Maatalouden geenivarojen arvo – tutkimustarpeiden arviointi meta-analyysilla

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Tiivistelmä

Maatalouden kasvi- ja eläingeenivarat köyhtyvät edelleen huolimatta siitä, että tietoisuus ja suojelutoimet ovat jatkuvasti lisääntyneet. Asiantuntevien päätösten teko geenivarojen suojelun painopisteistä ja laajuudesta vaatii taloustieteellistä tietoa, joka sisältää rahallisia arvioita sekä suojelun kustannuksista että hyödyistä. Vaikka kasvien siemeniä tai tuotantoeläimiä voidaan pitää yksityishyödykkeinä, niiden sisältämillä geenivaroilla on julkishyödykkeiden piirteitä, kuten olemassaoloarvoja kansalaisille. Julkishyödykeominaisuuksien vuoksi markkinahinnat eivät täysin kuvaa geenivarojen arvoa. Geenivarojen arvoa onkin aiemmassa kirjallisuudessa selvitetty käyttäen erilaisia arvottamismenetelmiä. Tutkimuksessa tehdään yhteenveto olemassa olevasta maatalouden geenivarojen arvoa käsittelevästä kirjallisuudesta ja niiden suojelun hyödyistä meta-analyysin avulla. Tavoitteena on arvioida, voidaanko suomalaisten kasvi- ja eläingeenivarojen arvoa päätellä aiemman kirjallisuuden pohjalta ja tunnistaa, minkälaista tutkimusta geenivarojen arvosta tarvitaan tulevaisuudessa. Aineisto koostuu 13 geenivarojen arvottamistutkimuksesta ja 63 maksuhalukkuushavainnosta. Aineiston perusteella eläingeenivaroja on arvotettu kasvigeenivaroja enemmän. Kaikki tutkimukset ovat arvottaneet geenivarojen *in situ* -suojelua. Eniten on arvotettu rotujen tai lajikkeiden yksittäisiä ominaisuuksia, mutta kohteena on ollut myös rotuja/lajikkeita ja suojeluohjelmia. Valtaosa tutkimuksista on tehty kehitysmaissa, ja aineisto sisältää ainoastaan kaksi arvottamistutkimusta Euroopasta. Suomesta ei ole saatavilla yhtään geenivaroja arvottavaa tutkimusta. Aineistoa analysoidaan meta-regression avulla. Selitettävä muuttuja on maksuhalukkuus geenivarasta, ja selittävinä muuttujina on arvotettavaa hyödykettä ja tutkittua väestöä kuvaavia muuttujia ja lisäksi tutkimuksen maantieteellinen ulottuvuus, arvottamismenetelmä, tutkimusvuosi ja otoskoko. Keskimääräinen maksuhalukkuus geenivaroista on kertasummana noin 42 dollaria kotitaloutta kohden. Maksuhalukkuus kuitenkin vaihtelee tutkimusten välillä varsin paljon. Karjageenivaroja arvostetaan enemmän kuin muita eläingeenivaroja. Maksuhalukkuus roduista ja suojeluohjelmista on korkeampi kuin yksittäisistä ominaisuuksista. Paikallisia rotuja arvostetaan enemmän kuin risteymiä tai eksoottisia rotuja. Olemassa oleva tutkimus ei tarjoa mahdollisuuksia päätellä geenivarojen arvoa Suomessa. Tuleva tutkimus voikin edistää usealla tavalla tietoisuutta maatalouden geenivarojen arvosta. Arviot *ex situ* -suojelun hyödyistä, kasvigeenivarojen arvosta, ei-käyttöarvoista, kuluttajien arvostuksista ja kehittyneiden maiden geenivaroista ovat aliedustettuina nykyisessä kirjallisuudessa. Kasvattamalla tietopohjaa uusilla tutkimuksilla parannetaan meta-analyysien luotettavuutta. Lisäksi mahdollistetaan tutkimusten tulosten entistä monipuolisempi käyttö tilanteissa, joissa tehdään päätöksiä aiemmin tutkimattomien lajikkeiden tai rotujen suojelusta.

Asiasanat: arvottaminen, geenivarat, maatalous, maksuhalukkuus, meta-analyysi, luonnonsuojelu

The value of genetic resources in agriculture: assessing future research needs

Introduction

One of the aspects of biodiversity conservation is the protection of genetic resources in agriculture. Plant or crop genetic resources (PGR/CGR) refer to the genetic material within cultivated species and other plant species that can be of value for food production and agriculture (Evenson et al. 1998). Animal genetic resources (AnGR) include all animal species, breeds and strains that are of interest in terms of food and agricultural production (Rege and Gibson 2003). Both PGR and AnGR continue to be lost despite the increasing awareness and action to protect them.

Making informed decisions on the appropriate focus and extent of conservation efforts requires economic information that includes monetary estimates on both the costs and benefits of conservation. Economic analyses, involving the valuation of conservation benefits, can guide resource allocation between the conservation of genetic resources and other efforts as well as between various types of genetic resources (Artuso 1998). In addition, valuation can assist in designing economic incentives for efficient conservation. Values can also be used as inputs for benefit and cost sharing arrangements (Wale 2008). Although the importance of economic analyses has been recognized, the literature on the value of genetic resources in agriculture is relatively limited (see e.g. Evenson et al. 1998, Drucker and Scarpa et al. 2003b and Rege and Gibson 2003).

Value estimates for genetic resources are not typically revealed by markets, which is the case for any other public or non-market goods (Gollin and Santaniello 1998). Such goods are seldom sold in the markets or their price does not completely indicate their value. Thus, the valuation of genetic resources necessitates the use of valuation methods designed for estimating non-market benefits. Both revealed preference (RP) methods, such as hedonic pricing, and stated preference (SP) methods, such as contingent valuation and choice experiment, are suitable for valuing genetic resources in agriculture. The focus of valuation can be on various aspects of genetic resources. It can be used to assign a monetary value to breeds or varieties and their traits. Other possible objects of valuation include general agrobiodiversity or conservation programmes of genetic resources.

The objectives of the present study are to review and summarize the existing literature on the valuation of genetic resources in agriculture. Based on current knowledge, we also attempt to identify what kind of future research is needed to improve understanding of the value of genetic resources. The existing valuation studies are compiled into a single data set and qualitatively described. Furthermore, the studies are quantitatively examined in the framework of meta-analysis.

Meta-analysis refers to methods and techniques that summarize the results of empirical studies. Glass (1976) is typically credited with introducing meta-analysis to the social sciences. The first applications in environmental valuation were conducted in the early 1990s (Smith and Kaoru 1990, Walsh et al. 1992). Since then, meta-analyses of environmental amenities have covered a variety of topics from air quality (Smith and Huang 1995) to recreational fishing (Johnston et al. 2006). To the best of our knowledge, there have been no previous meta-analyses of the value of farm genetic resources.

In the field of environmental valuation, meta-analysis is used for three general purposes: research evaluation and synthesis, hypothesis testing and benefit transfer (Smith and Pattanayak 2002, 277). Our emphasis is on evaluating and summarizing existing research and identifying future research needs.

This paper is organized as follows. The next section describes the data and methods used in this study, and it is followed by the results. Conclusions and recommendations for further research are presented in the final section.

Data and methods

Data

To summarize the existing studies on the value of farm genetic resources, we conducted an extensive literature research on the subject. We focused on those that used established valuation methods to provide monetary value estimates for genetic resources in agriculture. The object of valuation could be a breed or a variety, a specific trait or a conservation programme. Both PGR and AnGR were included. Based on the criteria, we identified 13 studies on the value of plant and animal genetic resources in agriculture. All publications were refereed journal articles. We first examined the data qualitatively and then extended the analysis to a quantitative analysis with meta-regression. One of the objectives in both approaches was to identify future research needs.

Descriptive analysis

In the descriptive part we reviewed the literature to obtain a more comprehensive understanding of the studies on the value of genetic resources in agriculture. Altogether 13 studies with 63 value estimates were evaluated and summarized. For this purpose, we used summary tables to describe the distribution of variables in our data sets. The qualitative analysis also provided descriptive statistics for the selection of variables available for the meta-regression analysis.

Meta-regression analysis

The quantitative method of analysis was meta-regression, which complement the descriptive analysis of the data. The meta-analysis aimed at explaining the willingness to pay (WTP) for farm genetic resources with a set of explanatory variables. Three meta-regression models were estimated: for all observations, positive (WTP) observations and animal observations.

The dependent variable in all meta-regression models was the willingness to pay for the genetic resource evaluated in the empirical study. Most value estimates were reported as household-specific and lump sums, and thus it was chosen as the base format. To make the WTP estimates comparable, they were all converted to US dollars using exchange rate data from the UN and the OECD.

The first set of explanatory variables described the valued environmental good. The valued genetic resource was depicted with the binary variables for crop/plant genetic resources (CROP), cattle (CATTLE) and agrobiodiversity (AGROBIOD), respectively. The next four variables described the focus of valuation, either local breeds (BREEDLOC), cross-breeds (BREEDCROS) and exotic breeds (BREEDEX) or conservation programmes (PROGRAM). The second set of variables described the geographic dimension of the study (LOCAL), the study population (GDP) and the valuation method (HP). The third set of variables consisted of other study-specific features. The variable YEAR was included to determine whether there was a systematic trend in WTP for genetic resources over the years and to captured the effect of inflation. SAMPLE represented the number of households or people that the willingness to pay estimation was based on.

All meta-regression models were linear and used weighted least squares. Each value estimate was weighted with the estimate weight (ESTW), which sums to one for a study. Weighting avoids giving disproportionate importance to those studies that had produced several value estimates.

In addition to identifying statistically significant factors that explain willingness to pay for genetic resources in agriculture, the estimated meta-regression models were used to illustrate their ability to give value predictions for scenarios of genetic resource conservation. In this case we calculated benefit estimates for the European examples to be able to evaluate the models' ability to produce feasible results on the area when there were only few observations.

Results

Descriptive analysis

Table 1 summarizes the features of the data with respect to the focus of valuation, geographic dimensions of the good, value categories and valuation methods and also provides an illustration of the variety of studies conducted and a basis for the evaluation of future research needs.

Our data indicated that animal genetic resources have been valued more often than plant or crop genetic resources. Cattle and pig genetic resources have received the most attention, as there were four studies on both of them. Other valued species included goats, sheep, horses and rice. There was also one study on general agrobiodiversity. All valuation studies were conducted to value the conservation of genetic resources *in situ*.

In most cases the focus of valuation was on specific attributes or traits of a breed or a variety, such as health-related issues, body conformation and weight, fertility, water-related issues or feed purchase requirements. Studies that focused on breeds or varieties have typically valued local breeds/varieties or landraces in comparison to the values of crosses or exotic breeds/varieties. Valuation studies on conservation programmes measured the value of protecting a local or an endangered breed/variety.

Genetic resources in agriculture are typically of regional or local importance. Thus the geographic scope of the valuation studies ranged from local to regional. The studies originated from Africa, Asia, Europe and South America. The distribution of GDP captures the ratio of observations from developed and developing countries. Most studies were conducted in developing countries, where people are more dependent on agriculture. Our data included only two valuation studies from Europe and none from the United States. This was quite surprising, as economic valuation is well established in the U.S.

Table 1. Summary statistics for the data

	Studies (n = 13)		Value estimates (n = 63)	
	Number	%	Number	%
Genetic resource				
Plant/crop	2	15.4	6	9.5
Animal	11	84.6	57	90.5
Species				
Cattle	4	30.8	27	42.9
Pig	4	30.8	20	31.7
Goat	1	7.7	4	6.3
Sheep	1	7.7	5	7.9
Horse	1	7.7	1	1.6
Rice	1	7.7	2	3.2
Agrobiodiversity	1	7.7	4	6.3
Focus of valuation[a]				
Attribute/trait	10	62.5	50	79.4
Breed/variety	3	18.8	9	14.3
Conservation programme	3	18.8	4	6.3
Geographic scope				
Local	4	30.8	9	14.3
Regional	9	69.2	54	85.7
Country				
Ethiopia	1	7.7	11	17.5
Hungary	1	7.7	4	6.3
Italy	1	7.7	1	1.6
Kenya	5	38.5	28	44.4
Mexico	3	23.1	12	19.0
Nepal	1	7.7	2	3.2
Vietnam	1	7.7	5	7.9
Value categories				
Use value	11	84.6	61	96.8
Use and non-use value	2	15.4	2	3.2
Valuation method				
Contingent valuation	3	23.1	4	6.3
Choice experiment	8	61.5	52	82.5
Hedonic pricing	2	15.4	7	11.1

[a] Three studies have valued both attributes and breeds/varieties.

Most studies of genetic resources in agriculture estimated values from the perspective of farmers or livestock-keepers. The focus was on use values, as only two studies estimated both use and non-use values. Valuation methods used included contingent valuation, choice experiments and hedonic pricing. Contingent valuation was used to value conservation programmes, and choice experiments and hedonic pricing to value breeds or varieties and their attributes.

Mean willingness to pay as a lump sum was approximately 42 dollars per household. The weighted mean, weighted by the sample size, was 38 dollars. The highest willingness to pay estimates were obtained from one of the two European studies, which estimated the value for general agrobiodiversity (Birol et al. 2006). The mean willingness to pay estimates for the three distinct data sets differed somewhat from each other, ranging from 37 to 49 dollars.

Meta-regression results

Table 2 presents the results of the meta-regression models for all observations, positive observations and animal observations. The results of the meta-regressions were fairly robust, as the signs and statistical significances of the variables were consistent across specifications. All models gave a reasonably good fit to the data, the R^2 statistic being between 0.63-0.71 and adjusted R^2 statistics between 0.54-0.64.

Most of the variables describing the valued good were statistically significant. The consistently positive sign of CATTLE indicated that cattle genetic resources were valued more highly than other AnGR. The variable AGROBIOD was significant and positive. The magnitude of the coefficient could be explained by the fact that the data set included only one study on agrobiodiversity, which was conducted in Europe and produced notably higher value estimates compared to other studies. CROP was negative but not statistically significant.

The second level of variables describing the environmental good indicated that willingness to pay for breeds was higher than for attributes or traits. The breed-related variables local breeds BRLOC, cross-breeds BRCROSS and exotic breeds BREXOT were all significant and positive. The relative magnitudes of the coefficients seem to indicate that local breeds were valued more highly than cross-breeds and cross-breeds more highly than exotic breeds. The variable for conservation program was consistently positive but significant only in the third data set that includes AnGR observations. Thus, the willingness to pay for conservation programmes seems to be higher than for attributes at least in the case of animal genetic resources.

Table 2. Meta-regression models

Liner regression, weighted least squares
Dependent variable in all models: willingness to pay for genetic resources in dollars

Variable	**Data set 1: All observations (n = 63)** Coeff.	Std. Error	**Data set 2: Positive observations (n = 51)** Coeff.	Std. Error	**Data set 3: Animal observations (n = 57)** Coeff.	Std. Error
(Constant)	-50.164*	28.485	-69.940**	34.493	-48.844*	26.470
CROP	-21.786	24.542	-23.411	27.223		
CATTLE	39.598***	11.536	48.454***	13.817	45.551***	12.388
AGROBIOD	169.585***	32.363	179.168***	36.794		
BRLOC	134.223***	28.074	137.215***	30.773	129.964***	26.431
BRCROSS	102.759***	28.074	105.751***	30.773	98.500***	26.431
BREXOT	87.611***	28.074	90.602***	30.773	83.352***	26.431
PROGRAM	30.778	24.684	34.741	30.932	20.404***	25.351
LOCAL	0.717	19.407	6.843	25.469	-1.344	18.139
GDP					2.154	2.255
HP	10.327	20.681	22.322	26.420	21.500	22.476
YEAR	6.461**	2.743	8.119**	3.449	7.330***	2.703
SAMPLE	0.046	0.059	0.058	0.065	-0.007	0.078
WTA	-8.858	15.376			-7.484	14.341
R^2	0.71		0.72		0.63	
Adjusted R^2	0.64		0.64		0.54	
F-statistic	10.075		9.177		7.022	

Of the other study-specific features, only the variable YEAR was significant. It was positive, indicating that later studies produced higher value estimates. This could imply an upward trend for willingness to pay for genetic resources. It should be noted that the variable also captured the change in the value of money over time, or inflation as the value estimates were not converted to the same base year.

The results from the meta-analysis allowed prediction of the willingness to pay for specific scenarios affecting genetic resources. Table 5 presents the value estimates for three genetic resource scenarios for our three data sets. The first scenario concerned the value of a local cattle breed in

Europe, the second was a scenario for maintaining general agrobiodiversity and third a conservation programme for crop genetic resources.

The willingness to pay estimates in Table 3 are presented as lump sums per household. Local cattle breed and agrobiodiversity received a notably higher willingness to pay than a crop conservation programme. Willingness to pay ranged from 206€ to 261€ for a local breed, from 202€ to 217€ for agrobiodiversity and from 42€ to 49€ for a crop conservation programme. The value estimates should be regarded as only indicative due to the limited amount of data.

The predicted values were larger compared to the mean willingness to pay estimates from the two European studies. The average willingness to pay for conserving an endangered horse breed was estimated at 30€ (Cicia, Dércole and Marino 2003). The predicted estimates for general agrobiodiversity were also higher than that observed in the Hungarian study of 143€ (Birol, Smale and Gyovai 2006). These disparities reflect the insufficient number of valuation studies, especially in Europe.

Table 3. Willingness to pay for different genetic resources

Scenario	Data set 1: All observations (n = 63)	Data set 2: Positive observations (n = 51)	Data set 3: Animal observations (n = 57)
Local cattle breed in Europe	206€	223€	261€
Maintaining general agrobiodiversity	202€	217€	NA
Conservation programme for crops	42€	49€	NA

Conclusions and discussion

The review indicates that despite growing interest in the economic valuation of farm genetic resources, empirical studies reporting monetary values are at present rare. Examination of the existing literature and the meta-analysis revealed a number of issues related to the current situation and the future research needs in the valuation of genetic resources.

All valuation studies in our data focused on the *in situ* conservation of genetic resources. If we wish to study whether to conserve genetic resources *in situ* or *ex situ*, we need information on the benefits and costs of both approaches. The value of *ex situ* conservation needs to be studied in the future. There was better knowledge of the value of animal genetic resources, as these types of studies have been more common. Monetary value estimates for plant genetic resources have been rare, and more research is needed. Of the valued species, cattle and pigs have received the most attention. The focus of valuation has in most cases been on attributes, whereas breeds/varieties and conservation programmes have received less attention.

There were only two European studies on the value of genetic resources in agriculture. In addition, they examined special issues, one focusing on an endangered horse breed in Italy and the other on general agrobiodiversity on small Hungarian farms. The generalization of these results to other contexts is difficult. Therefore, little can be inferred on the value of genetic resources in Europe.

Most studies have only estimated the use values of genetic resources from the perspective of farmers and livestock-keepers. This is reasonable on the grounds that the value of farm genetic resources mainly consists of use-related values. However, it is probable that the general public, at least in developed countries, values the protection of threatened or endangered genetic resources in agriculture in the same way it values the protection of wildlife. The magnitude of these non-use values is worth studying and it is one of the possibilities for future research.

There is a need to use the stated preference methods for estimating the non-use value component of genetic resources. Thus far, most studies have utilized choice experiments, which are well suited to valuing genetic resources due to its flexibility and ability to value the traits of breeds/varieties. However, contingent valuation could be used to value conservation programmes.

The identified future research needs can be summarized as follows. More value estimates are especially needed for *ex situ* conservation, plant genetic resources, Europe and the United States, non-use values and consumers. Further original research on these previously unstudied issues would increase our knowledge of the value of genetic resources. In addition, a large enough body of valuation literature on genetic resources in agriculture would make it possible to conduct benefit transfers.

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