, K., De Young, C., Soto, D. and Bahri, T. (Eds.), Climate change implications for fisheries and aquaculture: overview of current scientific knowledge. FAO Fisheries and Aquaculture Technical Paper. No. 530.Rome, FAO, pp. 151-212.

Dikmen, S., Alava, E., Pontes, E., Fear, J. M., Dikmen, B. Y., Olson, T.A. and Hansen, P. J. 2008. Differences in thermoregulatory ability between slick-haired and wild-type lactating Holstein cows in response to acute heat stress. Journal of Dairy Science 91(9), 3395-3402.

Eknath, A. E. and Acosta, B. O. 1998. Genetic Improvement of Farmed Tilapias (GIFT) Project Final Report, March 1998 to December 1997. ICLARM, Makati City, Philippines, pp. 75.

FAO. 2009. The State of Food and Agriculture. Electronic Publishing Policy and Support Branch, Food and Agricultural Organization of the United Nation, Rome. pp. 166.

FAO. 2012. The Global Foot and Mouth Disease Control Strategy. Food and Agricultural Organization of the United Nation, Rome, pp. 26. (http://www.fao.org/docrep/015/an390e/an390e.pdf)

FAO. 2013a. AQUASTAT. http://www.fao.org/nr/water/aquastat/water_use/index.stm, downloaded on November 16, 2013.

FAO. 2013b. Loss of biodiversity in livestock (animal biodiversity). Livestock and Environment Toolbox. Available at http://www.fao.org/ag/againfo/programmes/en/lead/toolbox/Indust/LossAgbi.htm, downloaded on November 25, 2013.

FAO. 2015. FishStatJ. http://www.fao.org/fishery/statistics/software/fishstatj/en#downlApp. Downloaded on September 6, 2015.

Garcia-Ulloa, M., Villa, R. L. and Martinez, T. M. 2001. Growth and feed utilization of the tilapia hybrid *Oreochromis mossambicus* x *O. niloticus* cultured at different salinities under controlled laboratory conditions. Journal of the World Aquaculture Society 32, 117-121.

Gebreyohannes, G., Koonawootrittriron, S., Elzo, M.A. and Suwanasopee, T. 2015. Genotype by environment interaction effect on lactation pattern and milk production traits in an Ethiopian dairy cattle population. Kasetsart Journal (Natural Science) 48, 38-51.

Gjedrem, T. 2012. Genetic improvement for the development of efficient global aquaculture: A personal opinion review. Aquaculture 344, 12–22.

Grandin, T. 1994. Solving livestock handling problems. Journal of Veterinary Medicine 89, 989-998

Green, D. M., Kiss, I. Z. and Kao, R. R. 2006. Modelling the initial spread of foot-and-mouth disease through animal movements. Proceedings of the Royal Society B: BiologicalSciences 7, 273(1602), 2729-35.

Haile, A., Joshi, B. K., Ayalew, W., Tegegne, A., Singh, A. 2009. Genetic evaluation of Ethiopian Boran cattle and their crosses with Holstein Friesian in central Ethiopia: milk production traits. Animal 3(4), 486-493. doi: 10.1017/S1751731108003868.

Henryon, M., Berg, P., Olesen, N. J., Kjaer, T.E., Slierendrecht, W. J., Jokumsen, A. and Lund, I. 2005. Selective breeding provides an approach to increase resistance of rainbow trout (*Onchorhynchus mykiss*) to the diseases, enteric red mouth disease, rainbow trout fry syndrome, and viral haemorrhagic septicaemia. Aquaculture 250, 621-636.

Hume, D. A., Whitelaw, C. B. A. and Archibald, A. L. 2011. Foresight project on global food and farming futures, The future of animal production: improving productivity and sustainability. The Journal of Agricultural Science 149, (Suppl. 1), 1-8 Doi:10.1017/S0021859610001188

IPCC (Intergovernmental Panel on Climate Change). 2007. Climate change 2007: the physical science basis. In: Solomon, S. Qin, D., Manning, M., Chen, Z., Marquis, M., Averyt, K. B., Tignor M. and Miller, H. L. (Eds.), Contribution of Working Group I to the Fourth Assessment Report of the Intergovernmental Panel on Climate Change. Cambridge, UK, Cambridge University Press, pp. 103.

Jones, H. E., Warkup, C. C.,Williams, A. and Audsley, E. 2008. The effect of genetic improvement on emissions from livestock systems. (Abstract) Proc. 59th Annual Meeting of the European Association for Animal Production Vilnius, Lithuania, pp. 28.

Julian, R. J. 1993. Ascites in poultry. Avian Pathology 22, 419-454.

Julian, R. J., Friars, G.W., French, H. and McQuinton, M. 1986. The relationship of right ventricular hypertrophy, right ventricular failure and ascites to weight gain in broiler and rooster chickens. Avian Diseases 31(1), 130-135.

Karaket, T., Poompuang, S., Na-Nakorn, U., Kamonrat, W., Hallerman, E. M. 2011. DNA microsatellite-based evaluation of early growth performance among strains of freshwater prawn *Macrobrachium rosenbergii* de Man. Aquaculture 311, 115-122.

Koonawootrittriron, S., Elzo, M. A. and Thongprapi, T. 2009. Genetic trends in a Holstein×other breeds multibreed dairy population in Central Thailand. Livestock Science 122 (2), 186-192.

Kutz, S., Garde, E., Veitch, A., Nagy, J., Ghandi, F. and Polley, L. 2004. Muskox lungworm (*Umingmak-*

strongylus pallikuukensis) does not establish in experimentally exposed thinhorn sheep (*Ovis dalli*). Journal of Wildlife Diseases 40(2), 197–204.

Lafarga-de la Cruz, F., Espinoza, A. A. and Gallardo-Escárate, C. 2013. Parentage assignment in hybrid abalones (*Haliotis rufescens* × *Haliotis discus hannai*) based on microsatellite DNA markers. Aquaculture Research 46, 216-225. DOI:10.1111/are.12169.

Lambin, E. F. and Meyfroidt, P. 2011. Global land use change, economic globalization, and the looming land scarcity. PNAS 108 (9), 3466-3472. www.pnas.org/cgi/doi/10.1073/pnas.1100480108

Limsuwan, C. and Chuchird, N. 2007. Taura syndrome virus disease in farm-reared *Penaeus monodon* in Thailand. Kasetsart Journal(Natural Science) 41, 319-323.

Long, C. R. 1980. Crossbreeding for beef production: Experimental results. Journal of Animal Science 51(5) , 1197-1223.

Mahapatra, K. D., Jana, R. K., Gjerde, B. and Sarangi, N. 2006. Lessons from the breeding program of rohu. Pp. 34-40, In: Ponzoni, R. W., Acosta, B. O. and Ponniah A. G. (Eds.), Development of Aquatic Animal Genetic Improvement and Dissemination Programs: Current Status and Action Plans, WorldFish Center Conference Proceedings 73, pp. 34-40.

Mahapatra, K., Gjerde, B., Sahoo, P. K., Saha, J.N., Barat, A., Sahoo, M., Mohanty, B. R., Ødegárd, J., Rye, M. and Salte, R. 2008. Genetic variations in survival of rohu carp (*Labeo rohita*, Hamilton) after *Aeromonas hydrophila* infection in challenge tests. Aquaculture 279, 29-34.

Mohlatlole, R. P., Dzomba, E. F. and Muchadey, F. C. 2015. Addressing production challenges in goat production systems of South Africa: The genomics approach. Small Ruminant Research 131, 43–49, http://dx.doi.org/10.1016/j.smallrumres. 2015.08.003

Muir, W. M. and Craig, J. V. 1998. Improving animal well-being through genetic selection**.** Poultry Science 77, 1781-1788.

Na-Nakorn, U., Chantsawang, S., Tarnchalanukit, W. 1994. Response to mass selection for resistance to *Aeromonas hydrophila* in *Clarias macrocephalus*. Journal of Applied Aquaculture 4(4), 65-74.

Na-Nakorn, U. 2013. Interspecific Hybrid Catfish in Thailand. In: Ruane, J., Dargie, J. D., Mba, C., Boettcher, P., Makkar, H. P. S., Bartley, D. M. and Sonnino, A. (Eds.), Biotechnologies at Work for Smallholders: Case Studies from Developing Countries in Crops, Livestock and Fish: FAO, Rome, pp. 149-155.

Norris, A. T., Bradley, D. G. and Cunningham, E. P. 2000. Parentage and relatedness determination in farmed Atlantic salmon (*Salmo salar*) using microsatellite markers. Aquaculture 182, 73–83.

Nukwan, S., Tangtrongpiros, M., Lawanyawut, K. and Veerasidth, P. 1990. Cross breeding between *Clarias macrocephalus* and *Clarias gariepinus*. In: Proceedings of the 28th Kasetsart University Conference, Fisheries Section, 29–31 January 1990, Bangkok, pp. 553–567.

Nuntawan Na Ayudhya, S., Assavacheep, P., Thanawongnuwech, R. 2012. One world – one health: the threat of emerging swine diseases. An Asian perspective. Transboundary and Emerging Diseases 59 (Suppl. 1), 9–17. doi:10.1111/j.1865-1682.2011.01309.

Ødegård, J., Baranski, M., Gjerde, B. and Gjedrem, T. 2011. Methodology for genetic evaluation of disease resistance in aquaculture species: challenges and future prospects. Aquaculture Research 42, 103-114.

Olson, T. A., Lucena, C., Chase Jr., C. C. and Hammond, A. C. 2003. Evidence of a major gene influencing hair length and heat tolerance in *Bos taurus* cattle. Journal of Animal Science 81 (1), 80-90.

Oltenacu, P. A. and Broom, D. M. 2010. The impact of genetic selection for increased milk yield on the welfare of dairy cows. Animal Welfare 19, 39-49.

Peacock, C. 2008. Dairy goat development in East Africa: A replicable model for smallholders? Small Ruminant Research 77, 225-238

Peacock, C., Ahuya, C. O., Ojango, J. M. K. and Okeyo, A. M. 2011. Practical crossbreeding for improved livelihoods in developing countries: The FARM Africa goat project. Livestock Science 136, 38-44.

Poff, N. L., Brinson, M. M. and Day Jr., J. W. 2002. Aquatic ecosystems & global climate change: potential impacts on inland freshwater and coastal wetland ecosystems in the United States. Pew Center on Global Climate Change, Arlington, Virginia, pp. 45.

Ponzoni, R. W., Khaw, H. L. and Yee, H.Y., 2010. GIFT: The Story since Leaving ICLARM (now known as TheWorldFish Center): Socioeconomic, Access and Benefit Sharing and Dissemination Aspects. FNI Report 14/2010. TheWorldFish Center, Penang, Malaysia, pp. 8.

Prayaga, K. C. and Henshall, J. M. 2005. Adaptability in tropical beef cattle: Genetic parameters of growth, adaptive and temperament traits in a crossbred population. Australian Journal of Experimental Agriculture 45 (7-8), 971-983.

Rahel, F. J. and Olden, J. D. 2008. Assessing the effects of climate change on aquatic invasive species. Conservation Biology 22(3), 521–533**.**

Rege, J. E. O., Marshall, K., Notenbaert, A., Ojango, J. M. K. and Okeyo, A. M. 2011. Pro-poor animal improvement and breeding-What can science do? Livestock Science136, 15-28.

Ridha, M. T. 2012. Preliminary observations on growth and survival of *Oreochromis spilurus* x GIFT *Oreochromis niloticus* F1 reciprocal hybrids in fresh and seawater. Aquaculture Research 45(3), 528-536.

Rijberman, F. R. 2006. Water scarcity: Fact or fiction? Agricultural Water Management 80, 5-12.

Sarakul, M., Koonawootrittriron, S., Elzo M. A. and Suwanasopee, T. 2011. Factors influencing genetic change for milk yield within farms in Central

Thailand. Asian- Australasian Journal of Animal Sciences 24, 1031-1040.

Sekino, M. and Hara, M. 2007. Individual assignment tests proved genetic boundaries in a species complex of Pacific abalone (genus *Haliotis*). Conservation Genetics 8, 823–841.

Stear, M. J., Bishop, S. C., Mallard, B. A. and Raadsma, H. 2001. The sustainability, feasibility and desirability of breeding livestock for disease resistance. Research in Veterinary Science 71 (1), 1-7. (http://www.sciencedirect.com/science/article/pii/S0034528801904965)

Tadesse, M. and Dessie, T. 2003. Milk production performance of Zebu, Holstein Friesian and their crosses in Ethiopia. Livestock Research for Rural Development 15 (3), 28-37.

Tantilertcharoen, R., Kiatipattanasakul, W. and Thanawongnuwech, R. 1999. A report of circovirus infection in pigs in Thailand. Thai Journal of Veterinary Medicine 29, 73-83.

Thanawongnuwech, R., Amonsin, A. Tatsanakit, A. and Damrongwatanapokin, S. 2004a. Genetics and geographical variation of porcine reproductive and respiratory syndrome virus (PRRSV) in Thailand. Veterinary Microbiology101, 9-21.

Thanawongnuwech, R., Thacker, B., Halbur, P., Thacker, E. L. 2004b. Increased production of proinflammatory cytokines following infection with porcine reproductive and respiratory syndrome virus and *Mycoplasma hyopneumoniae*. Clinical and Diagnostic Laboratory Immunology 11, 901-908.

Thodesen, J. and Gjedrem, T. 2006. Breeding programs on Atlantic Salmon in Norway-Lessons learned. In Ponzoni, R.W., Acosta, B.O. and Ponniah A.G. (Eds.), Development of Aquatic Animal Genetic Improvement and Dissemination Programs: Current Status and Action Plans, WorldFish Center Conference Proceedings 73, pp. 22-26.

Villegas, C. T. 1990. Growth and survival of *Oreochromis niloticus*, *O. mossambicus* and their F1 hybrids at various salinities. In Hirano, R. and Hanyu, I. (Eds.), Proceedings of the Second Asian Fisheries Forum. Asian Fisheries Society, Manila, Philippines, pp. 507–510.

Wachirachaikarn, A., Prakoon, W., Nguyen, T. T. T., Prompakdee, W. and Na-Nakorn, U. 2011. Loss of genetic variation of *Phalacronotus bleekeri* (Günther, 1864) in the hatchery stocks revealed by newly developed microsatellites. Aquaculture 321, 298-302.

Wongsathapornchai, K., Salman, M. D., Edwards, J. R., Morley, P.S., Keefe, T. J., Van Campen, H., Weber, S. and Premashthira, S. 2008. Use of epidemiologic risk modeling to evaluate control of foot-and-mouth disease in southern Thailand. American Journal of Veterinary Research 69(2), 240-251. doi: 10.2460/ajvr.69.2.240.