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SUBSTITUTION OF SOYBEAN IN ANIMAL NUTRITION ■ NEXT GENERATION SEQUENCING PROJECTS

■ YOUNG FARMERS IN HUNGARY

■ TEN YEARS AFTER EU ACCESSION ■ 2016 VALLEY OF ARTS FESTIVAL



# Social farms in Visegrad countries

## What is social farming?

Social farming is a farming practice that uses agricultural resources to provide social, health or educational care services for vulnerable groups of people, e.g. people with physical or mental health problems, disabilities, unemployment.

## Why social farming?

- it uses agricultural resources for improving the social, physical and mental well-being of people
- it diversifies the scope of farming activities and their role in society
- it provides farmers with new sources of income
- it enhances the image and utility of agriculture in the public eye



## Project aims:

- exploring social farm initiatives in Visegrad countries – Czech Republic, Hungary, Poland, Slovakia
- collecting of social farm best practices in Visegrad countries
- initiating international cooperation in the field of social farms

**Project duration:** October 2016 - September 2017

## Project partners:

- Szent István University – Gödöllő, Hungary
- University of South Bohemia - České Budějovice, Czech Republic
- Agricultural Advisory Centre – Kraków, Poland
- Slovak University of Agriculture – Nitra, Slovakia

**Project number:** Visegrad Fund's Standard Grant No. 21610041

**Visit our website for more detailed information:**

<http://socialfarm.gak.hu/>





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# SUBSTITUTION OF SOYBEAN WITH ALTERNATIVE SOURCES OF PROTEIN FOR FEED IN THE EU

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## ABSTRACT

The EU is dependent for 60% on imports of protein-rich feedstuffs and the self-sufficiency of soy products is just around 5-6%. The EU imports about 10% of soybean and 30% of the soybean meal available in the world market. Oilseed meals are also recognized as important protein feedstuff, however, for climatic and agronomic reasons, and the slow growth of the biofuels industry the EU is unable to increase considerably the production of oilseeds. Furthermore, the competitiveness of grain legumes in arable crop rotations is limited and yield increases would be needed to replace imported soybean products and this would also be needed for soybean production. The protein feed output by the biofuels industry is equal to about 65-70 million tonnes of soybean meal, or 30% of the global soybean meal production. In addition to the global production of 5 million tonnes of fishmeal per annum the global output of animal protein is around 13 million tonnes per year replacing about 18 million tonnes of soybean meals, or 10% of the global production of soybean meal. Protein levels in grass leaves are low, but bio-refineries of green leaves could potentially produce high protein content products and alfalfa protein extracts are commercially available on the market but in limited volumes. Recently, products of aquatic biomass have surfaced as potential protein sources for animal feed, however, at present production cost are too high for a market introduction. Insects are a well-known source of protein, but still much knowledge is yet to be collected to judge the real potential of insects as protein sources for animal feed. Improvement of cost effectiveness for the production of yeast and amino acid is needed to make them alternative protein sources. Soybean meal is still the most price competitive feed protein and will not be replaced by alternative protein sources in the next decade.

**keywords: protein feed, soya protein, alternative protein sources**

## INTRODUCTION

The EU is dependent for 60% on imports of protein-rich feedstuffs for which there are no substitutes in the short term. The self-sufficiency of soybean and soybean meal is just around 5-6% (European Commission, 2015). Protein-rich soybean meal is needed by livestock producers in the EU to achieve a balanced diet for their animals, especially as far as protein is concerned. Demands for soya from the EU differ to those from third countries with respect to the GM varieties grown, and which are authorised for import into the EU (USDA 2016a). The EU imports soybeans and soybean meal from the three large soybean producing and exporting countries – the USA, Brazil and Argentina – where the adoption rate of GM soybean reached between 89-99% and representing 80 to 90% of global production and exports of soybean and soybean meal (Popp et al. 2015). No real alternatives exist to imports from the three large producing and exporting countries – Argentina, Brazil and the USA – (FEFAC 2015a). The EU imports about 10% of soybean and 30% of the soybean meal available in world market. Though China is a biggest consumer of soybean meal in the world, however, it does not directly import meal but soybeans for crushing with a share of 62% of the global trade (USDA 2016b).

Around 480 million tonnes of feedstuffs are consumed by EU livestock on a year basis. Of this amount compound feed production has a 30% share (153 million tonnes a year). Soybean meal is the current main source of protein in the feed sector. The unique properties of soybean meal, namely the high protein content with high ileal lysine digestibility illustrates the dependency and associated risk in view of increasing demand and price volatility (FEFAC 2015b). The EU yearly imports around 19 million tonnes of soybean meal and 12 million tonnes of soybean of which some 10 million tonnes is processed into meal, taking total EU consumption of soybean meal to some 29 million tonnes (Tikász - Varga 2016). The EU soybean crop production stands at around

**Table 1: Protein yield per hectare in the EU.**

	Yield, t/ha	Protein content, %	Protein yield, t/ha
Soybean (BRA)	2.7	36.0	0.97
Pea (EU)	2.7	22.1	0.60
Rapeseed (EU)	3.0	21.6	0.65
Wheat (EU)	5.1	11.8	0.60
Wheat (World)	2.5	11.8	0.30

Source: Toepfer International, 2012; European Commission, 2014.

2 million tonnes (with around 1.6 million tonnes soybean meal). So only 5 % of the EU soybean meal consumption is produced in the EU (European Commission 2015). Total world consumption of soybean meal is around 210 million tonnes, so the EU is consuming around 14% (USDA 2016b). Total world meat production will continue to increase. thus, demand for protein sources for animal production will increase accordingly (FAO 2012). The widespread use of soybean meal in the animal compound feed industry and husbandry represents the high value of this product for meat, egg and dairy production. Alternatives should match this quality or have the potential to do so in the future. Many of the potential alternatives to soybean meal including even non-crop sources like insects, aquatic biomass (algae, duckweed), products from biorefineries (green leaves, alfalfa) yeast and amino acids have made their entry as a potential source.

## MATERIAL AND METHODS

The literature on the impacts of soybean expansions is already substantial, however, the alternative sources of protein for feed have received much less attention. The search engine Google Scholar and studies of international organisations are primarily used to collect the relevant literature. In addition, backward searches through bibliographies of academic studies and reviews as well as hand searching websites of international projects and conferences on protein feed are also applied. Since the rapid progress of this research field, literature is also limited to the papers mainly published after 2010. The literature reviewed is selective and critical. Highly rated journals and analysis of recognised international organizations (FAO, USDA, EC, FEFAC, RFA etc.) are the preferred choice. We carefully selected 23 papers which are considered as important or innovative studies, or comprehensive reviews offering us a big picture of protein feed production and use as livestock feed. The literature review is categorized into three topics:

- Soybean and soymeal production as livestock feed globally and in the EU.
- Alternative sources of feed protein.
- Outlook of replacing soya products with alternative sources of protein for feed in the EU.

## RESULTS

The question arises as to how grain legumes, for example peas with an average protein content of 22.1%, can replace soybean, which contain 36% of protein (Toepfer International 2012). An average of 1.6 ha of peas cultivated in the EU would be needed to replace a hectare of soybeans in Brazil. However, peas replace other crops and their protein output too, for example wheat. An average 1 ha of pea can replace 1 ha of wheat produced in the EU and 2 ha of wheat cultivated in other parts of the world where on average only half of the EU's yield can be achieved (Table 1). In order to replace wheat production of 1.6 ha in the EU, twice the 1.6 ha acreage would have to be cultivated elsewhere in the world. This means that wheat acreage of 3.2 ha is required in order to replace a single hectare of soybeans in Brazil. However, a reduction of the wheat acreage in favour of pulses would reduce the EU's export potential meaning other production regions around the world would have to fill this gap in production (ADM Germany 2015).

Increasing soybean production together with enhancing the range of protein crops cultivated in the EU, including grain legumes (mainly bean, field pea and lupins) and forage legumes (mainly alfalfa) is a strategy of the Common Agricultural Policy (CAP). For climatic and agronomic reasons, the EU is unable to produce most of the oilseed meal and other protein-rich feedstuffs required to feed its livestock. Imports of soybean meal could well be (partly) replaced by European soybeans. This crop is produced on some 0.8 million hectares with a production of 2,4 million tonnes a year in the EU (European Commission, 2015). But competitiveness of these crops to wheat and corn is not very good and yields need to improve to as high as 4-5 tonnes per hectare to replace imported soybean meal. Rapeseed and sunflower seed meal is also recognized as important protein feedstuff. For these meals the protein content is less than that of the soybean meal while it contains high levels of fibre, making the product less attractive compared to the soybean meal. According to the projection of the European Commission no change in the oilseed area is expected between 2015-2025.

Grain legumes like field peas, field and broad beans and lupins are all to some extent interesting alternatives to soybean meal. With the production of protein crops such



as field peas, field beans and lupins the EU can only replace just 5% of EU imports of soybeans and soybean meal (Popp et al., 2015). For the time being there is no prospect for developing large scale domestic production of protein rich plants. The production of grain legumes in the EU is around 4 million tonnes a year and out of that amount just 2 million tonnes are used by the compound feed industry (European Commission 2015). The grain legumes have high protein content but distinctively lower than the soybean meal and contents of methionine and lysine (essential amino acids) are also lower compared to the soybean meal. In addition, peas, beans and lupins are sensitive to diseases and pests and can only be grown in a wide crop rotation and therefore need much attention from farmers. At the moment the competitiveness of grain legumes in arable crop rotations in Europe is limited and yield increases are needed to replace imported soybean products and this would also be needed for European soybean production. The biofuels industry produces a high volume of protein feed. The ethanol industry produces worldwide an estimated 45 million metric tonnes of feed, including distillers grains (90%) and gluten feed and gluten meal (RFA 2014). In 2014 around 3.3 million tonnes of highly valuable animal feed (DDG, wheat gluten and yeast concentrates) was produced in the EU, which displaced nearly 10% of soybean and soybean meal imports by volume (RFA 2016; ePURE 2016). However, by generating high-protein animal feed as a co-product of ethanol reduces the need

for farmers to use imported animal feed, such as soya. About 7 million tonnes of soybean oil and 9 million tonnes of rapeseed oil is used in biodiesel production contributing to almost 28 million tonnes of soybean meal and 13 million tonnes of rapeseed meal output (Popp et al. 2016). Out of this 9 million tonnes or 70% was produced in the EU. The 6 million tonnes of rapeseed oil feedstock used for biodiesel production in the EU generates about 9 million tonnes of rapeseed meal as co-product, most of which is used for animal feed similarly, the 0.9 million tonnes of soybean oil has to be crushed from 4.3 million tonnes of soybeans generating about 3.4 million tonnes of soybean meal as co-product (USDA 2015). The share of oilseed meals as feed material in the compound feed industry reached 42 million tonnes in 2014 and the contribution of the biodiesel industry accounted for over 30% (FEFAC 2014). Taking into consideration that 210 million tonnes of soybean meal, 40 million tonnes of rapeseed meal and 15 million tonnes of sunflower seed meal is produced a year globally, the co-products of biodiesel production have a relatively high impact on the feed market (USDA 2016b). The protein feed output by the biofuels industry is equal to about 65-70 million tonnes of soybean meal, or 30% of the global soybean meal production. In addition to the global production of 5 million tonnes of fishmeal per annum the global output of animal protein is around 23 million tonnes per year replacing about 20 million tonnes of soybean meals, or 10% of the global production of soybean meal. Both the

Table 2: Crop and protein yield per hectare

	Protein content	Yield in the EU (DM/ha/y)	Protein yield (t/ha/y)
<b>Wheat (reference)</b>	11%	10 tonnes	1.1 tonnes
<b>Oilseeds – soybean</b>	40%	1.5-3 tonnes	0,6-1.2 tonnes
<b>Oilseeds – rapeseed</b>	25%	3 tonnes	0.75 tonne
<b>Oilseeds – sunflower</b>	23%	3 tonnes	0.7 tonne
<b>Legumes (pulses) – beans, peas, lupine</b>	17-35%	4-6 tonnes	1-2 tonnes
<b>Legumes (forage) – alfafa</b>	19%	13 tonnes	2.5 tonnes
<b>Leaves – grass</b>	12%	10-15 tonnes	1.2-2.0 tonnes
<b>Leaves – sugar beet leaves)</b>	12%	4,5 tonnes	0.5 tonne
<b>Cereals – oat</b>	12-15%	3-5 tonnes	0.4-0.75 tonne
<b>Pseudo cereals – quinoa</b>	12-18%	3 tonnes	0.4-0.5 tonne
<b>Macra algae – seaweed</b>	10-30%	25 tonnes	2.5-7.5 tonnes
<b>Micro algae</b>	25-50%	15-30 tonnes	4-15 tonnes
<b>Duckweed</b>	35-45%	30-40 tonnes	3-14 tonnes

Source: van Krimpen et al. 2015. Source: van Krimpen et al. 2015.

global production of co-products by the biofuels industry and animal protein (including fishmeal) is expected to increase just moderately in the future.

Protein levels in leaves are low, due to high moisture content, but bio-refineries of green leaves could potentially produce high protein content products, free of fibres that negatively influence digestibility (Molnár et al. 2016). At present, alfalfa protein extracts are commercially available on the market but in restricted areas. With products like grass and alfalfa experimentation is on-going but economic feasibility is still questionable at the current level of technology and market prices. Grass would be interesting because of the protein content of about 200 g per kg dry matter at a dry matter percentage of around 19% (Table 2). In all cases a considerable amount of water needs to be removed to produce an alternative to the soybean meal. Recently, products of aquatic biomass like duck weed, macro- and micro-algae have surfaced as potential protein sources for animal feed (Bachis 2015). However, digestibility figures are not available yet and at present production cost are too high to make bulk markets accessible to algae. Duckweed is also considered as a potential alternative because of the relative high protein content in the dry matter and with good amino acid profiles (Bachis 2015). With a dry matter content of 6-8% this potential protein source would need processing to produce a credible alternative to soybean meal (Table 2). However, for cows this product could be a roughage product, much like grass, and thus contribute to protein uptake. Nevertheless, digestibility studies are scarce, so digestibility is still to be investigated.

Insects (black soldier fly, house fly and meal worm) are a well-known source of protein. In the dry matter crude protein level can be higher than 50% and the animals grow fast on organic waste materials (Fitches 2015). Studies reported good amino acid digestibility of insects fed to animals, but still much knowledge is yet to be collected to judge the real potential of insects as protein sources for animal feed. If grown on waste material, insect protein could be price competitive, but at high production levels, the question will arise whether or not insect feed needs to be produced in an efficient way beyond organic waste sources. Also, little is known about processing cost of insects. Improvement of cost effectiveness for the production of yeast and amino acid is needed to make them alternative protein sources. Soybean meal is still the most price competitive feed protein and will not be replaced by alternative protein sources in the next decade improvement of cost effectiveness for the production of yeast and amino acid is needed to make them alternative protein sources. Soybean meal is still the most price competitive feed protein and will not be replaced by alternative protein sources in the next decade (Tacon 2015; Research and Markets 2015).

## DISCUSSION

Europe is so far highly dependent on animal protein imports for compound feedstuffs production particularly of soybean and soybean meal for mainly the poultry and pig sectors. In order to meet the animal protein supply needs, the EU appears inflexible especially in the area of green biotechnology embraced at large scale and fast speed in third countries. The EU has had several major trade disruptions already, regardless whether conventional or genetically modified protein sources are imported. The current EU ad-hoc management of GM-related matters has had a severe financial impact on many sectors, and has caused the need for authorities to handle crises. There is a risk of trade disruptions following asynchronous authorizations of GM-traits between the producing countries and the EU with leading to very high price increases when this disruption would refer to the USA, Brazil and Argentina suppliers simultaneously. In addition, a general increase of American soybean exports toward China inducing tensions on prices particularly for poultry and pig feeding.

Soybean meal is the current main source of protein in the feed sector. Meeting the global growing demand for animal proteins with limited availability of resources and with the need to reduce pressure on the environment is a worldwide challenge. Sustainability is an important driver for alternative sources of protein. There is growing concern about the production systems of soybean in part of the production area and the impact that these have on deforestation and soil decline amongst others. The replacement of soybean meal by other protein sources does not automatically imply that a sustainability gain is realized. For instance, the enlargement of the production of European soybean or grain legumes will be realized at the expense of wheat and maize in most countries. So to some extent this could be counteracted by increases of yield level, but to a larger extent it will imply import or reduced exports of wheat and maize from outside the EU. The mainstream feed value chain needs substantial amounts of price and quality competitive alternatives and it will take time and efforts to build up a supply chain large enough to meet these demands in the EU. Availability of industrial by-products reduces pressure on land compared to dedicated feed crops. Often the production of aquatic biomass is considered as not competing with the food value chains. However, aquatic biomass needs sunlight to be produced and that sunlight could also be used for other purposes (human food production). However, the present day situation looks different because European output of protein crops is restricted to niche activities, while supply-chain logistics are poor or nonexistent. Furthermore, the investments of the supportive industry (plant breeding) are low therefore an intensive co-operation between all stakeholders involved is needed.

Increasing soybean production together with enhancing the range of protein crops cultivated in European countries, including grain and forage legumes could be a long term strategy. Moreover, sunflower and rape meals are also recognized as important protein feedstuff. However, in the next decade, developments in the oilseed complex in the EU should be driven mainly by the expansion in the livestock sector and the consequent increase in demand for oilseed meals. This should trigger a shift towards more imports of soybeans and especially soybean meals, while domestic rapeseed and sunflower seed production is expected to stabilize. Protein crop production is expected to increase, given a favourable policy environment (with voluntary coupled support and the ecological focus area obligation) and strong protein demand from more intensive livestock production. However, it will continue to account for a limited proportion of total area.

## CONCLUSIONS

The EU is dependent for 60% on imports of protein-rich feedstuffs and the self-sufficiency of soy products is just around 5-6%. The EU imports about 10% of soybean and 30% of the soybean meal available in the world market. In the EU there will not be substitutes for imported protein-rich feedstuffs in the near future. Oilseed meals are also recognized as important protein feedstuff, however, for climatic and agronomic reasons, and the slow growth of the biofuels industry the EU is unable to increase considerably the production of oilseeds. Furthermore, the competitiveness of grain legumes in arable crop rotations is limited and yield increases would be needed to replace imported soybean products and this would also be needed for soybean production. The co-products of biodiesel production have a relatively high impact on the feed market compared to 210 million tonnes of soymeal, which is produced a year globally. The protein feed output by the biofuels industry is equal to about 65-70 million tonnes of soybean meal, or 30% of the global soybean meal production. In addition to the global production of 5 million tonnes of fishmeal per annum the global output of animal protein is around 13 million tonnes per year replacing about 18 million tonnes of soybean meals, or 10% of the global production of soybean meal. Protein levels in grass leaves are low, but bio-refineries of green leaves could potentially produce high protein content products and alfalfa protein extracts are commercially available on the market but in limited volumes. Recently, products of aquatic biomass have surfaced as potential protein sources for animal feed, however, at present production cost are too high to make bulk markets accessible to aquatic biomass. Insects are a well-known source of protein, but still much knowledge is yet to be collected to judge the real potential of insects as protein sources for animal feed. Improvement of cost effectiveness for the production of yeast and amino acid is

needed to make them alternative protein sources. Soybean meal is still the most price competitive feed protein and will not be replaced by alternative protein sources in the next decade.

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# AGRICULTURAL GENOMICS: AN OVERVIEW OF THE NEXT GENERATION SEQUENCING PROJECTS AT THE NARIC-AGRICULTURAL BIOTECHNOLOGY INSTITUTE IN GÖDÖLLŐ

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## ABSTRACT

Next generation sequencing technologies developed in recent years can produce vast amount of data about the sequence composition and variation of any nucleic acid fraction of the cell. In the last decade, the genome and/or transcriptome and other cellular nucleic acid compartments of a number of land plants and vertebrates was determined, including agriculturally important species such as barley, rice, wheat, potato, tomato, grape, cattle, pig, chicken and others. By analysing the obtained sequence data, a deeper insight into the biology, evolution and genome composition of the examined species became possible. Examining and comparing the data also can provide an opportunity to identify genes, which participate in the appearance of important qualitative and quantitative traits of farmed plants and animals. Based on sequence variations, the selection of DNA-based markers, which then can be applied in molecular breeding for the marker assisted selection of plants and animals with superior traits in order to develop elite varieties, is also possible. Here, we present a summary of miscellaneous agricultural genomics projects conducted at the Agricultural Biotechnology Institute, National Agricultural Research and Innovation Centre, Gödöllő, on various, agriculturally important species such as potato, grape, pepper, tomato, pea, wheat, tobacco, carp, pig, honey bee and foodborne pathogen bacteria. The outcomes of these projects would have practical considerations regarding these species.

**keywords:** agricultural genomics, crops, farmed animals, next generation sequencing, pathogenic bacteria, plant viruses

## INTRODUCTION

In the almost four decades that have gone since the full genome of bacteriophage X174 was sequenced in 1977<sup>1</sup>, the scientific discipline called genomics, of which aim is to study the structure and function of entire genomes, skyrocketed. Genomics is backed by rapidly evolving new DNA sequencing technologies, which are different to the traditional Sanger technique. Development of these new methods started in the second half of the 1990s and the first commercial DNA sequencer implementing a next generation sequencing (NGS) technology was brought to the market in 2005<sup>2</sup>. Since then, second and third generation NGS technologies appeared and were commercialised<sup>2</sup>. In contrast to the traditional experimental methods of (molecular) genetics, by which only relatively few genes can be studied simultaneously, by using NGS technologies the entirety of virtually any cellular nucleic acid compartment, such as the transcriptome, small RNAome and protein-bound nucleic acids can be examined. Since the cost of NGS was rapidly decreasing in the last ten years<sup>2</sup>, the technology became more and more affordable for the wider scientific community. While sequencing of the first human genome by Sanger technology took 13 years and about \$2.7 billion to complete<sup>2</sup>, today the genome sequence of a eukaryote can be determined in a matter of days and at around \$1,000. In parallel with this, the number of sequenced genomes increased rapidly. In June 2016, the NCBI genome database<sup>3</sup> contained genome data for 70,702 prokaryotes, 5,583 viruses, 7,250 plasmids, 8,252 organelles and 3,199 eukaryotes, of which 177 and 121 are land plants and mammals, respectively. Certainly, these land plants and mammals represent not only model but agriculturally important species too, including tomato, potato, grape,

wheat, barley, rice, cattle, pig, chicken and horse. These studies enlightened issues important in farmed plants and animals, for example evolution in tomato<sup>4</sup>, cattle<sup>5</sup>, chicken<sup>6</sup> and pig<sup>7</sup>, polyploidisation in grape<sup>8</sup>, genome organisation in wheat<sup>9,10</sup>, ruminant biology in cattle<sup>5</sup>, geographic adaptation of yak<sup>11</sup> and domestication in chicken<sup>12</sup> and pig<sup>7</sup>. Due to the decreased cost of NGS, large number of different varieties of the same species can be now sequenced, as it was implemented in the 3,000 rice<sup>13</sup> and 100 tomato<sup>14</sup> genomes initiatives or in the resequencing of large number of pig breeds<sup>7</sup>. Genome sequencing can also provide an enormous amount of information about single nucleotide polymorphism (SNP) and other structural variations of the DNA. Genomewide genotyping and selection based on these variants is already used in the practice for the so called “next generation breeding” of sheep and cattle to improve the selection of animals with better agriculturally important traits, such as disease resistance, meat and milk production and quality, reproduction and feed intake<sup>15,16</sup>. Although genomewide selection is more difficult in plants than in animals, its theory exists already, and therefore, a progress on this field seems to be realistic<sup>17</sup>.

At the Agricultural Biotechnology Centre, Gödöllő, the predecessor of the current Agricultural Biotechnology Institute of the National Agricultural Research and Innovation Centre, application of the NGS technology started in 2009, when the full genome of the three ‘Mangalica’ breeds was sequenced<sup>18</sup> representing the first fully sequenced mammalian genomes in Hungary. Here we present a summary of several genomics research projects between the period of 2009 and 2016 at our institute, in order to show how these projects can extend our knowledge about the biology of a number of species important for the Hungarian agriculture.

## GENOME PROJECTS AT THE AGRICULTURAL BIOTECHNOLOGY INSTITUTE

### Sequencing a virus resistance region in potato

Viruses are widespread throughout the world in both cultivated and wild plants. Potato (*Solanum tuberosum* L.) is the world’s fourth most important food crop, following maize, wheat and rice, and can be infected by more than 35 different viruses in the field<sup>19</sup>. One of the most detrimental viral pathogen of the cultivated potato is *Potato virus Y* (PVY) that can reduce tuber yield by up to 80 per cent<sup>20</sup>. Evolution has equipped plants with defence mechanisms to counterattack virus infections. Resistance genes (*R* genes) are central components of the surveillance system that perceives pathogens and induces cell defences. Host plants can exhibit incompatible or compatible interaction with the virus. In an incompatible interaction, the plants respond to viral infection with an extreme resistance (ER) or a hypersensitive resistance (HR) response<sup>21</sup>. ER is defined by three criteria: localisation of the virus to the primary infection site,

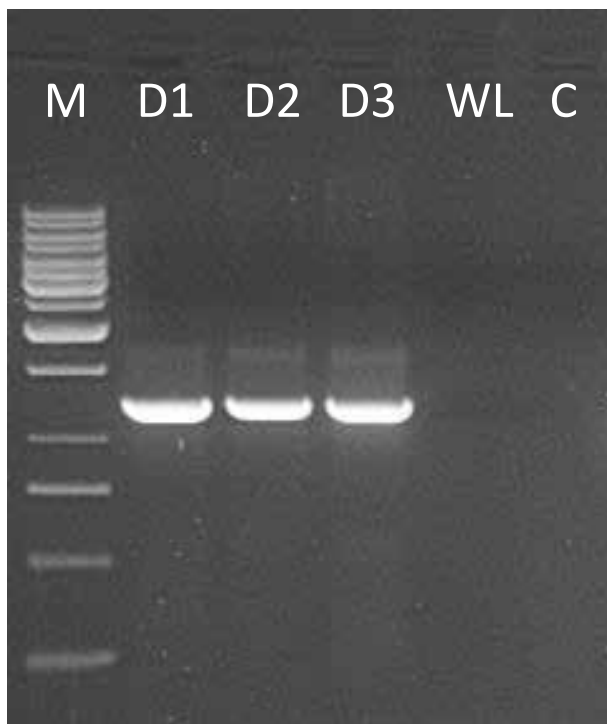


Figure 1: The PVY coat protein gene is expressed in infected susceptible ‘Desiree’ (D1 to D3) but not in resistant ‘White Lady’ (WL) potato (*Solanum tuberosum* L.) lines. M, DNA Ladder; C, uninfected ‘Desiree’.

limited virus replication, and little or no visible appearance of symptoms. In potato, ER against PVY is displayed by the *Ry* gene. The *Ry*-mediated resistance is effective against all strains of PVY and persistent as no PVY isolates that overcome *Ry* resistance are known<sup>21</sup>.

To date, three *Ry* genes have been mapped to potato chromosomes. One of them, *Ry<sub>sto</sub>*, is originated from the wild species *S. stoloniferum* and mapped to chromosome XII<sup>22,23,24</sup>. The Hungarian potato cultivar ‘White Lady’ harbours the *Ry<sub>sto</sub>* gene and is resistant to a wide range of viruses (Figure 1). To unravel the molecular mechanism underlying the *Ry<sub>sto</sub>*-mediated ER and facilitate breeding potato varieties with extreme virus resistance we aimed to isolate the *Ry<sub>sto</sub>* gene. To achieve this goal a map-based cloning strategy was employed. First, we localised the *Ry<sub>sto</sub>* gene to a 770 kb region on chromosome XII by genetic mapping. Then, a bacterial artificial chromosome (BAC) library was constructed from the ‘White Lady’ genome with an average insert size of 150 kb. Based on the *S. phureja* genome sequence<sup>25</sup> and six genetic markers, seven BAC clones overlapping the *Ry<sub>sto</sub>* region were isolated and sequenced. Comparative analysis of the sequences using the orthologous region of *S. phureja* and transformation of candidate genes into a PVY sensitive potato cultivar for functional analysis are underway.

### Virus diagnostics in plants by next generation sequencing

Virus diagnostics for perennial or woody plants, which are



propagated vegetatively, is a key tool for the production of virus free propagation material. Traditional virus diagnostic methods, such as ELISA and RT-PCR, can only detect the presence of virus of interest. For these tests, an antibody against any virus protein or sequence information about the virus genome is required. Next generation sequencing methods offer new perspectives for virus diagnostics. Since the nucleic acids of the host and the viral pathogen carry the same genetic code, sequencing of all RNA or DNA in a pathogeninfected plant sample will reveal the nucleotide sequences of both the host and the pathogen. In a single test, all viruses can be diagnosed even if they are new in a particular host or have not been described at all<sup>26</sup>. This metagenomic approach can describe the virome of the investigated plant.

Focusing on grapevine (*Vitis vinifera*), different platforms were used for the description of new viruses: Roche 454 for *Grapevine Syrah-1 virus*<sup>27</sup> and Illumina for *Grapevine virus F*. The later platform was also used to discover the viromes of a vineyard<sup>28</sup>. In these tests, dsRNAs were purified in order to eliminate host mRNAs.

RNA interference, the RNA based defence reaction of the infected plant, opened a new possibility in virus diagnosis by deep sequencing of the small RNA population of the infected plants<sup>29</sup>. During virus infection, virusoriginated small (21-25nt long) interfering RNAs, which have the same sequence as the infecting viruses, are formed by the immune system of the infected plant. When this defence process works efficiently, there are low amount of viral RNAs, but the number of viral specific small RNAs increases. Deep sequencing and bioinformatics analysis of the small RNA population extracted directly from field plants offers unique opportunity to identify viroids and viruses<sup>30</sup> even if they are alien in the plant or never described<sup>31,32</sup>.

Although NGS needs a major investment at the start, running costs are relatively high, but barcoding the libraries for pooled sequencing, improvement of data analysing pipelines and considerable reduction of the sequencing costs can make this method suitable for the diagnostics of large scale samples in the near future<sup>33</sup>. Using NGS

techniques, we made a virus diagnosis survey of grapevine plantations in Hungary and could identify and validate the presence of the recently described *Grapevine Pinot Gris virus* and *Grapevine Syrah virus*<sup>34,35</sup> (Figure 2).

### Genome wide mRNA and small RNA transcriptome profiling in *Capsicum annuum*

Plant development processes are under the highly coordinated and interconnected control of mRNAs and small regulatory RNAs<sup>36</sup>. One of the most intensively studied scientific fields in recent days is the exploration of small regulatory RNAs in plants and animals. The availability of NGS technologies opened a new way to study and understand complex RNA mediated regulatory processes<sup>37</sup>. It is inevitable for us to employ stateofart genomic sciences in order to harness the outcomes of genomewide data analyses of genomes and/or transcriptomes of important species and valuable national cultivars to understand their basic biological processes and/or improve of economically important traits.

Our genomics project to study pepper (*Capsicum annuum*), which is one of the most valued crop in Hungary, fits into the worldwide trend of studying not only model but crop plants too, in order to reveal the similarities and differences between species and provide information about the developmental aspects of economically important traits. Setting up crop sequence databases and analyses of the deposited metadata can also provide numerous economic and scientific benefits. In our project, deep RNAseq and sRNAseq technologies were used to determine the complex expression profiles of mRNAs (the transcriptome) and small regulatory RNAs, such as miRNA and siRNAs<sup>38</sup>, in different developing pepper fruit tissues. Using the obtained data sets, comparative bioinformatics approaches<sup>39</sup> were used to identify known and new pepperspecific regulatory small RNAs. The biological relevance of the promising candidate small RNAs are under investigation by wet laboratory techniques.

Comparative analyses of the ancient cultivar '*Tepin*', which has small fruits and different growing habit<sup>40</sup>, and modern cultivars are in progress in order to identify small RNAs and/or mRNAs playing pivotal roles in the development of economically important traits (Figure 3). This research will reveal not only important regulatory RNAs during the pepper organogenesis but will also provide mechanistic data on the general mode of action of small regulatory RNAs during the plant development. Identification of pepperspecific small RNAs and the connection of small RNA-mediated regulation of mRNAs to specific phenotypes would be valuable findings too. The comparative analyses of ancient and modern cultivars will provide information about the changes of mRNA and small RNA profiles during the transition of wild type traits to modern economically important traits, for example fruit size. The results might be also useful for the future improvement of economically important traits in pepper.

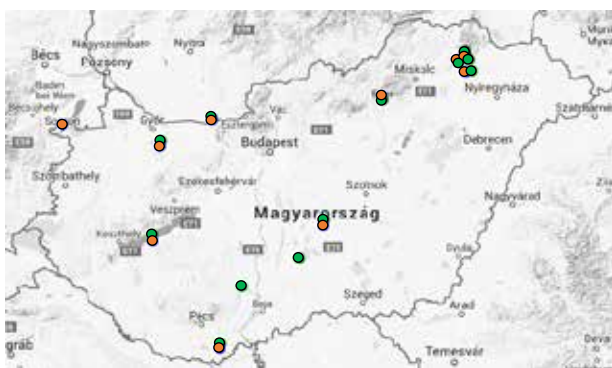


Figure 2: The occurrence of *Pinot Gris virus* (green circles) and *Grapevine Syrah virus1* (orange circles) in grapevine (*Vitis vinifera*) detected by NGS in wine regions of Hungary.



Figure 3: RNA-seq of the ancient 'Tepin' (top panel) and the modern 'Fehérözön' (bottom panel) varieties can unveil the regulatory mechanisms participating in fruit development in pepper (*Capsicum annuum*).

### Genome sequencing of grapevine

Grapevine (*Vitis vinifera*) is one of the most widely cultivated crops around the world for the production of both tablegrape and wine. It has hundreds of variations, of which only nine ('Cabernet Sauvignon', 'Chardonnay', 'Chenin Blanc', 'Merlot', 'Pinot Noir', 'Riesling', 'Sauvignon Blanc', 'Semillon' and 'Syrah') are considered as "classic" international varieties. However, since wine industry expanded enormously in particular across the New World countries in the last few decades, more and more grape varieties became widely distributed. Genome sequencing of *Vitis vinifera* 'Pinot noir' revealed that three ancient genomes contributed to the haploid grapevine genome<sup>8</sup>. This and the hybridisation-based grape breeding practices resulted in highly heterozygous varieties, whose precise origin is often not clear or disputable. Grape also has high proportion of

repetitive and transposon sequences. To discover these characters of grape varieties more fully, we have recently determined the genome sequence of twelve international and Hungarian grape varieties. Data analysis is being underway and we anticipate the discovery of such differences in the genomes of the sequenced varieties, which might be useful for the development of molecular markers for breeding, identification of varieties, and for evolutionary studies in grape.

### Amplicon sequencing in tomato and pea

Heterosis, which can positively improve a number of agriculturally important traits in crop plants, is mainly considered to involve multiple genes or QTLs. In this respect, the discovery that certain loss-of-function alleles of the *SP3D* gene caused fruit yield heterosis in tomato (*Solanum lycopersicum*) had a great significance and confirmed the overdominance hypothesis of heterosis<sup>41</sup>.

Since the effective alleles were obtained by mutagenesis and three generation breeding, we were interested whether such alleles might naturally occur in tomato and therefore could be used more directly to breed higher fruit yield varieties. To discover the genetic polymorphism of a single gene amongst large number of individuals, amplicon sequencing by NGS technologies was found to be more appropriate than traditional Sanger sequencing. In amplicon sequencing, PCR products are generated and pooled from the gene of interest from large number of individuals or varieties; then the pool is sequenced and data analysis is performed to identify DNA variations. By this strategy, the *SP3D* gene from almost 300 tomato varieties was sequenced, yielding more than 2000fold coverage of the gene per variety, which was adequate to identify even rare DNA polymorphisms. The method could be accomplished for a fraction of the cost of Sanger sequencing, in particular because the *SP3D* gene is about 5 Kbp long and therefore could not be sequenced in a single Sanger run. Although we could not identify any naturally occurring loss-of-function mutants in the selected gene, conclusions about regulatory SNPs could be drawn regarding correlation between the *SP3D* gene and tomato plant architecture. Using the same amplicon sequencing approach, the pea (*Pisum sativum*) orthologue of *SP3D* was also sequenced in more than 200 varieties, because of the interest in yield heterosis in other crops too.

### Wheat genomics

Bread wheat (*Triticum aestivum*) is one of the most widely farmed plants under temperate climates and has a great economic importance in Hungarian agriculture. Modern varieties often have a reduced performance in characters such as disease resistance or baking quality of the flour compared to older varieties, but they can be easily harvested mechanically. Thus, there are more and more efforts to combine the beneficial characters of new and old varieties in order to develop new elite wheat varieties.

'*Bánkúti*' is an old Hungarian wheat variety with a special grain storageprotein composition<sup>42</sup> and, therefore, it is suitable to produce flour with superior baking properties. We currently investigate several aspects of the wheat genome to support studies, of which aim is to incorporate the '*Bánkúti*' variety into new elite varieties with enhanced grain protein composition. Since the size of the hexaploid wheat genome is about 17 Gbp, 5times larger than the human genome, and most of it consists of repeats, its sequencing is very challenging. Thus, to compare the genome of six '*Bánkúti*' lines, in particular their storage protein genes, we have chosen to sequence only their exome<sup>43</sup>, the protein coding fraction of the genome. Highmolecular weight glutenins represent one of the most important major fractions of wheat storage proteins, encoded by highly homologous genepairs by the A, B and D genomes in hexaploid wheats. Therefore, it requires serious bioinformatics to match the protein alleles being present in the '*Bánkúti*' lines to their genes, and we are using different *in silico* tools to extract and group glutenin gene sequences in order to define glutenin gene families of different alleles. The major goal of our task is to develop putative DNA markers for the easy test of glutenin alleles in the early stage of development, as this is currently only possible by examining the protein composition of the mature grain.

In another study, we have sequenced the miRNA and mRNA fractions isolated from different stages of developing wheat grains in order to understand the involvement of miRNAs in the regulation of grain development. miRNA sequencing was performed by two different sequencing library preparation methods<sup>44</sup> (Figure 4), and now we are in a position to compare the miRNAome and the transcriptome of developing wheat grain.

#### Development of a new tool to quickly identify the function of plant genes

RNA sequencing (RNA-seq) allows quick, relatively cheap and high resolution qualitative comparison of complete mRNA profiles. Although RNA-seq assays can be used to identify differently expressed genes between any kinds of two samples, in plant biology it is most frequently applied to recognize mRNAs, which are controlled by a certain gene of interest. Comparing the transcriptome of a wild-type line of the *Arabidopsis thaliana* model plant and that of an *Arabidopsis* line in which the gene of interest is mutant, we can detect the mRNAs, whose expression is controlled by the gene of interest. However, generation of mutant lines are time consuming and frequently challenging since many genes are present in multiple, often functionally redundant, copies in the genome, thus inactivation of all of them are required for

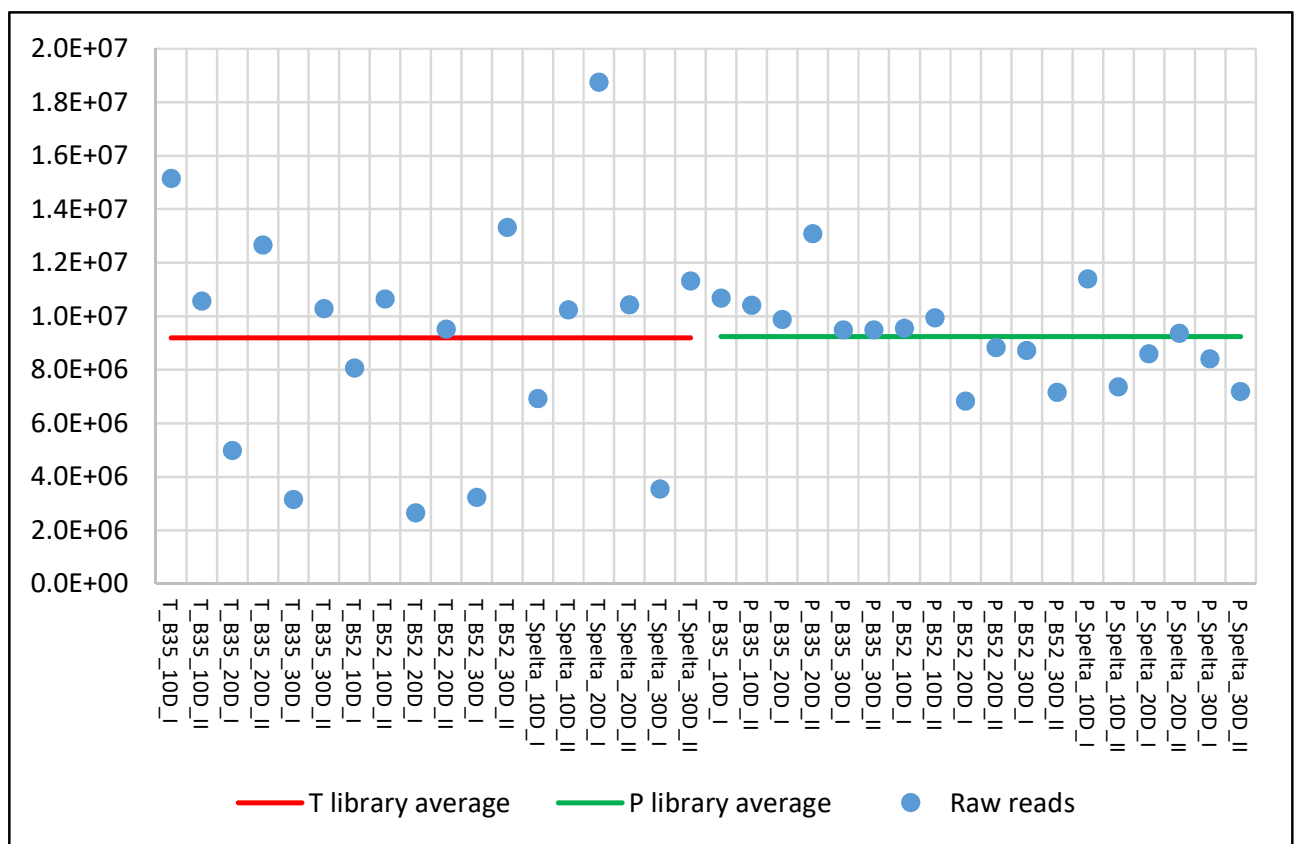


Figure 4: The number of raw small RNA reads and their average obtained by NGS of libraries constructed from total RNA (T library) and purified small RNA fraction (P library) in wheat (*Triticum aestivum*).



functional studies. Moreover, inactivation of essential genes is not possible.

Virus-induced gene silencing (VIGS) in the model plant *Nicotiana benthamiana* offers a quick and versatile alternative to the generation of mutant lines<sup>45</sup>. Using VIGS, we can inactivate multiple genes parallelly and thereby circumventing the problem of redundancy. Moreover, we can locally inactivate essential genes by VIGS. Briefly, if we insert a piece from the gene of interest (or pieces from genes of interests) into *Tobacco Rattle Virus*, and infect a *N. benthamiana* plant with it, the recombinant virus will systematically infect the plant. However, virus infection activates a defence mechanism called RNA silencing, which attacks the virus and selectively degrades the mRNAs of the plant gene, whose piece was inserted into the virus. Thereby in the upper leaves the gene of interest will be inactivated. Relevantly, more than one gene can be inactivated parallelly by VIGS<sup>45</sup>.

We hypothesized that comparative RNA-seq assay of VIGS inactivated lines can be an efficient tool to identify the function of plant genes. As a proof-of-concept experiment, we generated *N. benthamiana* plants in which only the phytoene desaturase gene (PDS) was inactivated by VIGS (it was the control line), and a second line, in which both the PDS and UPF1 genes were silenced<sup>46</sup>. UPF1 is an mRNA binding protein, which plays a critical role in a specific RNA metabolic pathway (called nonsense mediated mRNA decay, NMD) that eliminates aberrant RNAs and protects plant cells from viral pathogens<sup>47</sup>. Previously, in other laboratories the UPF1 controlled mRNAs by RNA-seq assays in *Arabidopsis* was determined<sup>48,49,50</sup>. mRNA samples from the PDS-silenced *N. benthamiana* control, and the PDS/UPF1 silenced test plants were isolated and sequenced, and then mRNAs, which were differentially expressed between the control and the test lines were identified. Preliminary results confirmed that VIGS lines can be used for comparative RNA-seq assays. Statistically significant overlap was found between the UPF1-controlled genes of *Arabidopsis* and *N. benthamiana*.

Our results indicate that RNAseq of VIGS lines is a realistic alternative approach to experiments that employ mutant lines. Moreover, the obtained data confirmed that a conserved set of genes are regulated by UPF1 in *Arabidopsis* and *N. benthamiana*. Furthermore, we could identify UPF1-regulated genes, which are absent in *Arabidopsis* but are present in most other plants. As VIGS-mediated gene inactivation offers many advantages relative to the generation of mutant lines, we believe that comparative RNA-seq assays of various VIGS plants can help us to understand the function of plant genes. This knowledge could be also used to accelerate plant breeding.

### **Application of the third generation Nanopore MinION sequencer in plasmid biology**

Combating the antibiotic resistant pathogenic bacteria

began in the early antibiotic era. Antibiotic resistance genes often occur in mobile genetic elements and their horizontal spread is probably facilitated by the general use of antibiotics. One of the most efficient mechanisms in horizontal gene transfer is conjugation, which is widespread among naturally occurring plasmids. Large resistance plasmids are the major factors in rapid acquisition of multidrug resistance (MDR) by pathogenic bacteria<sup>51</sup>. The broad-host-range conjugative plasmids of IncA/C family are the most prevalent MDR vectors among enteric bacteria, including the potential zoonotic foodborne pathogens *Salmonella*, *Klebsiella*, and *Escherichia* causing a threat for human and animal healthcare<sup>52,53</sup>. Comparative genomics of IncA/C plasmids revealed that their conserved backbone, which encode genes of maintenance and conjugative transfer, share a more than 99 % homology, while their accessory modules are resistance islands (RIs) that are highly variable and often composed of transposons and integrons<sup>54</sup>.

The presence of repetitive elements on plasmids and bacterial chromosomes pose a serious challenge for NGS since repeat regions longer than a read are barriers for sequence assembly. The recent developments with third generation sequencing platforms can result in reads long enough to span repetitive elements and therefore facilitate to solve assembly problems. Two decades ago, it was suggested that DNA molecules could be sequenced by monitoring

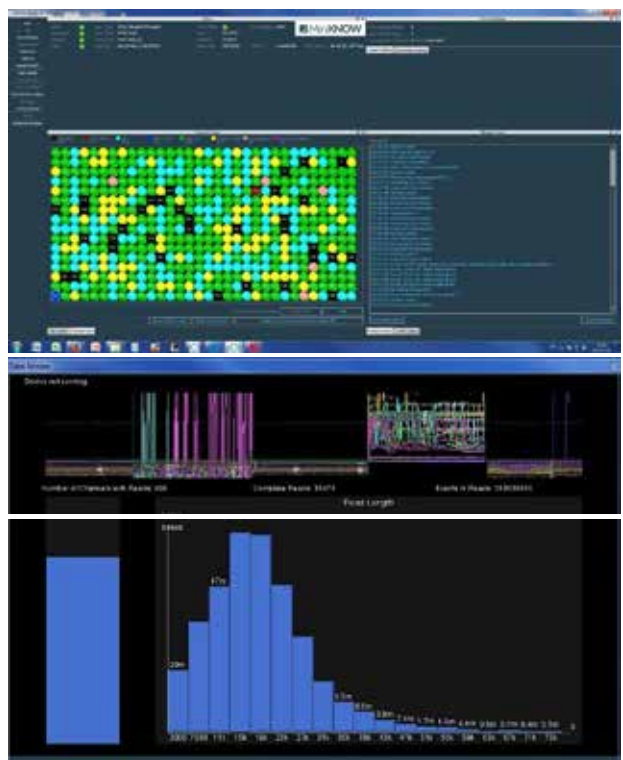


Figure 5: Sample pictures of the computer interface of MinION sequencing that show the active protein pores in green (top panel) through which DNA strands pass, and the electric signal produced for each passing base (middle panel) from which reads with different length are computed (bottom panel).

their movement through nanopores<sup>55</sup>. The MinION device developed by Oxford Nanopore Technologies (ONT) is a nanopore-based sequencer in which  $\alpha$ -haemolysin pores are embedded in a membrane<sup>56</sup>. DNA molecules passing through the pores generate sequencedependent alterations in the ionic current that can be used to deduce the sequence<sup>57</sup> (Figure 5). The main advantages of the MinION platform over other NGS technologies are the production of very long (there is no theoretical limit of read length) and unbiased reads, low investment cost per device, portability, flexible run and reduced turnaround time, while its major limitation is the relatively high error rate. Even though the accuracy of MinION reads generally remains below 90%, they are suitable for *de novo* assembly of complete genomes<sup>58</sup>, scaffolding NGS contigs<sup>59</sup>, metagenomic studies and real-time epidemiological investigations<sup>60</sup>.

Participating in the MinION Access Program initiated by ONT in 2014, the technology was used to sequence large (>170 kb) single copy IncA/C plasmids. We have constructed the complete sequence of two “archaic” plasmids isolated from hospital samples in the late 1960s and identified their spontaneous rearrangement products too. Both plasmids carry RIs composed of complex array of transposons that include numerous resistance genes. The comparative analysis of these plasmids suggested that they represent an ancient form of the IncA/C lineage. It was also revealed that the observed plasmid rearrangements are associated with transposons residing on RIs. Mapping of whole plasmid sequences and rearrangements may elucidate the origin of members of the IncA/C family, and help to understand plasmid evolution. MinION platform appears to be a valuable tool in bacterial genomics and it will be also applied for generating complete genome sequences in the future.

### Genomics of tolerance against *Aeromonas hydrophila* in carp

Worldwide, the most important cultured freshwater fish species are carp, tilapia, and catfish. The farming of common carp (*Cyprinus carpio*) in Europe is highly concentrated to central and eastern countries. In Hungary, carp has been traditionally farmed since the 19th century.

*Aeromonas hydrophila* is a gram negative bacterium associated with diseases mainly found in freshwater fish and amphibian. It causes substantial mortality in fish farms worldwide and is one of the most important pathogens of carps<sup>61</sup>. Defence against pathogenic microorganisms in animals occurs by either resistance or tolerance<sup>62</sup>. Both mechanisms can increase the fitness of an infected individual, but resistance does limit pathogen fitness, whereas tolerance does not.

NAIK-HAKI (Research Institute for Fisheries, Aquaculture and Irrigation Szarvas, Hungary) maintains a living genebank of common carp populations and we have used families from that genebank with tolerance against *Aeromonas*

*hydrophila*<sup>63</sup> in our experiments. Bacterial challenge with *Aeromonas hydrophila* was performed in genetically different carp families to study nonspecific immune responses and the level of specific antibodies<sup>64</sup>. Phagocytic activity of leukocytes, plasma lysozyme activity and specific antibody titre were higher in the resistant than in the sensitive families following infection with *A. hydrophila*.

The genetic background of the tolerance against *A. hydrophila* is still unknown. However, a network biology approach identified differential gene expression in carp head kidney, which is an important immune and lymphatic tissue in fishes, between tolerant and susceptible phenotypes in response to the pathogen. In that study, global gene expression response to *Aeromonas* sp. infection was investigated in Atlantic salmon, using a custom cDNA microarray consisting of over 4000 different amplicons. Several informative genes were identified and revealed to encode humoral components of the innate immune system. Other genes identified in this study were not previously associated with infection. Several genes with no known homologs were also uncovered<sup>65</sup>.

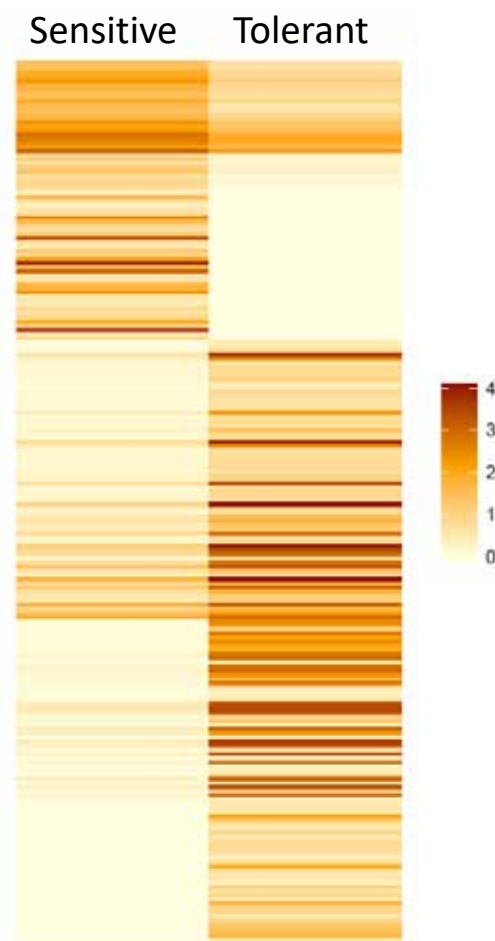


Figure 6: Heatmap of differentially expressed genes in sensitive and tolerant carp families challenged by the bacteria *Aeromonas hydrophila*. Each horizontal line represents a single gene; darker colour indicates stronger expression.

Our aim was to find genetic markers/genes expressed differently without experimental bacterial challenge in carps of different genetic background using NGS methods. Three representative individuals were selected from both tolerant and sensitive families. Total RNA from the main immune tissues head kidney and spleen were purified. A conventional mRNAseq analysis was performed followed by bioinformatic analysis. Differentially expressed genes were selected based on the criteria of displaying a larger than 2fold difference (adjusted p-value < 0.01) between the tolerant and susceptible animals (Figure 6).

Our results showed that more than one hundred transcripts were differently expressed in both tissues. Further bioinformatical analysis is in progress to investigate those factors/genes which express differently and are functionally important in the defence against the pathogen *A. hydrophila* in carp.

### Apicultural genomics

Honeybee (*Apis mellifera*) is an important animal species for humans. It has been maintained, fed and transported by beekeepers for a long time back in history. The products of honeybees have been used as food and medicine for hundreds and thousands of years<sup>66</sup> and bees are also essential in the pollination of many plants and agricultural crops<sup>67</sup>. Moreover, the species is an important experimental organism to study the development, behaviour and genetics of animals.

A suite of genomic tools has been developed for honeybee, including a nearly saturated genetic map based on RAPDs<sup>68</sup>, microsatellites<sup>69</sup> and AFLPs<sup>70</sup>, and a recently completed genomic sequence<sup>71,72</sup>. The assembly and annotation of genome sequences had greatly enhanced our knowledge

about the biology, phylogenetic relationships and population structures of the sequenced species, and contributed to our understanding of human biology too. However, since only a few Metazoan genomes can be considered as complete, there is still room for improvement of most genome assemblies.

We have sequenced the genome of Hungarian honeybee specimens, which resulted in up to 13x median autosomal coverage. Comparative analyses of the genomes of Hungarian and other available bee specimens are underway. About seventeen million SNPs, of which approximately eightyeight thousands are specific to Hungarian bees, were identified. Several hundred thousands of INDELs and STRs were also identified. Hopefully, the identified genome variations can be used to develop molecular markers for species and subspecies identification, recognition of valuable behavioural traits and tolerance against bee pathogens (Figure 7).

### 'Mangalica' pig genomics

The first pig (*Sus scrofa*) genome assembly was released in 2009<sup>73</sup> and mainly based on a few international breeds. However, local/rare/old breeds are also important for niche meat industries and therefore have an impact on local economics and communities. Thus, the deepest possible knowledge about their genetics and genomics is desirable to fully exploit their potential. 'Mangalica' is such an old breed, which has been developed in the Carpathian Basin and is being kept for a long time not only in Hungary, but in also other countries, for example Austria, Germany, Romania, and Switzerland. It was also introduced into Britain and the USA too, in which countries and in Japan 'Mangalica' pork is a highly valued product, while in Spain 'Mangalica' legs are used for ham production.

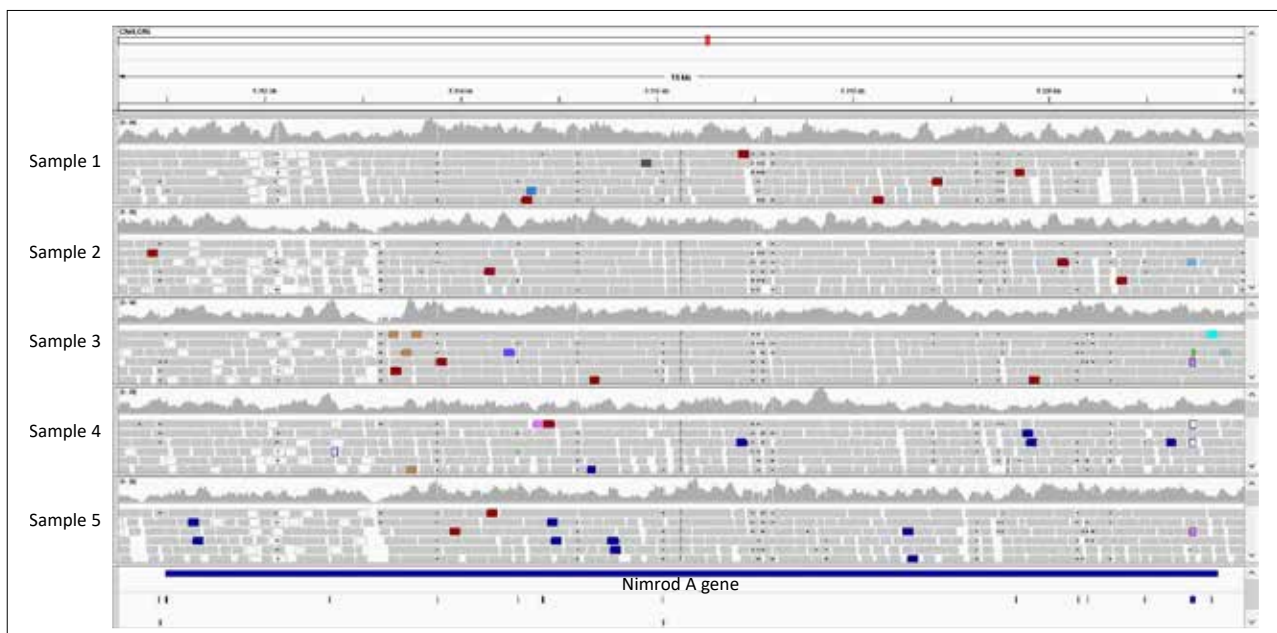


Figure 7: NGS reads (grey rectangles) aligned to the Nimrod A gene of five genome sequenced Hungarian honeybee (*Apis mellifera*) samples and the positions of designed molecular markers (coloured boxes).



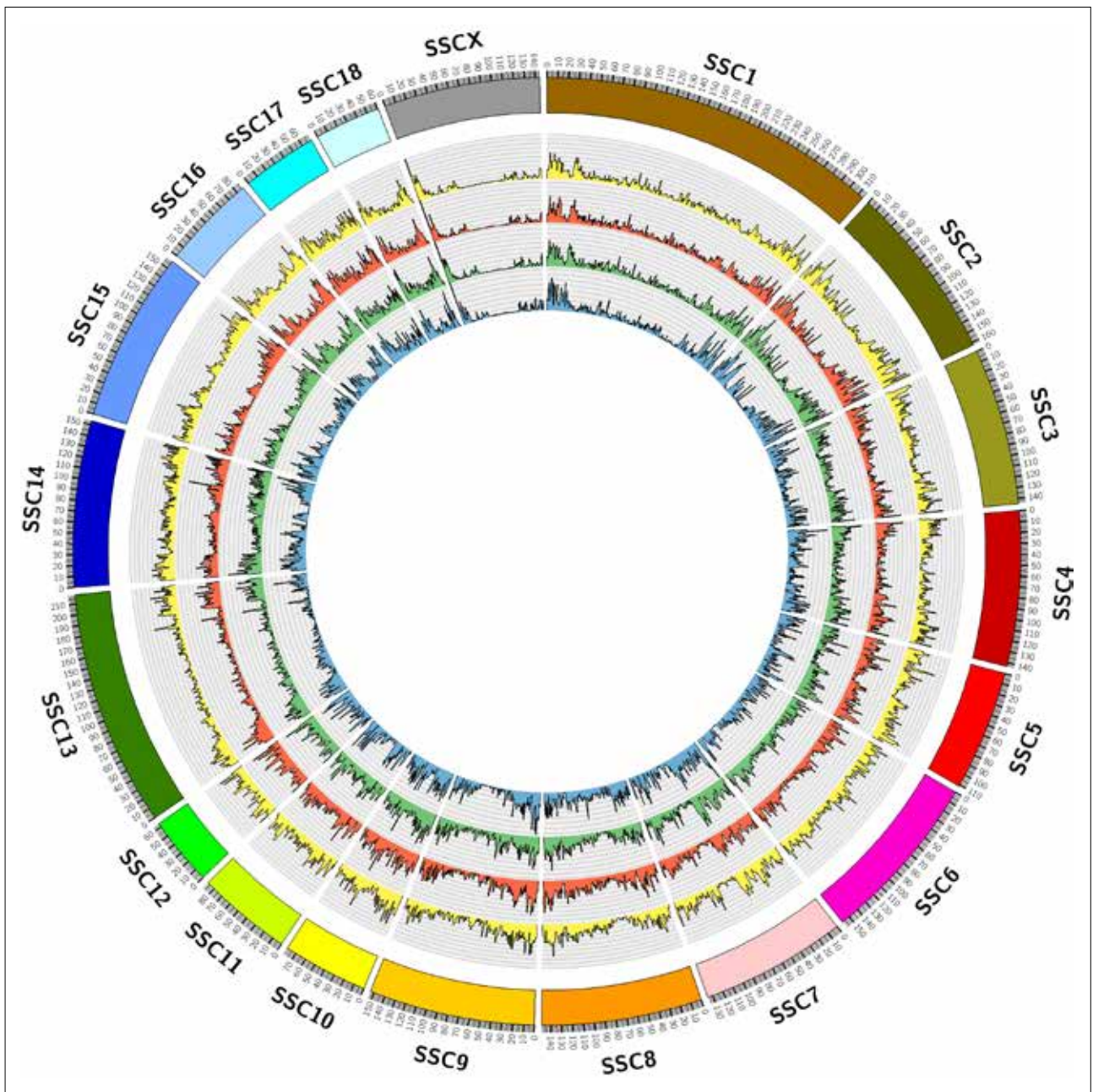


Figure 8: The distribution of SNPs on the chromosomes of the 'Blond', 'Red' and 'Swallowbelly' *Mangalica* (yellow, red, and green circles, respectively) and the 'Duroc' (blue circle) breeds.

To provide a genomic background for the Hungarian '*Mangalica*' industry, the genome of a male animal of each '*Mangalica*' breeds, 'Blond', 'Red' and 'Swallowbelly', and of a 'Duroc' male for comparison, was sequenced by using Illumina's pairedend technology during a project run by the MANGFOOD consortia. The sequencing resulted in more than 10-fold coverage of the genomes of the individuals<sup>18</sup>, which was deep enough for a detailed analysis. By employing bioinformatics, the obtained genome sequences were analysed for the presence of small (Figure 8) and large structural differences between the breeds<sup>18</sup>. Compared to the lean 'Duroc' breed, '*Mangalica*' is a

fattytype of pig with marbled meat of high market value, thus the genomic differences between '*Mangalica*' and 'Duroc' were studied in details at the nucleotide level (single nucleotide polymorphism, SNP), with particular emphasis to fatrelated genes. A number of '*Mangalica*' specific nonsynonymous SNPs, which causes amino acid change in the protein coding exons of genes, were identified in genes associated with fatrelated QTLs and pathways<sup>18</sup>. Since nonsynonymous SNPs can influence protein function, they might have a particular role in the fatty body and meatcharacter of '*Mangalica*' pigs<sup>74</sup>. In addition to the genome sequencing, we also performed a largescale

genotyping of about sixty thousand SNPs in 78 'Mangalica' and 60 other pigs of different breeds. The vast amount of data obtained in these projects is a rich source of genomic information for developing DNA-based markers for different purposes such as molecular breeding and meat adulteration, phylogenetic and population genetic, genomewide association and genomic selection studies, all having of a great potential for agricultural practice.

## ACKNOWLEDGEMENT

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# THE SITUATION OF YOUNG FARMERS IN HUNGARY

## - THE RESULTS OF TWO STUDIES -

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### INTRODUCTION

In the framework of cooperation between Agricultural and Rural Youth Association, Hungary (Agrya) and the Hungarian Central Statistical Office (KSH), we launched a joint study in 2012 on the Hungarian situation of young farmers. As a result of our joint study, the niche publication presents how their number, demographic composition and their farming circumstances had changed in the period since the general agricultural census (GAC) in 2000. An online survey by a questionnaire was also a part of the study about the correlations of generational change in agriculture by questioning young people who are working, establishing businesses in the sector or envisage their

future in it. In 2014-2015, work continued by studying young farmers in the horticultural sector in cooperation with AgroStratégia. We show the results, important conclusions of the two studies in the article.

### I. THE SITUATION OF YOUNG FARMERS IN HUNGARY

#### *The number of farms, the proportion of young farmers*

In Hungary between 2000 and 2010, the structural realignment of agriculture involved a significant reduction of the number of farms. A part of those who liquidated their farms en masse remained in the sector in the form of business organisations but most of them “got too old”

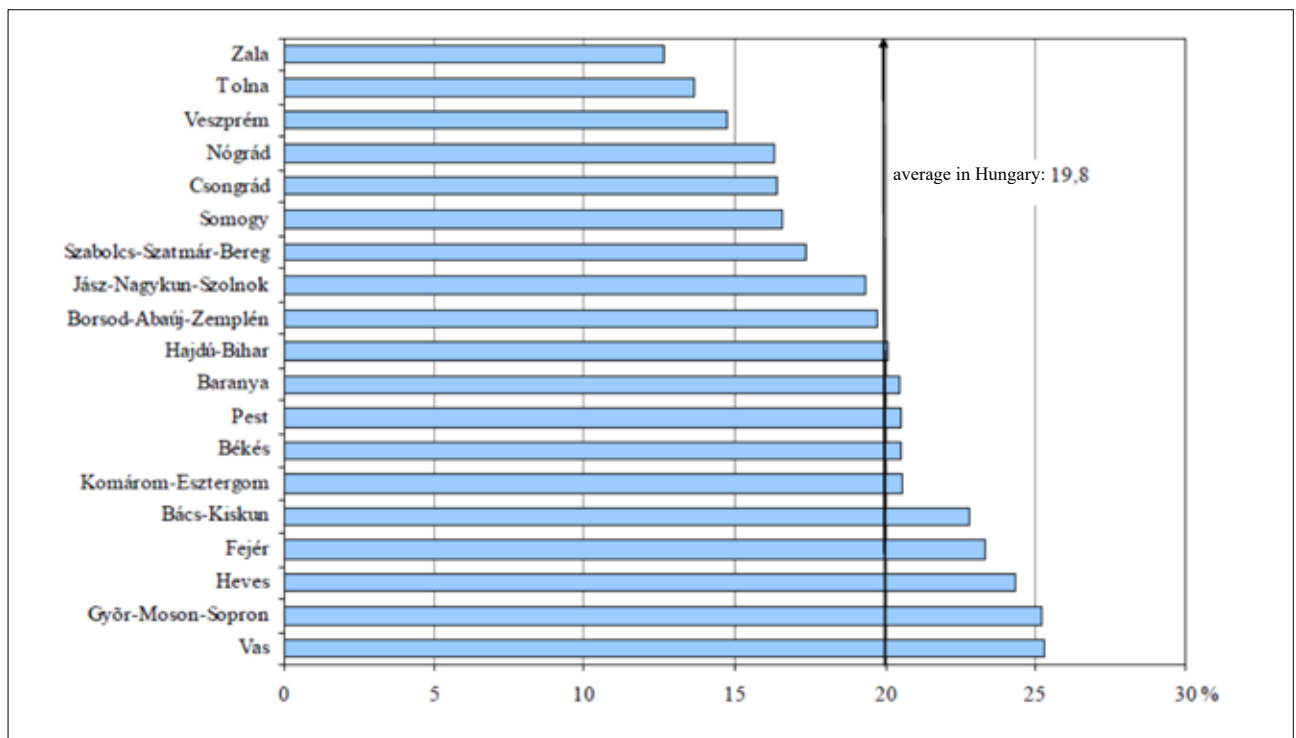


Figure 1: The rate of business organisations with less than 10 people with a young leader, 2010

or abandoned agricultural activity because of another reason (e.g. lack of funding, problems with selling).

According to the general agricultural census (GAC) in 2010, almost 568 thousand individual farms and almost 9.2 thousand business organisations conducted agricultural production or service activity, 40% less than at the time of the GAC in 2000. During this 10-year-long period, these two forms of farming changed in opposite directions: while the number of business organisations had increased by almost a third, the number of individual farms had decreased by four-tenths.

In 2010, almost three-quarters of business organisations doing agricultural production employed less than 10 people, their number had increased by 34% in ten years. In almost fifth of these – a bit more than 6000 business organisations –, the leader of the farm was younger than 40 years old.

In 2010, a little more than 76 thousand farmers who were younger than 40 years old conducted agricultural production on individual farms, half than ten years before. The number of young farmers decreased in Nógrád, Győr-Moson-Sopron és Heves Counties the most and in Szabolcs-Szatmár-Bereg County the least. In 2010, the age composition of individual farmers was more disadvantageous than in 2000, individual farms were characterised by ageing instead of generational change. In 2010, the proportion of young farmers under 40 barely surpassed 13%.

In EU statistics, young farmers are those who are younger

than 35 years old. It is true for this demographic that between the census of 2000 and 2010, adversarial processes had happened from the perspective of generational change: the proportion of young farmers had decreased by a somewhat bigger rate than the EU average. In 2010, Hungary was in the 7<sup>th</sup> place among the EU-27 regarding the number of farms of those who are under 35, while it was in the 3<sup>rd</sup> place ten years earlier. In 2010, those who are under 35 used 11 hectares of agricultural land on average that is still less than EU average (14 hectares).

### Composition by sex

During the ten years studied, the number of men among young farmers had decreased much more (by 54%) than the number of women (by 26%), therefore the rate of men had decreased by 7 percent on average between 2000–2010. Men-women ratio shifted the most, around 10 percent in the age group of 20–24 and 25–29 years olds to the advantage of women. This tendency can be observed at those under and over 40 but ratios changed by much less – less 2 percent on average.

The good news is that the ratio of women increased in every county among young farmers between 2000–2010.

### Professional qualifications

The composition of under-40 young people leading business organisations with less than 10 people is somewhat

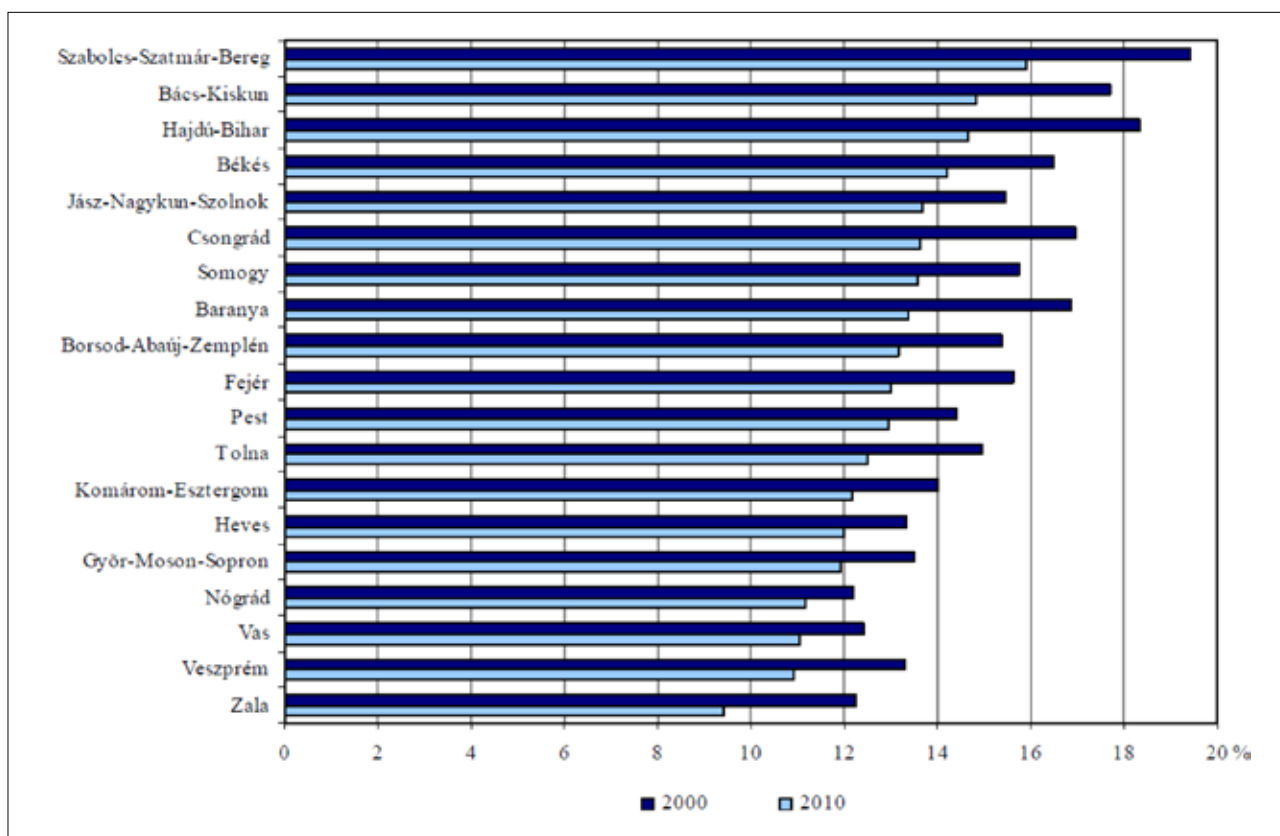


Figure 2: The proportion of young farmers per county



different than in the case of older leaders. In 2010, 37% of young leaders had a qualification from higher education, 27% from secondary education and 8% from primary education but almost every fifth business organisation leader only had practical experience and almost 7% have not gained even that. Among the older farmers, the rate of those who had agricultural qualification from secondary

education was lower (24%) and every fourth had only practical experience.

The agricultural schooling level of individual farmers is much lower-levelled. In 2010, the rate of those with higher education diplomas was around 3% in the case of both young and older farmers. The rate of the former ones had increased by around 2% but the proportion of the

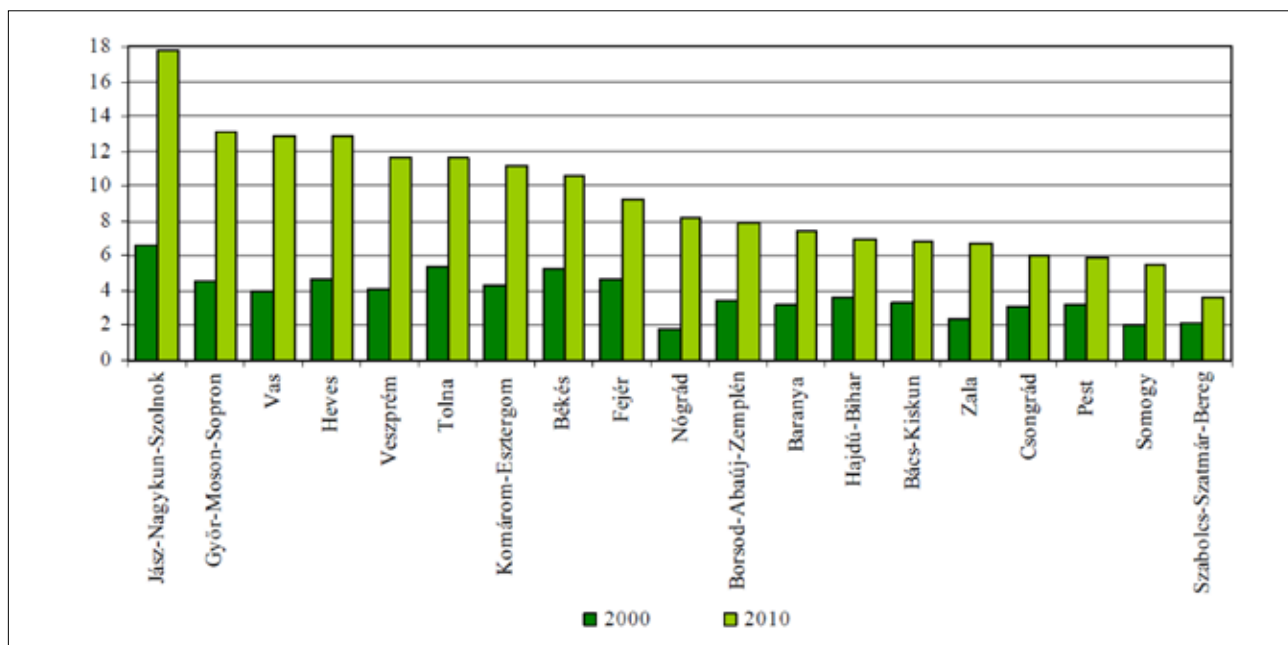


Figure 3: Average size of arable land of young farmers per county

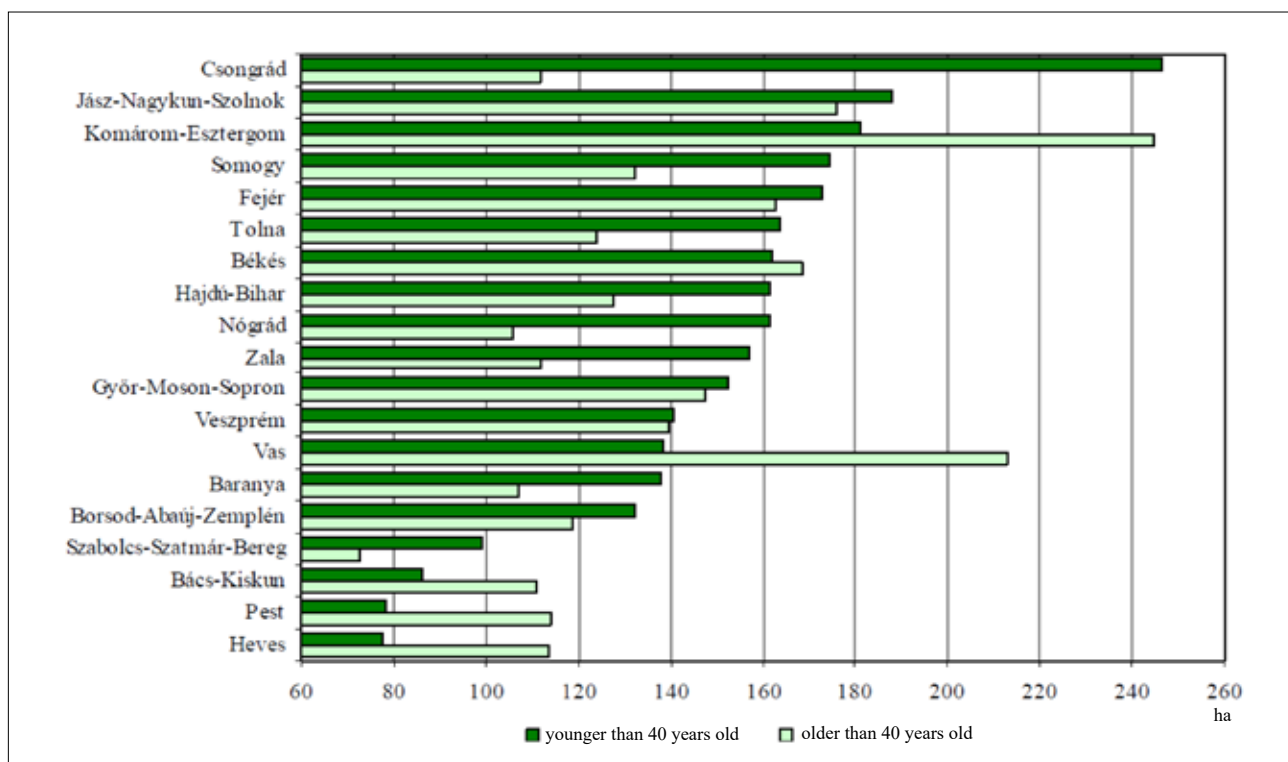


Figure 4: Average size of agricultural land of business organisations with less than 10 people according to the age of its leader per county, 2010

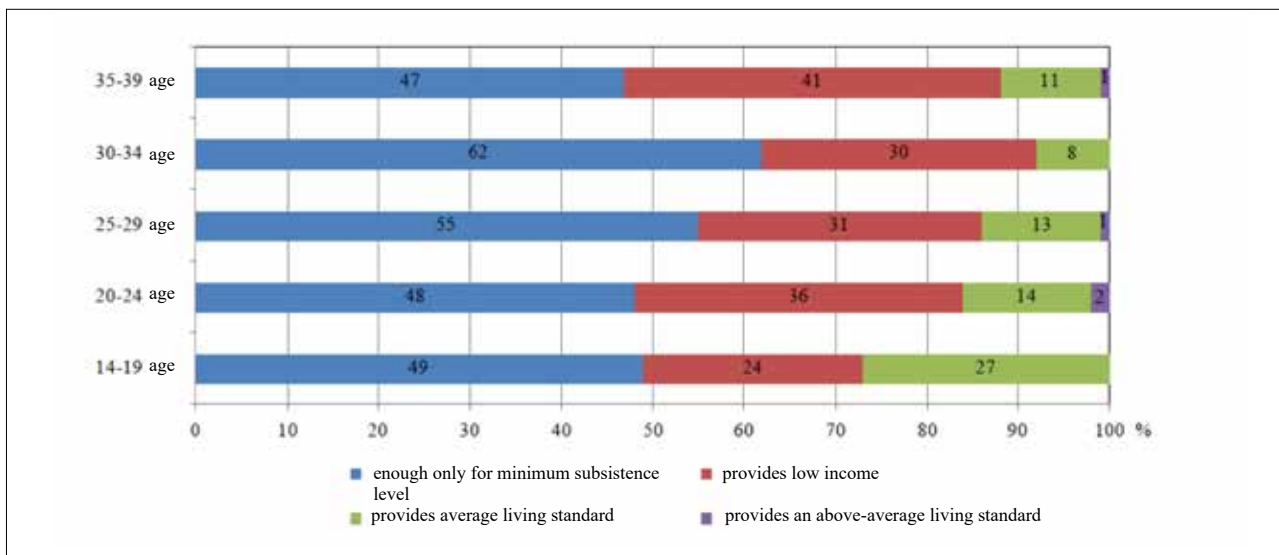


Figure 5: View on income situation by age group, 2012

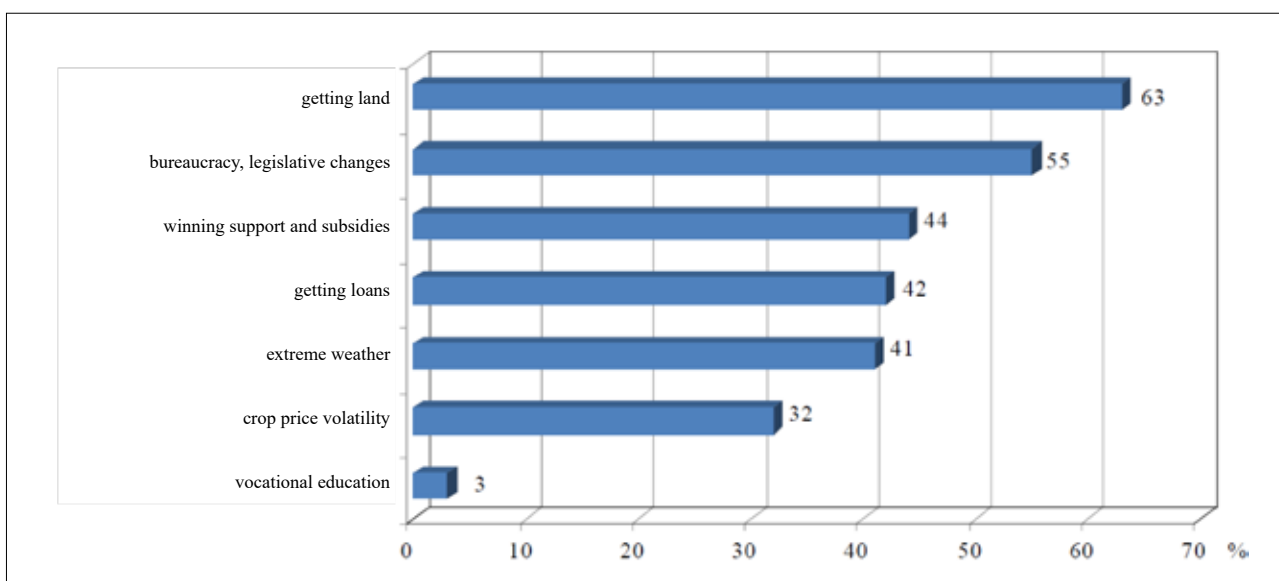


Figure 6: Main obstacles hindering farming, 2012

latter ones increased by even less during the 10 studied years. The rate of farmers with secondary level education had not really changed in either age group: 9% among those under 40, and almost 6% for those who were 40 or older. In 2010, most of the individual farmers, almost seven-tenths were farming without any qualifications, based only on practical experience, while this rate was close to 80% among the older ones.

### Land use

The size of agricultural land used by youth had not changed significantly in the country. In 2010, an individual farmer under 40 cultivated more than twice the size of agricultural land on average than 10 years before. The crop structure of field crops at individual young farmers was dominated by cereals. Due to the general appreciation of oilseeds

(sunflower, rapeseed), the proportion of industrial plants had increased significantly (by 10 percent) between 2000-2010. The structural shift during the ten years resulted in profile clearing; the composition based on production type had been realigned in a way that the weight of exclusively plant-cultivating farms had increased by the same rate that the weight of mixed-profile farms decreased. Composition based on the goal of farming significantly shifted towards those who primarily product to sell.

### Online questionnaire survey

Our primary goal with the questionnaire survey was to examine what are the personal motivations, expectations that characterize young farmers behind the tendencies shown by the data of GAC. We wanted to study among others what are their biggest obstacles in farming, what

is their opinion on income and how open are they to innovation. Questionnaires of more than 500 young farmers have been processed.

In the years when calls for applications for young farmer start-up support were open, the business-starting will of youth who envisaged their future in agriculture increased. Due to this, a significant amount of businesses were launched both in 2008 and 2010.

The number of those who chose agricultural activities was influenced significantly by the income situation in the sector. To make it appealing, there is a need for support especially at the start to reach the wanted income level. According to most respondents, income in the first years of farming is barely enough to sustain themselves, only a tenth of them said that their income from agriculture provides an average mean of life. The opinion on current and future income situation is much more advantageous, respondents have positive expectations, they count on the increase of income from agriculture.

Getting land was regarded to be the biggest problem among the obstacles of farming, bureaucracy and legislative changes were indicated at the second place by responders. There is an intensive need among farmers for preferential loans, interest subsidies and guarantees for loans.

The will of young farmers to innovate, their positive view on the future is supported by that 85% of those who were asked want to invest to their farm in the next five years. Those who have qualification from secondary education have the most will to expand (98%), this rate is 88% for those who had primary education and 82% for those with higher education.

Two-thirds of those who were asked want to expand their farming activity in the next five years by alternative income-gaining activity (e.g. processing, bioenergy production, tourism service). Young farmers have the will for diversification, they are open to new, auxiliary activities beside farming.

## II. YOUNG FARMERS IN HORTICULTURE

Our joint study with KSH and AgroStratégia in 2014/2015 focused on those who have found their call in horticulture and wants to describe the sector of horticulture. Based on the results, we get a glimpse of employment opportunities in horticulture, we tried to uncover the motivation of those concerned, their openness to innovation and developments, and we also tried to get answers to the reasons of low will for cooperation. The joint study by AGRYA and AgroStratégia consisted basically of a survey by questionnaire and deep

interviews. The wider contextualisation and appropriate interpretation was grounded on the analysis of KSH that describes the general situation of sectoral actors leaning on official statistical sources.

### Main conclusions of the study

At the time of the last farm structure census (FSC) in 2013, a total of 491.3 thousand farms were registered. Beside the 8800 business organisations, 482.5 thousand individual farms conducted agricultural activity. The number of farms decreased by 15% relative to the previous census in 2010 and halved compared to 2000, primarily the number of individual farms diminished. The number of agricultural establishments listed as horticultural ones that are relevant from the perspective of the study (according to typology: 2. specialist horticulture, 3. specialist horticulture outdoor and 163. specialist field vegetables) was a total of 86.6 thousand, 82% of which were cultivating plantations (mainly fruits and vegetables), 11% of various horticultural activities (typically cultivating in greenhouses, flowers and ornamental plants), and 7% with arable land production. Between 2010 and 2013, the number of agricultural establishments of this type had decreased by 14%, and 21% since the start of this millennium. The number of workers in this sector decreased much more moderately than in the case of all the farms. Furthermore, the number of specialised horticultural establishments had decreased the least during the 13 years. Generally, there has been a kind of specialisation, as a result of the realignment, the share of horticultural establishments out of all the agricultural establishments had increased from 11% in 2000 to 18% in 2013.

The share of young gardeners was 12% in 2013; there were a total of 10.5 thousand establishments led by someone younger than 40 years old. There is no significant deviation related to other farms because this rate is 13% in their case.

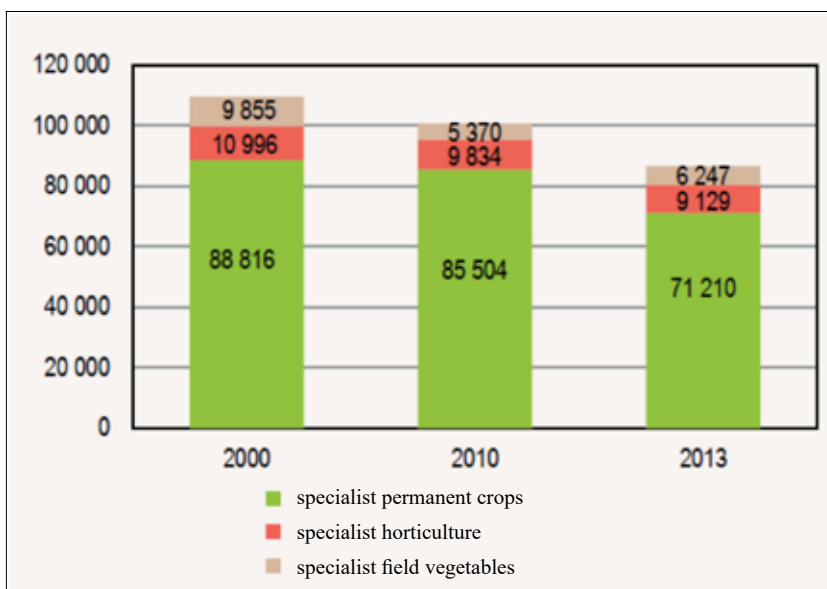


Figure 7: The number of agricultural establishments categorised under horticulture



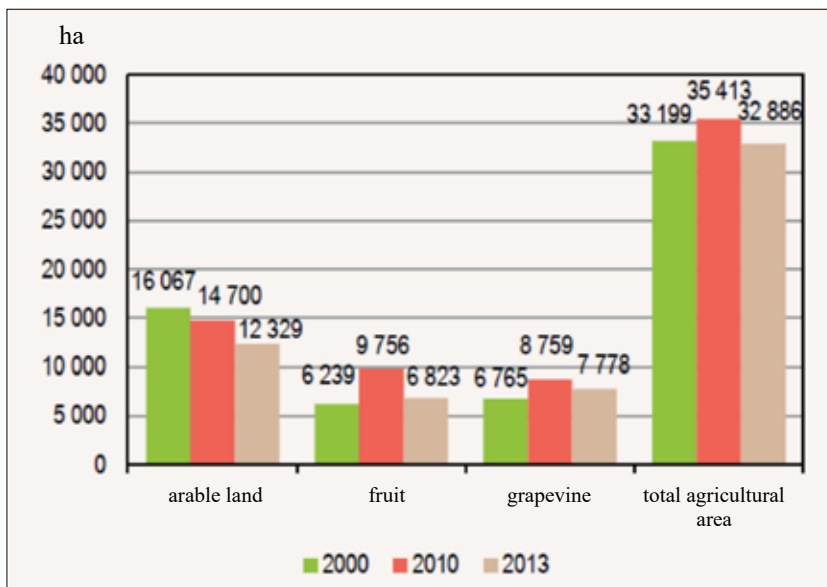


Figure 8: The average size of agricultural area among young farmers

The share of youth was the highest for field vegetables (19%), it was 16% for horticultural establishments and the lowest for permanent crops (11%). The share of fruit farmers who are plenty and have the biggest weight was average (13%) while it was 9.7% in the case of the also significantly numerous vineries.

- The average farm size of young farmers is somewhat bigger than the average of all farmers.

- The employment potential of young gardeners is significantly higher than average but ageing is also apparent here as it is typical to the whole of agriculture.

- The education level of young gardeners is significantly better compared to other farmers, even to all gardeners. Among them, the share of people with secondary (10%) and higher educational qualifications (5,6%) was higher.

- Horticultural establishments used 195 thousand hectares of agricultural land in 2013. 17% of land used for horticulture was cultivated by young farmers.

The average age of respondents of the online questionnaire was 33 years, four-fifths of them were men. Most of them were individual farmers.

- More ownership changes can be expected in the next five years than in the previous five years.

- 38% of those who currently sell only in Hungary plan to export in the next five years.

- Approximately two-thirds of respondents resort to advisory services (mostly in the field of pest control, applications for support and subsidies, farming technology, administration and other (e.g. ecological farming, agri-environmental farming)).

- 73% of the farms represented by the respondents had investment in the last five years. Those who did not invest in the last five years mainly identified a lack of own resources, the uncertainty of the future and the lack of external funding as reasons.

- The overwhelming majority (94%) plans investment in the next five years. Those who invested in the last five years are more inclined to do so again (95%) than those who did not. The average financing of the planned investment: 43% own resources, 12% loan, 45% support.

- The majority of respondents (57%) is not a member of a producer organisation. The advantages identified by members: common market action, better input material prices, foreseeable payment terms, security, better means of selling, plus points for support or subsidy applications. Reasons by non-members: there was no need, there is no producer organisation nearby, bad experiences with functioning, over-administration, lack of trust.

- 74% of those who do not use renewable energy sources plan to do so in the future.

- 82% of respondents plan to hire new employees in the near future.

- The most important conditions to expand the activity and to create new jobs were identified as foreseeable market and economic environment, the availability of investment support, preferential loans, making land buying and lease, support for employment and simplifying the administration of employment.

The results of the joint survey support the fact that the horticultural sector (especially farms led by young farmers) has an important role in creating jobs and agricultural output. Young gardeners plan investments and expansion, support available between 2015-2020 can provide a good basis for that.

### III. THE HARDSHIPS OF GENERATIONAL CHANGE

Statistics unequivocally show that similarly to most EU member states, the Hungarian farmer society is ageing, there are not enough young people in the sector. Although there are some young people who start farming without any antecedent, from ground zero, but they are in minority. The real venues for generational change are those family farms where farming has been conducted for many decades. There are a lot of hardships even in the latter case. We see the biggest problem in that they usually do not talk about that in the family or business, they are not preparing to change ownership. But with conscious preparation, the process could be made more smooth. There is a lack of good examples, too: there are only a few farms where changing the baton was done without

hiccups. The hardships are well-represented by that they encompass a wide area: from the proper knowledge on duty rules through sustaining supported investments to even emotional, psychological aspects. Showing the way, examples or a simple legal forum where they can talk about these could be welcome in such a situation. It is apparent that external help is needed the most here.

Regarding the financial aspect, there are more options for support to stimulate young farmers (e.g. young farmer start-up support, higher support intensity for investments, etc.), these were and are available in the coming years. We hope that on the long term, these measures can significantly help generational change. More should be done on loaning start-up businesses because this is still the weakest leg of financing.

In order to solve problems hindering farming, starting a farm, young farmers formulated various suggestions during our previous surveys that reflect on the factors that mostly

make their situation hard. The remarks can be basically divided into three main groups: getting land, financing, and legal, regulatory environment are those areas where changes are mostly needed.

Beside these, professional, community-building events are what can help this process where young farmers can gain strength mainly from each other.

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The publications are available at [www.agrya.hu](http://www.agrya.hu), [www.ksh.hu](http://www.ksh.hu) and [www.agrostratega.blog.hu](http://www.agrostratega.blog.hu).

# TEN YEARS AFTER EU ACCESSION: THE AGRICULTURAL PERFORMANCES OF NEW MEMBER STATES

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In 2004, 10 new member states joined the European Union. The tenth anniversary provides a good opportunity to evaluate the agricultural performance of each country and to take stock of the results achieved. Despite the relevance of the topic, only a limited number of research projects were concerned with the agricultural effects of the accession. The goal of the article is to quantify the agricultural performance of the new member states and to compare the results achieved as well as to set up some kind of a performance ranking. Which countries made use of the advantages of the accession the most (common market, budget, etc.)? Which ones lagged behind concerning agricultural performance? These are the questions I am seeking answers to. To achieve the goal mentioned above, the article introduces the methodology used and analyses in detail the performances achieved in agriculture, agri-environment and rural economy. After that, I introduce the ranking made and then try to uncover the reasons behind different performances.

Literature on the effects of accession from an agricultural aspect is quite scant. Möllers et al. (2011) examined the change of the agricultural structure and change of rural quality of life of the region. They made numerous agricultural policy conclusions and recommendations in the light of experiences so far, especially in the of the currently ongoing debate on the future of the Common Agricultural Policy. In their article, Gorton et al. (2009) prove why is the Common Agricultural Policy unsuitable to solve the rural development problems of the region. In their comprehensive study, Csáki-Jámbor (2013) analysed the effect of EU membership on the agriculture of new member states and according to their results, each member state used the available opportunities differently beside the basically positive effect. Kiss (2011) made the similar conclusion in his article, underlining that accession meant an incentive for the agriculture of the new member

states but strong market competitiveness had negative effects in many cases. Kapronczai (2010) analysed the comprehensive effect of accession on Hungarian agriculture while Hegedűs-Kiss (2014) examined the effects of 10 year long EU membership on Hungarian agricultural trade. They found that accession increased the balance of Hungarian agricultural balance and the intensity of agricultural trade ties with the EU27, hinting at greater integration.

To achieve the goal of the article, I use an innovative agricultural analysing tool, the agricultural performance index. The index is similar to indicators used by international organisations to measure the economical-environmental performances of different countries (e.g. WEF Competitiveness Index, WEF Environmental Performance Index – WEF, 2014). The basis of the similarity is that the organisations mentioned above also rank the performances of countries based on different indicators, analysing their changes. In light of this, the article uses 15 indicators, five out of these measure agricultural, five agri-environmental and five rural economy performances. As far as I know, the method has never been used to the whole of agriculture.

The article examines the agricultural performances of new member states between 2001-2012 by comparing the average of the 2001-2003 period with the average of 2010-2012. All 15 indicators are calculated for each country examined and their average will be the agricultural performance index. To handle negative values (of changes over time), the result of the country with the lowest average is added to the corresponding result of all the countries (in other words, the changes between 2001-2003 and 2010-2012), and then the performance of each country is expressed as the rate compared to the best-performing one. This method enables us to give 100% for the best country in the indicator in question (in other words, the country with the most positive change) and then less and less for the worse-performing ones. The five indicators belonging to each subcategory provide a chance to measure



**Table 1: Description of used indicators**

Name	Measure	Source	Positive impact if the indicator is:
Agricultural performance			
Net production value/ha	euro/ha	EUROSTAT	+
Cereal yield	ton/ha	FAOSTAT	+
Milk yield	litre/cow/year	FAOSTAT	+
Farm income	million euros	EUROSTAT	+
Agricultural trade balance (HS2)	million USD	WITS	+
Agri-environmental performance			
Emission of greenhouse gases	million tons	EUROSTAT	-
Size of organic area	hectare	EUROSTAT	+
Nitrogen use	ton	EUROSTAT	-
Phosphorus use	ton	EUROSTAT	-
Permanent meadows and pastures	1000 ha	FAOSTAT	+
Rural performance			
Rural population	1000 people	FAOSTAT	+
Rural employment	%	EUROSTAT	+
Difference between urban and rural income	euro/person	EUROSTAT	-
Highway density	km/1000km <sup>2</sup>	EUROSTAT	+
Rate of early school leavers	%	EUROSTAT	-

Source: own edition

the agricultural, agri-environmental and rural economical performance, and then the average of the 15 indicators (or in another way, the average of the three subcategories) compose the agricultural performance index. I chose the indicators based on recommendations in literature and the availability of data (see the indicators in Annex 1).

The method above is suitable to measure and compare the agricultural performance of new member states after accession because it is made of comparable data from official sources and it measures performances based on that. The countries with the highest aggregate value (so with the best performance) have made use of the opportunities of accession the best while those with the lowest values have made the worst. Since we examine the performance of each country relative to itself, the differences of already existing capabilities do not have any role. Data is basically from the databases of Eurostat (Eurostat, 2014) but sometimes I also use the data of FAO (FAO, 2014) and the World Bank (WITS, 2014), too. Since the study concentrates on the 2004 accession round, Bulgaria, Croatia and Romania are not included in the study despite being EU member states. Cyprus and Malta are also not examined because of the relatively small weight of their agricultural sector.

According to the results – although every country won with the accession – Poland, Estonia and Lithuania are undoubtedly winners in agriculture while Slovakia, Latvia

and Hungary were less able to make use of the agricultural opportunities offered by EU membership. But sectoral performances are quite different. The Baltic states and Poland show the best agricultural performances while in this respect, Slovakia stood in the last place behind Hungary by a bit. But Slovenia, the Czech Republic and Slovakia made use of the advantages of accession from an agri-environmental aspect while here, the Baltic countries are unequivocally seen as tail-enders in sharp contrast with their agricultural performances. Regarding rural economic performances, Poland, Slovakia and the Czech Republic are standing on the virtual while the state of the countryside improved the least in Lithuania, Latvia and Hungary in the last 10 years.

The differences in the performance of the agricultural sector in each country can be traced back to many reasons. The article identified the differences of the starting positions, different structures of economy, different land and farm policies, the agricultural privatization process, the amount of foreign capital, the use of pre-accession programmes, the transparency and variability of national agricultural policies and macro-environment.

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# UNCONVENTIONAL SUMMARY OF THE 2016 VALLEY OF ARTS FESTIVAL

TAMÁS EPERJESI

'backyard host'

Ottó Herman Institution, Directorate of Nature Protection, Landscape Sustainment and Community Development

*Short summary from "A Falu" ("The Village"), 2016 Autumn, Page 49-56*

*Let us start a new dialogue about how to rebuild the future of our planet. We need a discussion that unites us all because the environmental challenge that we are experiencing and its human roots concern us all and we are all interested in it. [...] We need new, universal solidarity." Pope Francis: Laudato si' 14.*

**Ottó Herman Institute (OHI)** and its predecessors have represented themselves for years at the *Valley of Arts Festival* that may have become the most important festival for the Hungarian public. The programme series awaits those who are interested with a lot of performances, concerts, plays and handicraft exhibitions but also awareness-raising, knowledge-disseminating presentations, conferences, fora and discussions, too. In the last few years, the employees of the background institution of the *Ministry of Agriculture (MoA)* participated in the Kapolcs-centered cultural festival to strengthen conscious, responsible thinking. Our topics included not only protecting and preserving the environment but also social cohesion, strengthening solidarity. In the spirit of taking social responsibility, last year was the first when our background institution represented itself under the name of Ottó Herman after NAERDI (National Agricultural Advisory, Educational and Rural Development Institute).

Also in 2015 – thanks to the professional relationship established during years of camping at Csórompuszta – we vivified the wood installations made by the young international architects and designers of the "*Hello Wood Project*" in Vigántpetend. The wooden structures made in the international camp were an excellent setting for the fora organised by the employees of our Institute, too.

The successes of 2015 established a basis to let the Institute autonomously operate a courtyard for the duration of the whole festival for the first time. We chose the Catholic Church of Kapolcs – a filial church of the Parish of Vigántpetend – to be its venue. The programme

started every day at 11.30 with a special mass, piety, worshipping, followed by a forum discussion organised around a previously chosen topic each day.

It was humbling that in the first days of the festivals, the distinguished representatives of the Reformed (Calvinist) Church were our guests, therefore we were able to greet bishop *Károly Fekete, Eszter Dani*, the head of the Missionary Bureau of the *Reformed Synod*, and *Attila Kocsis*, the director of the *Hungarian Reformed Church Aid (HRCA)*. In the second part of the festival representing the Catholic Church, temple director *Ádám Füzes*, the leader of the *Károly Kanter Adult Education Institute*, the president of the *Ecclesia Cooperative* was the leader of our spiritual programme. For the last three days of the programme series, our guest was Methodist pastor *Zsófi Pásztor* and *Zoltán Pásztor*, the laic prefect of the Hungarian Methodist Church.

Many refer to the thoughts of *Pope Francis* published in summer 2015 just as the "green" encyclical because the thoughts represented in it connect the problems of our environment with the problems of our values and our relationship to each other. We named the programme series resembling a free university as Ottó Herman Creation Protecting Podium Discussion. In it, we discussed every day from 12.30 at the temple garden about preparations for climate change, the contemporary extinction of species, social solidarity, transforming local communities and eco-social movements. Our topics also included: the role of churches in rural development, the activity of charity services, greenways, natural parks, the development of local economy, youth work and volunteering – at home and also in the world.

In this spirit, the work of the Eco-congregation in the framework of the Reformed Church was introduced by *Boglárka Szűcs*. Biologist *András Victor* also had a presentation as an activist of this movement, analysing human intervention, the changing of the world due to human actions, the nature and as its part, human activity.









We hosted professor *József Forgács* (*Joseph P. Forgas*), member of the Australian and Hungarian Academy of Sciences, one of maybe the most respected social psychologist, who held a highly acclaimed presentation about the development and nature of preconceptions, meeting with great interest.

Led by Prima Primissima Junior award-winning actor-director *Rodrigo Balogh* and *Tamás Szegedi*, the members of *Independent Theatre* and the activists of Panna Czinka Folk High School presented their special interactive performance, the "School of Senses". In our yard, we were able to greet *István Loránd Szakáli*, the deputy state secretary of MoA responsible for agricultural development and "hungaricums" (unique Hungarian specialties). We discussed "value catalogues", the Value Keeper Movement. Here, coordinator of Hungaricum Committee and president of Pannonian Value Keeper Foundation *Zsolt Horváth*, and the mayor of Taliándörögd representing also the "Éltet Balaton-felvidék" LEADER LAG *Tibor Hoffner* were also present. The importance of addressing the youth was emphasised by *Gabriella Bazsó* and *Viola Horváth* based on the youth value keeper movement.

The role of churches in local economy and rural development was the topic at the fourth day. *Csaba Latorcai*, the deputy state secretary of the *Office of the Prime Minister* responsible for pilot programmes, *Miklós Vecsei*, the deputy president of the *Hungarian Maltese Charity Service* and *Tamás Sáringer-Kenyeres*, the newly appointed president of the *Hungarian National Rural Network* accepted our invitation amongst others. During the forum, we debated the current results of local economy development programmes supported by religious organisations, especially the problems and achievements of the social cooperative at Gyulaj led by *Németh Nándor* and coordinated by the Maltese charity service. Pastor *Róbert Polgár* who was also present detailed the community developing effects of the parish of Murakeresztúr and the Integrated Community and Service Space that has been created by the church. As a Reformed pastor of Hajdúnánás, *Áron Kocsis* introduced the farmers market programme of the HRCA as well as the successes of the local economy and "koruna of Bocskai" as a currency operated with the help of the local government.

We showed the operating experiences of the non-governmental organisation encompassing the work of spatial and rural development (National Association of Multicommunity Development Organisations, NAMDO) with the help of president *Gábor Csikász* and secretary-general *Viktória Bencze*. In the framework of the same forum, *Rita Kandikó*, the deputy president of NAMDO talked about the work of volunteers, the programmes of the European Voluntary Service, the actions and work of the Black Army Youth Association in Nagyvázsony.

Expecting the interest of many, an own podium day presented the activity of the Environmental Directorate of the Ottó Herman Institute. Led by director *András Béres*, numerous participants were able to hear about the effects of climate change, the opportunities to prepare for it.

The second weekend of the Hungarian Valley of Arts Festival started with one of our most high-profile programmes in our courtyard. At our podium discussion, we were able to get to know the local and central governmental actors of protecting nature and the environment, the activity of national and natural parks, greenways with our guests. We were able to greet *Zsolt V. Németh*, the state secretary of MoA responsible for the environment, agricultural development and hungaricums, *Dávid Mezőszentgyörgyi*, the director-general of Ottó Herman Institute, *Zoltán Puskás*, the director of the Balaton Highlands National Park, *Béla Báthly*, the president of the Hungarian Natural Park Association and *Krisztina Budai*, the president of Greenway Methodology Association, too. During the discussion, beside the landscape-sustaining, value-conserving role of local communities and the development concept of natural parks, the importance of the activity of greenways organised by including the public also emerged. During this, president Béla Báthly detailed the activity of the nine Hungarian natural parks. Krisztina Budai reported on two milestone successes of the greenway movement, "Fabulous" Hetés Greenway – organised from both sides of the Hungarian-Slovenian border – getting the Landscape Award of the Council of Europe and the EDEN Award of the Mecsek Greenway operating around Pécs.

Director Zoltán Puskás representing the local *Balaton Highlands National Park* introduced our programmes to improve eco-tourism. He especially highlighted that during the festival, they operate the "Green of Arts" courtyard with Ottó Herman Institute and *Green Zugoly Association*. Here, one can participate in knowledge-disseminating presentations and interactive games or tours with leaders and value registering at the geopark of the Balaton Highlands during the whole duration of the festival. State secretary Zsolt V. Németh introduced the central government programmes to activate local communities, conserve the landscape such as revitalising abandoned vineyards, gardens, the Farmstead Development Programme, but he also regarded registering unique landscape values as a part of value assessing and conserving activity of local communities to be important. Director-general of HOI Dávid Mezőszentgyörgyi told that as a leader of a ministerial background institution, he thinks that it is essential to be represented at every event, festival that concerns environment and nature protection, the problems and solution opportunities of the Hungarian countryside and closely related to that, agriculture. In order to disseminate knowledge and shape attitude on this topic,

he regards it to be important to let more and more people know the work, the career results of Ottó Herman who is still considered to be a polymath.

At the penultimate day of the festival, *Katalin Sipos*, the Hungarian director of *WWF* talked about the effects and prospects of the extinction of animals and plants, the change of the biosphere we know today. At the same day, *Mihály Kálóczi* introduced their actions to get the cultural landscape world heritage label for the Balaton Highlands. Everyone present agreed that these discussions can serve protecting our environment, spreading conscious thinking.

At the closing day of the festival, a summarising discussion took place as a free university in Csórompuszta. Architect and co-founder of Hello Wood Movement *Péter Pozsár* talked about innovation in rural regions, the initiatives of local communities and the prospects of social activity as a guest. Human ecologist *Mátyás Révai*, landscape

architect and deputy president of Hungarian Landscape Architect Association *Klaudia Máté* were present as well as the employees of HOI and activists of the Black Army led by president Rita Kandikó. Catholic pastor Ádám Füzes emphasised the importance of cooperation for good issues as the leader of Károly Kanter Adult Educational Institute. He hinted at that the goals of churches aimed at protecting what has been created should be more in synch with the aim of natural protection and consciousness of Ottó Herman Institute, therefore religious organisations could be partners in joint action. Methodist pastor Zsófi Pásztor and Zoltán Pásztor, the laic prelate of the church talked about volunteering and the will to act for the community, the strong presence of those who have faith. They viewed the goals set to be efficiently reached by thinking in a network, conscious presence.

Participants of the closing discussion agreed that the presence related to the programme series of Valley of Arts brought many positive results and steps forward.



