Review

Agricultural genomics and sustainable development: perspectives and prospects for Africa

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The genomes of various organisms have now been fully sequenced, including human and representative microbial, insect, animal and plant genomes. The research challenge in the post-genome era is to establish how genes and proteins function to bring about changes in phenotype. Some of these phenotypes, and products obtainable through modern biotechnology, are of crucial importance within the context of sustainable development of African economies. The greatest ultimate impact will be in agricultural genomics, especially for marker assisted selection and breeding programs in crop and animal agriculture, development of animal disease diagnostics and vaccines, crop genetic engineering to overcome abiotic and biotic stresses and for improvement of the nutritional quality of major food staples. It is imperative that African countries become key players in the "gene revolution" since the cost of leaving them behind may be higher than the cost of empowering them to become players in mastering and benefiting from biotechnology. This paper highlights the potential impact of the latest advances in modern biotechnology, including genomics and bioinformatics, on sustainable development, in line with the goals of the New Partnership for Africa's Development (NEPAD). These include acceleration of economic growth, eradication of widespread and severe poverty and efforts to halt the marginalization of Africa in the globalization process.

Key words: Genomics, modern biotechnology, agriculture, sustainable development, Africa.

INTRODUCTION

It has been noted by many experts that African countries, which lost out on the "Green Revolution", may yet again lose out on the current "gene or biotechnology revolution" unless these countries somehow manage to keep up with advances in biotechnology (Devries and Tonniessen, 2001; Machuka, 2001a; Wambugu, 1999). According to the United Nations (UN) Report of the Secretary General released in May 2003, "the cost of leaving some countries behind may be higher than the cost of empowering them to become players in mastering and benefiting from biotechnology". The purpose of this paper is to highlight the potential impact of the latest advances in modern biotechnology, particularly genomics, on sustainable development in Africa. The term sustainable development is used in a broad sense to include poverty alleviation, food security, enhanced health and environmental care systems, promotion of industrialization and economic productivity. Emphasis is placed on the applications of recent advances, rather than details of the underlying science itself, in order to portray the potential benefits and concerns associated with current practices in agricultural biotechnology. An attempt is made to discuss the issues within the context of global development goals, current biotechnology status, technology transfer and opportunities for biotechnology (technology) development in Africa. This is in tune with goals of the New Partnership for Africa's Development (NEPAD) which aims to promote and

accelerate growth and sustainable development, to eradicate widespread and severe poverty and to halt the marginalization of Africa in the globalization process.

THE STIGMA OF POVERTY, HUNGER, MALNUTRITION, LAND DEGRADATION AND RISING POPULATION GROWTH

According to the World Bank, approximately 1.2 billion people globally are absolutely poor, living on less than US$1 per day. Nearly twice this number live on less than US$2 per day. Environmental degradation, hunger, malnutrition, mass starvation, disease (especially HIV/AIDS) and death are phenomena regularly experienced by millions of people in Africa. Estimates released by the Food and Agriculture Organization (FAO) of the United Nations in November 2003 state that there are 842 million poor and chronically undernourished people worldwide. The majority of these people barely survive on less than a dollar a day. Out of the 650 million Africans, 250 million are chronically undernourished, over 40 million children are severely underweight, 50 million suffer from vitamin A deficiency, while 65% of women of child bearing age are anemic. About 90% of Africa's poor are rural, resource-poor farmers, their families, and the landless poor who depend on agriculture for their livelihoods. The rest are mostly urban, jobless slum dwellers. Women produce 70 to 80% of the food in Africa compared with 65% in Asia and 45 % in Latin America and the Caribbean. Between 1970s and 1990s, per capita food production in Africa declined at a rate of 2% per year (Pinstrup-Anderson and Garret, 1996). Despite this trend, population growth continues at a rate of 2.8% annually, against declining economic growth and reduced investments in agriculture (Conway and Toennienssen, 1999). The natural resource base of suitable land, water, forests and biodiversity which largely determines the potential of agriculture, are under severe threat. It is estimated that 80% of the land in Africa is threatened by degradation, while 2 million hectares of forest are lost annually (Scherr, 1999). Water and wind erosion, loss of soil nutrients, overgrazing, salinization, acidification, pollution, compaction and waterlogging, are some of the factors that lead to environmental degradation, especially land degradation and deforestation. The figures and trends outlined above are truly worrying. And yet this miserable scenario has been the subject of much research, with the aim of getting Africa out of its quagmire of poverty, environmental degradation and a host of other problems, many of which are largely precipitated by socio-political causes that are beyond the scope of this discussion (Haddad et al., 1995; Pinstrup-Anderson et al., 1995). In order to obtain solutions to these problems, and to understand how biotechnological tools may be applied, it is useful to track past events or ¨revolutions¨ that appear to have acted as vital catalysts in helping

other countries elsewhere to achieve food self-sufficiency, especially the Green Revolution in Asia.

ENERGY AND WATER REVOLUTIONS SPAWNED THE GREEN REVOLUTION

Over 200 years ago, during the early decades of the industrial revolution, the English economist (Reverend) Robert Thomas Malthus suggested that human population growth would outstrip food production since population increases faster than the means of subsistence. Although this may be partly true, the discovery of energy sources, notably coal and natural gas, spawned an "energy revolution" that impacted positively on the means of agricultural production in a way that enabled food production to match or even potentially outstrip population upsurges in Europe and North America (Manning, 2000). The ability to manufacture nitrogen and other fertilizers ("fertilizer revolution"), and to mechanize agriculture, especially through use of irrigation ("water or irrigation revolution") has allowed countries such as Israel to become self sufficient in food production in otherwise hostile environments (Bump and Baanante, 1996). Whereas about 40% of the global population did not have adequate food supplies in the 1960s, approximately 20% of the current global population does not have enough food in 2003 (IFPRI, 2003). However, the number of people lacking adequate food remains the same, and this number is largely composed of the poor in sub-Saharan Africa (SSA, Dalgado, 1997).

The term Green Revolution refers mainly to the large increases in grain production achieved by certain underdeveloped areas, particularly India, Pakistan and the Philippines from the late 1960s (Manning, 2000). This fete was accomplished through the use of high yielding hybrids, chemical fertilizers, new crop management strategies and harvesting methods. Although questions have been raised about the environmental "sustainability" (e.g. soil integrity) of Green Revolution practices, all are agreed that countries that successfully underwent this Revolution changed from being net food importers to net exporters of grain to date (Conway and Toenniessen, 1999). But can the success of the Green Revolution be repeated on a global scale, in many diverse agroecosystems, and in an equitable, sustainable and environmentally friendly manner? If such a "Doubly Green Revolution" is possible, how shall we ensure that SSA, which needs it most, does not miss out? And for the sake of this discussion, what role will biotechnology and genomics play? From the very outset, one thing seems certain - that the gene revolution is only a part, albeit invaluable, of a holistic, integrated, multidisciplinary approach needed to address the constraints highlighted above (Dalgado, 1997; Machuka, 2001b; Serageldin, 1999). In the following sections, I briefly summarize the

salient scientific research advances and trends in plant and animal agricultural genomics and the implications of these advances for sustainable development in SSA. Tissue culture-related technologies that do not involve direct DNA manipulations, such as micropropagation, haploidy and embryo culture, are not covered.

ELEMENTS OF THE AGRICULTURAL GENE(-OMICS) REVOLUTION

The genome of any organism represents the sum of all the genes in that organism (Vukmirovic and Tilghman, 2000). Structural genomics is concerned with the elucidation of the nucleotide base composition of gene sequences, whereas functional genomics focuses on how genes are regulated and expressed, at the level of DNA, RNA (trancriptome) and protein (proteome) (Eisenberg et al., 2000; Lockhart and Winzeler, 2000). The aim of genomics is to discover genes that code for Mendelian and complex traits, and to utilize the knowledge gained from such studies to address problems in fundamental (e.g. biochemical and developmental biology) and applied biology (e.g. agricultural, industrial, medical and environmental applications) and product development. However, there is no fine line between basic and applied genomics and proteomics research since most basic research often has direct bearing on applied sciences. For example, basic biochemical studies of oil, protein, starch, cellulose synthesis and secondary metabolism, or research in developmental biology of fruit ripening, fertility, seed development and growth characteristics have obvious applications in crop agriculture and forestry at the farm, field and post-harvest storage levels (Somerville and Somerville, 1999).

Large-scale genome sequencing projects

Large scale DNA sequencing can be performed on genomic DNA or on complementary DNA (cDNA). Using these strategies, the genomes of many organisms have now been either fully or partially (as expressed sequence tags or ESTs) sequenced and resultant sequences deposited in nucleotide or protein data banks, many of which are freely accessible on the internet. One notable achievement was the landmark completion of the human genome sequence in 2001, in addition to several representative microbial, insect, animal and plant genomes (Adams, 2000; The Arabidopsis Genome Initiative, 2000). The completed human genome is expected to facilitate identification of all genes that contribute to human disease. In the drug industry, many pharmaceutical companies are valued at hundreds of billions of dollars, much of which depend on their ability to exploit genomic information in developing blockbuster drugs (pharmacogenomics). In animal agricultural genomics, advances in the use of cloned and transgenic animals in research programs will have a profound impact in many areas such as development of new diagnostics and vaccines and enhanced growth characteristics and reproductive performance. Another key area will be understanding the genomes of microorganisms that are important to the productivity and sustainability of agriculture and forestry, and to the safety and quality of the world's food supply chain.

As will be discussed later, high *volumes* of genome data is accompanied by an even much greater increase in *complexity* of such genome data, thus creating the need to appreciate both the scale of the challenge of large genome analysis and the limitations of current gene prediction methods and understanding. Another feature of large-scale sequencing projects is that they are very expensive and often require forging partnerships from the private and public sector, and may involve different countries, as is the case for the Human and Arabidopsis Genome Projects. So far, African countries have been left behind in these initiatives, except in a few cases involving International Centres such as the International Rice Research Institute in the Philippines and the International Livestock Research Institute in Kenya, which participate in the rice and trypanosome sequencing programs, respectively, on behalf of developing countries. The reason for this scenario is that well funded structural and functional genomics programs in the North largely focus on organisms and applications that bring economic returns on public and private sector investment for those countries.

Genome mapping and molecular marker technologies

Humans have genetically modified plants and animals for as long as they have cultivated crops or kept livestock. This has heppenned either inadvertently or through structured breeding programmes. Traditional plant and animal breeding uses phenotype (e.g. crop yield, or milk production) to predict and select genotype, i.e, specific crop variety or animal breed. The phenotype is the product of distinct genotypic and environmental effects. Phenotypic selection based on traits that are conditioned by additive allelic effects has now been overtaken by marker-assisted selection (MAS). MAS relies on the existence of heritable genetic or molecular (usually DNA) markers that are associated with economically important traits (Darvasi and Soller, 1994). The predictive value of genetic markers used in MAS depends on their inherent repeatability, map position, and linkage with economically important traits [quantitative or qualitative] (Staub et al., 1996). The major advantage of MAS is that it provides a potential for increasing selection efficiency by allowing for earlier selection and reducing population size used during selection. Not only is the efficiency and precision of

breeding enhanced, but costs are also reduced. MAS of many important food and cash crops, trees and important farm animals now allows new cultivars and breeds to be developed far more rapidly than the "hit and miss" approach typical of conventional selective breeding programmes (Ribaut and Hoisington, 1998).

In addition to genome data, the physical maps of many crops, pathogenic microorganisms and some livestock are now available, for example for corn, rice, some viral, bacterial and fungal species and cattle. Efficient use of genome data from such organisms offers unprecedented potentials for crop and animal improvement. Among cereal grasses, there is very high synteny, in terms of gene structure and order, e.g. between rice, wheat, corn, millets and sorghum (Gale and Devos, 1998). By taking advantage of comparative genomics, it should be possible to establish genetic and physical maps of so-called African orphan crops such as tef, sorghum and millets (Ware, 2002). The extensive seed banks of these African crops can be used to initiate large-scale breeding programmes that utilize molecular markers to accelerate the evaluation of the outcome of the crosses (Young, 1999). One example is the accumulation of several desirable traits (also called pyramiding) in the same genotype (Lambalk, 1999). Another good example is marker-assisted backcrossing (MABC) programmes which utilize mapped markers to select backcross progeny that have the highest percentages of the recurrent parent genome and the minimum number of donor parent segments (Frisch, 1999). By using new MAS strategies and software tools for precise genetic mapping, high-resolution chromosome haplotyping and extensive phenotyping, it is now possible to create novel, superior crop varieties and livestock breeds in what Peleman and van der Voort (2003) have termed "breeding by design". However, this will require prior understanding of the molecular genetic control of agronomically important traits and the allelic variation that exists at loci controlling those traits, before the molecular breeder is able to design superior genotypes "*in silico*". Lastly, it should be mentioned that most of the technologies being developed for MAS are also applicable in the evaluation, conservation and use of biodiversity, including microbial, animal and plant genetic resources.

Animal agricultural genomics

Cloning and transgenic animal research has attracted a lot of attention, particularly since the cloning of Dolly the sheep. Although human cloning is banned, the use of cloned and transgenic animals and insects is now being done routinely in several laboratories around the world. Use of cloned animals may be useful in creating "herds" with uniform product characteristics (Visscher et al., 2001). So far, the area that already has had impact is the use of transgenic animals such as chickens and cattle to produce pharmaceutical or therapeutic proteins in eggs and milk (Gluck, 2000). Though difficult to predict with certainty, the overall global impact of transgenic and cloning technologies in animal agriculture is expected to be low, compared with crop agriculture and forestry. In animals, the complexity of multiple organs, tissues, and cell types, combined with mechanisms of cross-communication complicate all studies aimed at improvement. Another problem is the lower degree of totipotency exhibited by animal cells, making regeneration scientifically harder and more expensive to perform (Hines, 1997). In addition, ethical and religious considerations pertaining to any form of genetic tampering are more rigorously pursued with animal and human subjects than with other organisms. However, the greatest impact of genomics is being realised in the development of new diagnostics and vaccines for animal diseases and in the production and use of animal feeds.

Many vaccines and growth hormones are amenable to recombinant DNA manipulations, hence allowing avenues for development of animals, especially livestock breeds, with enhanced growth characteristics (McKeever and Rege, 1999). For resource-poor farmers in Africa, utilization of improved disease control strategies through use of disease resistant livestock and improved diagnostics, vaccines and therapeutics for disease prevention and treatment would greatly help secure livestock assets, with the greatest impact likely to be felt among pastoralist communities in the arid and semi-arid regions. In trying to achieve these objectives, it is crucial to target local genetic resources rather than exotic livestock genotypes as sources of useful genes, as illustrated by presence of disease resistance genes in locally adapted West African dwarf goats and Maasai sheep (International Livestock Research Institute, Nairobi, http:/www.cgiar.org/ilri). Use of genomics tools to address these constraints would increase productivity, farmers' income and food security, while also reducing chemical and drug usage and hence improving environmental health and sustainability. Production of transgenic animals with improved traits such as enhanced reproductive performance, disease resistance and tolerance to environmental stresses is still not a reality, although knowledge about the genetic and biochemical control of such traits make current research towards achieving these goals realistic and achievable in the long term.

As with the Green Revolution, there has been an equally powerful revolution in the field of animal feed efficiency (feed conversion and nutrient partitioning) and nutritional requirements arising from advances in animal genetics. For example, it now takes less than 1 pound of feed to produce one pound of weight gain in broiler chickens, whereas it took 6 pounds of feed to produce the same increase in weight 100 years ago (Gordon, 1996). These improvements in animal feed have been

made at the level of both macronutrients and micronutrients or as pharmaceuticals (Kellems and Church, 1998). Macronutrients, namely carbohydrates, lipids and proteins (amino acids) constitute the bulk of feedstuffs, and are primarily used as energy sources. Micronutrients (e.g. minerals and vitamins) are organic or inorganic compounds present in small amounts and essential for good health. Increasingly, bioproduction of these substances is through recombinant DNA tools utilising the latest knowledge in both structural and functional genomics (Bonneau and Laarveld, 1999). Examples include dietary supplements, such as vitamin D and E (antioxidant), amino acids (e.g. methionine to improve immunity), enzymes (e.g. to improve digestion and remove antinutritional metabolites and toxins), antibiotics and growth hormones (to improve health and enhance growth rate). Other advances include use of prebiotics and probiotics to improve gut microflora.

In the developed countries, a very significant proportion of crops, especially corn, are grown for animal feed in the form of hay, silage, forage or grain. In these countries, genetic modification of crops to enhance feed value has reached farmers. Such crops include silage corn with reduced lignin content to enhance digestibility, oil rich corn and corn with enhanced protein content (Mazur et al., 1999). Crops having reduced non-digestible components such as the oligosaccharides stachyose, raffinose and galactose, or with enhanced resistance to fungal pathogens, or a combination of these traits, would certainly be welcome, especially to overcome contamination of feeds by mycotoxins.

To date, many animal gene sequences, including over 250,000 cattle genes and more than 150,000 pig genes (www.nbfgc.msu.org) are available in public databases such as the Institute for Genomic Research (TIGR, Rockville, Maryland). In the coming decades, the vast amount of information gained from functional genomics studies will help to: 1), target relevant genes for drug studies; 2), develop effective therapies for disease treatment; 3), determine what hormones and metabolites are involved in animal responses to environmental and developmental cues; 4), determine true impacts of husbandry practices on animal health; 5), determine true impact of genetic selection on animal health; 6), find harmful and beneficial forms of genes for genetic selection, and; 7), guide strategies for transgenic research to improve animal health (Paul Coussens, Centre for Animal Functional Genomics, Michigan State University, personal communication). These examples provide sufficient evidence to spur future investments in animal genomics to address areas related to production, product quality, food and feed safety and health. Uptake of these new technologies in Africa is imperative not only for solving constraints but also for helping to diversify animal agriculture while at the same time promoting crop-livestock integration as a way forward for uplifting rural economies (Haan et al., 1997; Machuka, 2003).

Plant genomics and systems biology

In addition to marker-assisted breeding discussed above, identification of the genes conferring the agronomic traits to our crop and forest plants and engineering of novel traits will be the base of a sustainable agriculture, forestry, industry and environment care (Campbell et al., 2003; Diouf, 2003; Mazur et al., 1999; Somerville and Somerville, 1999; Walbot, 1999). Methods of gene identification include direct sequencing of genomic DNA and ESTs, gene disruption and trapping strategies, and differential display (Bellen, 1999; Reuber and Ausubel, 1995; Ross-McDonald, 1999; Springer, 2000). Furthermore, several methods to analyze RNA (trancriptomics or RNA profiling), proteins (proteomics) and metabolic pathways (metabolomics) at a large scale are now routine and continuously being improved (Pandey and Mann, 2000; Richmond and Somerville, 2000). Use of highthroughput technologies such as microarray and gene chips for expression profiling and improved tools of analytical organic chemistry (e.g. nuclear magnetic resonance spectroscopy or NMR, gas chromatography-mass spectroscopy, GC-MS, liquid chromatography-MS or LC-MS and time-of-flight-MS or TOF-MS) allow the establishment of profiles of all metabolites present in specific plant cells and tissues. The later approaches will allow unravelling of biochemical pathways, identification of genes encoding biosynthetic enzymes and production of secondary and intermediar metabolites in crop plants (Girke et al., 2003; Katagiri, 2003; Sweetlove et al., 2003). Given the ever-increasing knowledge and information pertaining to genomics, new bioinformatics and computational biology tools are needed to analyze, interpret and utilize the enormous body of data and knowledge generated.

With major breakthroughs in genomics and analytical chemistry, plant biologists are now aiming to integrate transcriptomic, proteomic and metabolomic datasets using bioinformatics tools in sufficient detail that affords system-wide predictions of plant development in response to both genetic and environmental perturbations. This new era of "systems biology" is probably the ultimate undertaking in terms of attempting to manipulate or improve plant traits for agricultural uses in an environmentally sustainable manner. One key trait that has defied scientific unravelling is the phenomenon of heterosis (Bircher et al., 2003). A systems biological approach to define how plant genomes interact to create phenotype is needed to arrive at a final resolution of this phenomenon.

Typically, target traits for genetic improvement fall into three classes, namely, input (agronomic) traits, output (nutritional quality) traits and physical traits. Agronomic traits are both biotic (e.g. resistance to diseases, parasites, insects, nematodes and weeds) and abiotic (e.g. better adaptation to heat, drought, salinity, acidity, heavy metals, water logging and nutrient [especially

nitrogen and phosphorus] availability). Output traits include content and quality of starch, protein, oil, nutritional elements (Mazur et al., 1999). Physical traits include plant architecture, shelf life and podshattering (Ait-Ali et al., 2003). In future, the most challenging studies with immediate impact on crop and tree agriculture will include regeneration (totipotency) and transformation capacity, vegetative seed production (apomixis), seed molecular biology, haploid plants; heterosis or hybrid vigour, symbiotic nitrogen fixation, parthenocarpy, plant architecture, flowering and drought resistance. For example, many genes controlling plant architecture and flowering time, and which have potential utility in crop improvement in Africa, have been characterized (Delmer, 2003). Some of these genes can be either up- or down-regulated in transgenic plants to dramatically alter such properties as stem strength and length, leaf size and shape, the form and polarity of organs such as fruits and flowers, the activity of various meristems, root branching patterns, the cell division cycle that plays a big role in determining the overall rate of plant development and genes controlling circadian rhythms, flowering time, and vernalization (Howell, 1998). As an example, introduction of one or several possible dwarfing genes to the tall East African Highland banana may reduce the size of this important fruit crop. Also, over-expression of gene(s) that can shorten the cell division cycle could speed up the otherwise very long growth cycle of this crop.

New technologies and strategies that rely on mechanisms such as transcriptional and post-transcriptional gene silencing are increasingly being used to address economic crop constraints in ways that were hitherto not contemplated (Covey, 2000). One such technique involves the silencing or down-regulation of specific genes by double stranded RNA (dsRNA) through a technology referred to as RNA-mediated interference or RNAi (Fire and Mello, 1998). In some cases, it has been shown that the presence of just a few molecules of dsRNA is sufficient to knock-down the expression of a gene that is homologous to the dsRNA. This approach opens up many avenues for utilizing already large amounts of specific genomic and cDNA sequences encoding known functions, in agricultural genomics with respect to priority constraints of economic value. Of particular importance to Africa will be manipulation of genes involved in abiotic stress mechanisms, especially drought stress and water use efficiency (Bruce et al., 2002; Zhang et al., 2000). It is now becoming clear that gene expression associated with dehydration (and freezing) stress involves both abscisic acid (ABA)-dependent and ABA-independent signal transduction pathways. Overexpression of ABA induced genes is thought to result in enhanced stomatal responsiveness leading to closure of stomates (and henced enhanced "staygreen" phenotype) during water stress (Laporte et al., 2002).

Presently, plants engineered with genes that encode enzymes that synthesize osmoprotectants (Penna, 2003) or genes that encode transcription factors such as the CBF/DREB family, provide the most promising economically viable technology to have applicability beyond the "prove of concept" phase (Bill Goure, Mendel Biotechnology Inc.®, California, personal communication; Kasuga et al., 1999; Michael Thomashow, www.aspb.org). Mendel Biotechnology (California) is currently licensing WeatherGard™ genes which are regulatory (CBF/DREB) genes that allow plants to be engineered to be more tolerant to drought. This is an opportune time to test these technologies in the farmers's fields through genetic transformation. Many research groups have also isolated genes from dessication tolerant plants such as the resurrection plant in South Africa, a desert moss that can slow its activity down to zero when water is scarce, and revive from almost complete dehydration (Gardner, 2002). ABA induced genes have also been identified from the model moss *Physcomitrella patens* through a pilot EST sequencing project (Machuka et al., 1999). Other strategies include manipulation of specific genes that control the pattern of root branching, to create deeper, perhaps more branched roots to increase the surface area for water absorption, and/or in combination with use of desiccation stress-inducible promoters.

Directly, or indirectly, plants provide all of humanity's food, most of which comes from only a few crops, namely rice, maize and wheat. Over many years of crop agriculture, the focus has been on agronomic traits such as yield, productivity and pest resistance, while nutrient content has largely been ignored, with the result that most food staples are severely limited in nutritional composition. As noted above, 250 million out of 650 million Africans are chronically undernourished, over 40 million children are severely underweight and 50 million suffer from vitamin A deficiency, while 65% of women of child bearing age are anemic. To alleviate these problems, research is underway to fortify food staples to enhance levels of essential and non-essential micronutrients and macronutrients, such as vitamins (e.g. A, C, E, folate), minerals (e.g. iron and zinc) and proteins. Examples include cereals and sweetpotato with enhanced levels of vitamins and/or proteins in their seeds and tubers, respectively (Beyer and Potrykus, 2001; Beyer et al., 2002; Potrykus, 2001; Wu et al., 2003; Ye et al., 2000). This field of nutritional genomics takes advantage of the many genes that have been cloned for vitamin pathways and for the synthesis of many other "nonessential" compounds and macronutrients (Dellapena, 1999; 2001). In future, it should possible to directly manipulate the content and composition of many nutrients in staple African food crops such as cassava, sweetpotato, banana, cowpea, maize, millets and sorghum. Other benefits will include lowering the levels of antinutrients (e.g. phytic acid), toxins (e.g. cyanide in

cassava) and allergens in seeds, food grains, leaves and tubers (Graham et al., 2001; Tada et al., 1996). Transgenic plant production of edible vaccines and antibodies (plantibodies), as well as products of therapeutic, pharmaceutical and industrial value, is also possible (Hood et al., 1997; Mason and Arntzen, 1995; Smith, 1996). Products with industrial uses include latex, oils (palm, soja, rape seed), speciality oils and waxes, sugars, starch, cellulose, wood, monomers for biodegradable plastics, etc. (Somerville and Somerville, 1999). Although this field of "molecular farming" is still a long way to go, it has the potential to spur rural agro-industrialization and enhance crop diversification for new uses, and hence to increase sources of income for resource poor-farmers who depend on agriculture for their livelihoods (Motto et al., 2003).

MAJOR CONCERNS

Public concerns about bioengineering fall within five categories: (i) safety issues related to human health, food safety and antibiotic markers (ii) concerns about detrimental environmental impacts such as loss of biodiversity, gene transfer to wild relatives, non-target effects arising from insect resistant crops and escape of bioengineered crops (iii) regulatory concerns, such as unsatisfactory regulation, labelling policy and the right to choose (iv) economic concerns, such as control of biotechnologies by big multinational companies and rich nations resulting in limited impact on developing countries, especially on small and medium family farmers in Africa (v) ethical concerns. Some of these concerns are legitimate, others clearly result from lack of information and/or misinformation about the technology, whereas others are deliberately not genuine. But however the case may be, these concerns largely determine whether or not biotechnology is accepted and/or adopted by end-users, mainly farmers, industry and consumers. It is not the intention of this short review to discuss detailed responses to these concerns, but suffice it to say that there is no scientific evidence so far to suggest that bioengineered crops pose unique hazards compared with conventional agriculture and breeding (Scott and Wilkinson, 2001). Indeed the precision of recombinant DNA technologies and our current knowledge about gene regulation, makes these technologies much more predictable than random mixing of genes that occurs through conventional breeding.

Data from first generation transgenic crops shows significant economic and environmental benefits, such as increased yields, easier weed control, reduced pesticide use on insect tolerant crops and reduced soil erosion resulting from non-tillage practices when growing herbicide tolerant crops (James, 2002).

However, it must be noted that no technology is risk-free, hence the concerns mentioned above need to addressed through sound science rather than mere emotion and unfounded speculation. Furthermore, it is important that these concerns are also raised and addressed with respect to classically bred crops and agricultural practices. One reason for doing this is because we know that many conventionally bred crops such as tomatoes, cassava, broccoli and potato contain unsafe levels of toxins, allergens and/or other antinutrients that have been ignored by those who claim that bioengineered foods which have undergone and passed rigorous food safety tests are (still) not safe to eat (Kleter and Peijnenburg, 2003). Responsible use of modern biotechnology must also take into account societal (including ethical and religous) values, trust, familiarity, controlled risk and tangible benefits to the consumer. So far, scientists have mostly followed scientific rationality and thereby failed to understand that public opinion follows not only science but also other "non-scientific" considerations. It is therefore imperative to educate and make the public aware of the importance of science in decision making by moving from "educating the public" to engaging with the public, through discussions with stakeholders such as farmer, consumer and regulatory organisations. In all this, the consequences of NOT applying modern biotechnology tools in agriculture must be explained. In Africa, the fruits of biotechnology are still far off, and yet we seem to be in blind danger of terminating this technology before it even germinates!

CONCLUSIONS AND WAY FORWARD

It can be argued that the major twin problems of food insecurity and dire poverty in Africa will not go away until water security is achieved, to allow rural populations to have adequate year round water supplies for safe drinking and irrigated agriculture. As priorities, improving crop and animal genetics to cope with environmental and biotic stresses, such as water deficits, heat and animal diseases, should be part of an integrated holistic approach for enhancing agricultural sustainability and poverty eradication. Application of nutritional genomics for biofortification of food staples has great potential to reduce hunger and malnutrition on the continent. To attain these benefits, increased educational and research efforts are needed by government agencies, charities and foundations for development, enhancement and/or adoption of genomics, computational biology and bioinformatics tools in agriculture, food and healthcare delivery systems. Furthermore, partnerships need to be forged between African research institutions and international, public and private sector genomics and breeding efforts. The New Partnership for Africa's Development (NEPAD) can play a key role in providing stewardship of this effort, by facilitating the generation and use of cutting-edge science and technology by the

continent's researchers to enable them to develop products aimed at solving African problems. The recently launched Biosciences Facility for Eastern and Central African will serve as a test case for NEPAD's leadership. The Facility has been constituted as a centre of excellence in biosciences (including genomics), and will be hosted by the International Livestock Research Institute (ILRI), in Nairobi, Kenya. Finally, it has to be hoped that the enormous financial resources being spent annually on endless biotechnology debates be channeled into useful research to address the urgent needs facing the dying rural poor who make up over one third of Africa's population. Currently financial resources are overwhelmingly skewed in favor of public awareness and acceptance concerns, and for development of policy frameworks, while there is hardly a single independent laboratory in the whole sub-Saharan Africa's national sector systems, with capabilities to undertake state-of-the art genomics research for development (RfD). This trend continues in spite of the fact that there are far more well trained scientists in biotechnology RfD than in the auxiliary areas of IPR and biosafety, many of whom choose to work in advanced laboratories in the North due lack of facilities in their own countries.

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