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The value of genetic resources in agriculture: a meta-analysis assessing existing knowledge and future research needs

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The protection of genetic resources in agriculture is an important aspect of biodiversity conservation. Knowledge of the value of genetic resources can contribute to determining the appropriate focus and extent of conservation. This study reviewed and summarised literature on the economic value of genetic resources using meta-analysis. Altogether, 22 studies were used to describe current knowledge on the value of genetic resources. Furthermore, 14 studies with 93 value observations were examined with a meta-regression model to identify variables that explain the willingness-to-pay (WTP) for or willingness-to-accept (WTA) loss of genetic resources. Grain genetic resources were ascribed lower value compared to animal genetic resources (AnGR) and agrobiodiversity, and the values of breeds or varieties and conservation programmes were higher than the value of individual attributes. Future research should address the gaps in knowledge that are relevant for policy-making. This particularly includes improving knowledge on the value of plant genetic resources (PGR), obtaining value estimates for maintaining genetic diversity in Europe and the United States, estimating the relative magnitude of use and non-use values and determining the value consumers place on genetic resources and diversity in agriculture. An extensive database with valuation literature on genetic resources that fulfils the requirements for benefit transfer is essential to utilise value information more efficiently in decision-making situations.

Keywords: agriculture; conservation; genetic resources; meta-analysis; valuation; willingness-to-pay; willingness-to-accept

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). According to the FAO (1996), the loss of diversity in PGR has been substantial and the process of genetic erosion continues. The main cause of the erosion is the replacement of local varieties by improved or exotic varieties and species (FAO 1997). It has been argued that the loss of AnGR may be a more serious problem than the loss of crops due to the small gene pool and the rarity of wild relatives (Rege and Gibson 2003). Mainly due to the marginalisation of traditional production systems and local breeds, 20% of animal breeds are classified as 'at risk', while population data are unavailable for 36% of breeds (Rischkowsky and Pilling 2007).

Making informed decisions on the appropriate focus and extent of conservation efforts requires information 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 and benefit and cost sharing arrangements (Wale 2008).

The value of genetic resources is not typically revealed by markets, as genetic resources are not directly traded in the markets or their price does not completely indicate their value (Oldfield 1989; Brown 1990; Drucker et al. 2001). Thus the valuation of genetic resources requires the use of valuation methods designed for estimating non-market benefits. Valuation methods aim at eliciting individuals' willingness-to-pay (WTP) or willingness-to-accept (WTA) compensation for the environmental good in question. WTP can be used to measure the value of desirable attributes or improvements in the conservation of genetic resources. Conversely, WTA is suitable for measuring the compensation needed for accepting undesirable traits or participating in conservation programmes that generate yield reductions.

Revealed preference methods (RP), mainly hedonic pricing, elicit the value of goods through consumer behaviour in markets by estimating the value of animal or plant characteristics or the value of specific varieties or breeds from market prices. Stated preference (SP) methods, such as contingent valuation (CV) and choice experiments, employ surveys to elicit individual preferences and WTP. CV is useful in valuing conservation programmes, and choice experiments can be used to value attributes, breeds or varieties and conservation programmes.

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In the economic valuation of genetic resources it is typical to distinguish between use and non-use values. Use values can be further classified into direct use and option value. For genetic resources, direct use value refers to productive activities and to their use in breeding (Gollin and Evenson 2003; Roosen et al. 2005). Option value, sometimes also referred to as indirect use value in the context of genetic resources, relates to the future uses of genetic materials, such as future breeding and the development of new traits (Roosen et al. 2005). Non-use values consist of existence value, bequest value and altruistic value. Existence value means that people may simply value the existence of certain breeds or varieties without ever using them. Bequest value and altruistic value refer to the value placed on preserving genetic resources for future generations and for others in the current generation, respectively. It has been argued that non-use values, elicited only with stated preference methods, may be more important for AnGR than PGR (Gollin and Evenson 2003).

Although the importance of economic analyses has been recognised, the literature on the monetary value of genetic resources in agriculture is relatively limited (see e.g. Evenson et al. (1998); Rege and Gibson (2003)). For example, Drucker et al. (2001) and Roosen et al. (2005) describe the possible values that genetic resources may have and present techniques to measure them. Several issues make the valuation of genetic resources in agriculture challenging, including uncertainties related to the future requirements of genetic resources, the possible future problems in agriculture and the consequences of the loss of genetic resources (Wale 2008). The measurement of option value and non-use values is difficult, and the only available methods for this purpose are stated preference surveys. Most of the world's genetic resources are found in developing countries, where economic valuation has to overcome additional problems.

We used a meta-analysis (Glass 1976) to summarise the results of empirical studies. In environmental valuation, a meta-analysis is used for three general purposes: research evaluation and synthesis, hypothesis testing and benefit transfer (Smith and Pattanayak 2002, p. 277). The first applications in environmental valuation were conducted in the early 1990s (Smith and Kaoru 1990; Walsh et al. 1992). Meta-analyses of genetic diversity include those by Loomis and White (1996) and Richardson and Loomis (2009), who examine the economic value of rare and endangered species, and Nijkamp et al. (2008), who review valuation approaches from the perspective of biodiversity conservation and present a meta-analysis of biodiversity values. However, to the best of our knowledge, there have been no previous meta-analyses of the value of genetic resources in agriculture.

Information on the value of genetic resources is rather fragmented, as it largely consists of separate case studies conducted in various contexts. Our purpose is to summarise and take stock of the existing literature. This

also enables us to consider the type of future research needed to improve understanding of the value of genetic resources.

In our study, the valuation studies on the use and existence of genetic resources were compiled into a single data set and described qualitatively. Furthermore, the studies were quantitatively examined with meta-regressions. In addition to identifying statistically significant factors that explain WTP or WTA 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. We considered methodological and econometric issues in meta-analysis pointed out by Nelson and Kennedy (2009), such as the heteroskedasticity of the variances of the dependent variable, and correlation within and between primary studies.

This paper is organised as follows: The second section describes the data, comprising empirical valuation studies of genetic resources, as well as discussing the methods used in this study. The third section presents the results of the descriptive analysis and the meta-regressions. Discussion and recommendations for further research are presented in the final two sections.

Data and methods

Data

To summarise the existing studies on the value of farm genetic resources, we conducted an extensive literature research on the subject. The studies were searched from databases such as CAB Abstracts, ISI Web of Knowledge, EconLit, Agricola, FSTA and IFPRI BioConserv bibliography. The searches were conducted in 2009, and the data were supplemented with a second round of searches in early 2010. Literature from the 1980s to the present was searched, and we included journal articles, book chapters and also publications from the 'grey' literature in the data. Both PGR and AnGR studies were selected. During the first stage, the information retrieval was maintained on a general level and the keywords used were *genetic resources* and *valuation*. From the search results those empirical studies that used established valuation methods (i.e. CV, choice experiments, hedonic pricing (HP)) to provide monetary value estimates for genetic resources in agriculture were included in the data set. The object of valuation could be a breed or a variety, a specific trait or a conservation programme. The purpose was to obtain an understanding of the benefits (or in some cases negative benefits) of conserving genetic resources. Cost-based estimates were excluded from the analysis to enable comparisons of the costs and benefits of conservation.

Based on the aforementioned criteria, we identified 22 studies on the value of PGR and AnGR in agriculture (see Appendix 1). We first examined the data qualitatively and then proceeded to quantitative analysis with meta-regression. One of the objectives in both approaches was to identify future research needs.

Descriptive analysis

In the descriptive analysis we reviewed the literature to obtain a more comprehensive understanding of the studies on the value of genetic resources in agriculture. Summary tables were used 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 complements the descriptive analysis of the data. Only studies reporting either a WTP or a WTA for the genetic resource were included in the meta-analytic data. The data set comprised 14 studies with 93 value estimates. Studies that were considered unsuitable for the meta-analysis included those that presented the value estimates as percentage changes in yields (Evenson 1998; Rao and Evenson 1998; Birol and Villalba 2006) or only at the aggregate level (Gollin and Evenson 1998a, 1998b). The study by Jabbar and Diedhiou (2003) was omitted because the article does not report the currency or the year of the value estimates.¹

The meta-analysis aimed at explaining the value of farm genetic resources with a set of explanatory variables. We constructed two data sets for the meta-regressions from the available material. The first data set was the largest, comprising all studies and value estimates that could be found. Both AnGR and PGR were included, as were WTP and WTA estimates.

Following a recommendation by Nelson and Kennedy (2009), a more homogeneous data set including only AnGR was constructed. It comprised 12 studies and 65 observations.

The dependent variable in the meta-regression models was the WTP for the genetic resource or the WTA compensation evaluated in the empirical study. To make the value estimates comparable, they were all converted to international dollars using the purchasing power parity (PPP) conversion rate. In addition, the values were adjusted to the year 2008 with country-specific consumer price indexes (CPI). This year was used because the subsequent PPP and CPI figures are estimates.²

The data also included WTA and negative WTP estimates. The absolute values for these estimates were used in the meta-regressions, and they were distinguished from the most common positive WTP values with separate dummy variables for both measures.

The explanatory variables included in meta-regression models typically describe the characteristics of the environmental good, the population studied, the methodology used and other study-specific features. Most explanatory variables in our meta-regressions were binary, meaning that they could only take the values 0 or 1.

The first set of explanatory variables described the valued environmental good. At the first level, PGR were

separated from AnGR with the binary variables GRAIN and AGROBIOD for grains and agrobiodiversity, respectively. At the second level, the focus of valuation was depicted with the variables BREEDVAR for observations of the value of specific breeds or varieties and PROGRAM for observations that capture the values of conservation programmes or scenarios. The base case was that the value was estimated for an attribute or a trait.

In the AnGR model the valued good was described with the dummy variable CATTLE for cattle genetic resources and BREDEXOT, BREEDCROSS and BREEDLOC for exotic breeds, crossbreeds and local breeds.

The second set of variables described the geographic and temporal dimension of the study and the study population. The geographic scope was captured with the binary variable LOCAL, which separated local from regional studies. MULTNAT was only included in AnGR models, and distinguished those studies that were conducted in multiple countries. The variable YEAR was included to determine whether there was a systematic temporal trend in WTP or WTA for genetic resources. The variable describing the study population was gross domestic product (GDP), which obtained the value one for those countries where GDP was above 10,000 dollars per capita per year and 0 otherwise. GDP figures were expressed in 2008 international dollars, and the original GDP figures from the study year were adjusted to the year 2008 using country-specific CPIs.³

Variables for HP, CV and combined stated and revealed preference (SPRP) described the valuation method. These were compared to the choice experiment method, which was the base case.

The variables WTA for willingness-to-accept estimates and NEGWTP for negative willingness-to-pay estimates were included in all models to test whether there was a significant difference between the value concepts.

Only a rather small number of variables could be included in the meta-regressions due to the small amount of data and multi co-linearity. Those variables describing the environmental good were considered as the first priority, and other variables were included as long as they did not cause significant problems with multi co-linearity. Variance inflation factors (VIF) were considered, and a VIF of 10 was regarded as the threshold (O'Brien 2007). Thus, the VIF were below 10 for all variables in all models.

All meta-regression models were linear and used weighted least squares. Each value estimate was weighted directly with the sample size (SAMPLE) to address the heteroskedasticity of variance in the WTP or WTA estimates. Those WTP or WTA estimates having smaller variances are more reliable (Nelson and Kennedy 2009), and the variances were proxied using the sample sizes from the original studies. The Breusch–Pagan test rejected the homoskedasticity of variances for both data sets, and thus heteroskedasticity-robust standard errors were calculated in all models.

As one primary valuation study produces multiple WTP or WTA estimates, some degree of within-study correlation is probably present. The simplest method to deal with this is to include only one observation from each study (Nelson and Kennedy 2009), but this would have lead to a drastic reduction in the meta-analysis sample. Instead, averaging of the estimates was occasionally used. For example, when values were calculated for different areas within one country, the average value was used. If WTP (or WTA) was calculated separately for cows and bulls, the value was also averaged to a single estimate. The study on agrobiodiversity provided the largest number of estimates, and it was separated with its own dummy variable.

Results

Descriptive analysis

Table 1 summarises the features of the data with respect to the focus of valuation, geographic dimensions of the good and valuation methods. The descriptive statistics of the explanatory variables from the studies included in the meta-analysis are presented in Table 2. Both tables also provide an illustration of the variety of research conducted and a basis for the evaluation of future research needs.

Our data includes more valuation studies on AnGR than PGR/CGR. This stems from at least two reasons. First, as noted by Koo et al. (2004), it is difficult to estimate the marginal benefits associated with each conserved plant germplasm, especially the non-use value components. Second, AnGR have received considerable interest during recent years, and a special issue of *Ecological Economics* (2003, Vol. 45) presented several case studies on the value of animal genetic resources. For PGR, the economic values were in several studies associated with yield changes and thus could not be included in the data.

Of the different species, cattle and rice genetic resources have received the most attention. Other valued species included pigs, goats, sheep, horses, maize and coffee, while one study examined general agrobiodiversity. *In situ* conservation was valued more often than *ex situ* conservation.

In most cases the focus of valuation was on specific attributes or traits of a breed or a variety, such as health-related issues (disease resistance, health status, frequency of illness), body conformation and weight, fertility, water-related issues (frequency of bathing or watering, drought tolerance) or feed purchase requirements. Studies that focused on breeds or varieties typically valued local breeds or varieties in comparison to crosses or exotic breeds/varieties. Studies on conservation programmes measured the value of protecting a local or an endangered breed or variety, or estimated the benefits of improved cultivars.

Genetic resources in agriculture are typically of local importance. Thus the study area was in most cases local or regional. Few studies were conducted at the national

Table 1. Summary statistics for the data used in this study.

	Studies (n = 22)	
	Number	%
Genetic resource		
Plant/crop	9	40.9
Animal	13	59.1
Species		
Cattle	7	31.8
Pig	3	13.6
Goat	1	4.5
Sheep	1	4.5
Horse	1	4.5
Rice	5	22.7
Maize	2	9.1
Coffee	1	4.5
Agrobiodiversity	1	4.5
Focus of valuation ^a		
Attribute/trait	14	53.8
Breed/variety	5	19.2
Conservation programme	7	26.9
Geographic scope		
Local	5	22.7
Regional	12	54.5
National	4	18.2
International	1	4.5
Continent		
Africa	10	45.5
Asia	5	22.7
Europe	2	9.1
South America	4	18.2
Several continents	1	4.5
Valuation method ^b		
Choice experiment	11	45.8
Contingent valuation	3	12.5
Hedonic pricing	4	16.7
Combined stated and revealed preference	1	4.2
Other	5	20.8

Notes: ^aThree studies valued both attributes and breeds/varieties and one study both attributes and conservation programmes. ^bOne study used three different valuation methods.

or international level. The studies originated from Africa, Asia, Europe and South America, and one of them covered several continents. 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 United States.

Most studies on genetic resources in agriculture estimated values from the perspective of farmers or livestock-keepers. In most cases, the emphasis seemed to be on use values, although the estimated value categories were not always mentioned. Many studies focused on private values only, and merely one study reported that it estimated both use and non-use values (Cicia et al. 2003). In the valuation of genetic resources, use values are typically associated with producers and non-use values with consumers (Gollin and Evenson 2003), a fact that was also observable in our data.

Table 2. Variable descriptions and summary statistics ($n = 93$).

Variable	Description	Mean	SD
WTP	Dependent variable, mean WTP or WTA in 2008 international dollars	379.60	709.067
SAMPLE	Sample size, continuous	278.68	130.806
GRAIN	1 if the valued genetic resource is a grain, 0 otherwise	0.02	0.146
AGROBIOD	1 if the valued genetic resource is agrobiodiversity, 0 otherwise	0.28	0.451
ANIM ^a	1 if the valued genetic resource is animal, 0 otherwise	0.70	0.461
BREEDVAR	1 if the object of valuation is a breed or a variety, 0 otherwise	0.10	0.297
PROGRAM	1 if the object of valuation is a conservation programme, 0 otherwise	0.17	0.379
ATTRI ^a	1 if the object of valuation is an attribute, 0 otherwise	0.73	0.446
CATTLE	1 if the valued AnGR is cattle, 0 otherwise	0.42	0.496
BREEDXOT	1 if the valued AnGR is an exotic breed, 0 otherwise	0.03	0.178
BREEDCROSS	1 if the valued AnGR is a cross-breed, 0 otherwise	0.03	0.178
BREEDLOC	1 if the valued AnGR is a local breed, 0 otherwise	0.04	0.204
LOCAL	1 if the geographic scope is local, 0 if regional	0.10	0.297
MULTNAT	1 if the study is conducted in multiple countries, 0 otherwise	0.09	0.282
YEAR	Study year, continuous ranging from 1 (1998) to 9 (2006)	5.90	2.006
GDP	1 if the country's gross domestic product is above \$10,000 per capita per year, 0 otherwise	0.38	0.487
HEDONIC	1 if the valuation method is HP, 0 otherwise	0.10	0.297
CV	1 if the valuation method is CV, 0 otherwise	0.04	0.204
SPRP	1 if the valuation method is combined stated and revealed preference, 0 otherwise	0.09	0.282
CE ^a	1 if the valuation method is choice experiment, 0 otherwise	0.77	0.420
WTA	1 if the value measures WTA, 0 otherwise	0.32	0.470
NEGWTP	1 if the value measures a negative WTP, 0 otherwise	0.12	0.325
POSWTP ^a	1 if the value measures a positive WTP, 0 otherwise	0.56	0.499

Notes: WTP, willingness-to-pay; WTA, willingness-to-accept; AnGR, animal genetic resources; HP, hedonic pricing; CV, contingent valuation; SD, standard deviation. ^aIndicates the omitted variable.

Valuation methods used included CV, choice experiments, HP, combined revealed and stated preference methods, changes in yields, avoided costs and determination of the value of an increase in improved varieties. CV was used to value conservation programmes, and choice experiments and HP to value breeds or varieties and their attributes. In all cases the valued attributes were related to the use of the breed or variety, regardless of the valuation method.

The first priority in genetic resource valuation appears to have been to establish values for different kinds of genetic resources. In addition, methodological tests were conducted to examine the heterogeneity of preferences between different groups of people in choice experiments (e.g. Ouma et al. 2007; Omondi et al. 2008a; Roessler et al. 2008). Stated preference results were also validated by comparing them to revealed preference data (e.g. Scarpa et al. 2003a; Omondi et al. 2008b).

The increasing interest in economic analyses of genetic resources is apparent in the observations, as most studies were published and also conducted in the 2000s. The majority of studies were refereed journal articles. A few book chapters and discussion papers were also included.

Table 2 presents the descriptive statistics for those observations that were included in the meta-regressions. Most of the studies in the data produced several value estimates. The reasons for multiple value estimates were

that studies presented values for several traits, different breeds or varieties or multiple conservation programmes. The number of value estimates from a single study varied from 1 to 26. Figure 1 presents the distribution of the WTP and WTA estimates after conversion to absolute values. The mean value for a genetic resource was approximately 380 dollars per household as a lump sum and the median was 53 dollars. The weighted mean, weighted by the sample size, was 383 dollars. All values are presented in 2008 international dollars.

Table 3 presents the descriptive statistics on the value estimates for the two data sets and separately for WTP and WTA. It is noteworthy that the WTA estimates were significantly higher than the WTP estimates. According to the Kolmogorov–Smirnov test, the distributions were statistically different with respect to their location and shape.⁴ The highest value estimates were obtained from one of the two European studies, which estimated the WTA for general agrobiodiversity characteristics (Birol et al. 2006a; Birol et al. 2006b). The higher estimates for WTA compared to WTP is expected, as WTA studies on losses of resources generally tend to produce higher estimates, a phenomenon referred to as loss aversion (Kahneman et al. 1991; Tversky and Kahneman 1991).

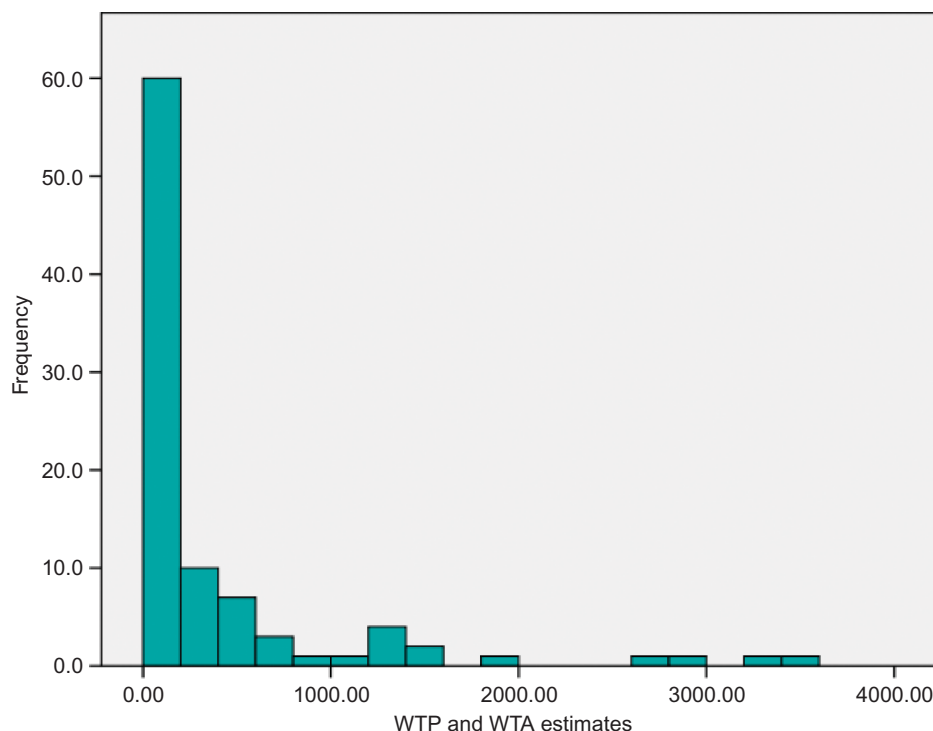


Figure 1. The distribution of the willingness-to-pay (WTP) and willingness-to-accept (WTA) estimates.

Table 3. Willingness to pay (WTP) and willingness to accept (WTA) from the two data sets (all and animal genetic resources (AnGR) observations).

WTP/WTA per household in 2008 international dollars	Value measure	Mean	Median	Standard error of mean	Minimum	Maximum
All observations ($n = 93$)	WTP	89.6	31.4	17.8	0.14	682.8
	WTA	988.7	613.0	181.3	16.3	3480.3
AnGR observations ($n = 65$)	WTP	92.5	18.3	31.8	0.45	682.8
	WTA	638.6	626.3	350.7	16.3	1285.3

Meta-regression results

The focus of the meta-analysis was on determining which variables were significant in explaining the WTP or WTA for genetic resources and the signs of the variables. The robustness of the results between the data sets was also of interest. Due to the limited amount and the heterogeneity of the meta-analytic data, marginal values should be regarded with caution. Apart from the variable WTA, there were no strong prior expectations regarding the signs of the variables.

Table 4 presents the results of the meta-regression models for all observations and Table 5 for AnGR. The results are presented for both unrestricted and restricted models. Restricted models include all variables describing the valued good, regardless of their significance, and exclude other variables that were not significant at the 10% level in the unrestricted models.

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 0.57 and 0.74 and adjusted R^2 statistics between 0.53 and 0.69. The F -statistics were between 3.69 and 9.44, indicating overall significance for all regressions.

The variables describing the valued good were statistically significant only in the data set that includes all observations. GRAIN was negative, indicating a lower WTP or WTA for grains compared to AnGR and agrobiodiversity. The significant positive coefficient on the variable BREEDVAR shows that breed and varieties are valued higher than individual attributes, which seems plausible. PROGRAM was significant and positive, which signifies a higher WTP or WTA for conservation programmes than attributes.

Other study-specific features were also significant in explaining WTP and WTA in both data sets. The variable YEAR was significant and negative, indicating that values have declined over time. Other meta-analyses on environmental goods have displayed both negative and

Table 4. Meta-regression models for all observations.

Variable	Model 1, unrestricted		Model 2, restricted	
	Coefficient	Standard error	Coefficient	Standard error
(Constant)	667.483***	211.532	635.325***	166.159
GRAIN	−174.060*	102.966	−163.280	98.478
AGROBIOD	297.367	361.490	122.710	300.924
BREEDVAR	112.316**	54.292	115.768**	54.290
PROGRAM	1186.205***	404.051	1140.139***	383.212
LOCAL	−35.801	82.553		
YEAR	−79.656***	27.080	−75.957***	21.896
GDP	−408.171***	131.222	−387.312***	103.951
HEDONIC	−73.098	293.597		
CV	−1165.692***	421.253	−1156.242***	395.021
SPRP	−527.847	363.654		
WTA	505.967**	81.027	519.180**	249.768
NEGWTP	−165.579**	211.532	−170.049**	80.282
R^2	0.606		0.576	
Adjusted R^2	0.547		0.531	
F -statistic	7.04		9.44	

Notes: Linear regression, weighted least squares, all observations, $n = 93$. Dependent variable: WTP or WTA for genetic resources in international dollars. *, ** and *** Variables are significant at the 10%, 5% and 1% levels, respectively.

Table 5. Meta-regression models for AnGR.

Variable	Model 3, unrestricted		Model 4, restricted	
	Coefficient	Standard error	Coefficient	Standard error
(Constant)	876.604***	285.776	915.226***	254.455
CATTLE	−71.520	99.370	−92.600	79.863
BREDEXOT	67.166	89.515	91.147	87.003
BREEDCROSS	113.306	124.532	137.287	123.771
BREEDLOC	112.304	123.649	128.544	115.275
LOCAL	−130.024	120.123		
MULTNAT	−63.497	81.097		
YEAR	−96.252***	31.674	−103.174***	28.575
GDP	−562.104***	211.031	−594.303***	175.073
HEDONIC	−347.814**	154.550	−345.463**	147.112
CV	109.339	175.909		
WTA	458.024*	229.733	457.307*	231.532
NEGWTP	−162.394*	93.663	−159.774*	80.564
R^2	0.742		0.734	
Adjusted R^2	0.683		0.690	
F -statistic	3.69		4.65	

Notes: Linear regression, weighted least squares, AnGR observations, $n = 65$. Dependent variable: WTP or WTA for genetic resources in international dollars. *, ** and *** Variables are significant at the 10%, 5% and 1% levels, respectively.

positive trends in values (see e.g. Johnston et al. (2003); Lindhjem (2007)). Possible explanations for the negative sign include changes in preferences over time, the development of valuation methodology, which has lowered the estimated values (Johnston et al. 2005), and changes in the publication selection process (Van Houtven et al. 2007).

The variable describing the income level of the country, GDP, was consistently significant and negative in the models. A positive effect of income on WTP is generally expected. It should be noted that GDP correlates positively with the value estimates, as high estimates were found in the Hungarian study (Birol et al. 2006a; Birol et al. 2006b),

which is separated with its own dummy variable. Some high value estimates were also found in low GDP countries, which could explain the observed negative sign for GDP.

The valuation methods were also significant in determining the values, but the results differed somewhat between the data sets. Although HP was negative in both data sets, it was significant only in the AnGR models. CV was negative and significant in the more encompassing data set. This seems to indicate that choice experiments have produced higher estimates than other methods, a finding also reported by Richardson and Loomis (2009).



Table 6. Willingness-to-pay (WTP) for different genetic resources.

Scenario	WTP in 2008 international dollars
Protecting an animal breed in Europe	506
Maintaining general agrobiodiversity	629
Conservation programme for grain	343

WTA was positive and statistically significant in determining the values in all models, confirming the result obtained in comparing the means for different value measures. NEGWTP was negative and significant in both data sets.

Due to the non-significance of the variables describing the valued genetic resource in the AnGR models, it is reasonable to use the results from a model that includes all observations to predict the benefits from specific scenarios affecting genetic resources. Thus, the restricted model including all observations was used in the predictions. Table 6 presents the value estimates for three genetic resource scenarios. The first scenario concerned a programme to conserve an animal breed in Europe, the second was a scenario for maintaining general agrobiodiversity and third a conservation programme for grain genetic resources. The values were predicted as WTP instead of WTA to obtain more conservative estimates. Variables CV and LOCAL were specified at their mean values for each scenario. GDP was defined to be above 10,000 dollars per capita per year for all scenarios. The variable YEAR was specified to be 2008.

The WTP estimates in Table 6 is presented as lump sums per household. Agrobiodiversity received the highest WTP, followed by the European animal breed and the crop conservation programme. This might indicate a preference for a comprehensive approach on genetic resource conservation, although it should be noted that the results on the value of agrobiodiversity are based on only one study. WTP ranged from \$343 to \$629 per household. The value estimates should be regarded as indicative due to the limited amount of data.

The predicted values were generally quite large compared to the value estimates from the original studies, especially for the crop conservation programme. These disparities reflect the insufficient number of valuation studies for some genetic resources.

Discussion

This study examined and summarised the existing information on the value of AnGR and PGR in agriculture by means of qualitative and quantitative analyses. The review indicates that despite growing interest in the economic valuation of farm genetic resources, empirical studies reporting monetary values are at present rare. We found 20 studies on AnGR and PGR, 14 of which could be included

in the meta-analysis, altogether providing 93 value estimates. Examination of the existing literature revealed a number of issues relating to the current situation in the valuation of genetic resources, and was useful in determining future research needs for genetic resources in agriculture.

The meta-regressions revealed that the focus of valuation has had a significant effect on the value of genetic resources. Grain genetic resources were valued lower compared to AnGR and agrobiodiversity, and the values of breeds or varieties and conservation programmes were higher than those of individual attributes. In addition, the value measure (WTP, WTA) had an effect on the value estimates and values seemed to have declined over time.

A challenge is that although different genetic resources, geographic locations and valuation methods were covered in the studies, the possibilities to generalise the findings are in many cases modest. Most of the studies were location- and species-specific and accurately described only limited circumstances. The number of studies on certain genetic resources and from particular geographical areas was so low that it is difficult to conclude much on the value of protecting genetic resources there. For example, only two European studies were found 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 generalisation of these results to other contexts is difficult.

Most studies estimated the use values of genetic resources from the perspective of farmers and livestock-keepers. Although it has been argued that the value of farm genetic resources may mainly consist of use-related values (Gollin and Evenson 2003), the relative magnitude of use and non-use values in AnGR and also PGR is still unknown. It is probable that the general public, at least in developed countries, holds both use and non-use values for the protection of threatened or endangered genetic resources in agriculture. The magnitude of these non-use values compared to use values is worth studying, and is one of the possibilities for future research.

There is a need to use stated preference methods for estimating the non-use value component of genetic resources. Thus far, most studies have utilised choice experiments, which are well suited to valuing genetic resources due to their flexibility and ability to value the traits of breeds or varieties. However, CV is useful in valuing conservation programmes. Combining stated preference and revealed preference methods can also be considered a promising future research direction (Smale et al. 2006).

Regarding the meta-analysis, more and better data would reduce multicollinearity and enable the inclusion of more explanatory variables. Not all variables describing certain genetic resources were significant, which may stem from the limited number of observations for these genetic resources, such as different species or breeds and varieties.

The low number of studies from high income countries is problematic, as conclusions cannot be made concerning the effect of income on WTP or WTA for genetic resources. However, the number of studies was adequate for estimating the meta-regressions and calculating the regression based WTP estimates. The meta-analysis revealed a higher value for conservation programmes and breeds and varieties over individual attributes. It also gave methodological insights showing choice experiments to produce higher values for genetic resources.

Conclusions

Based on existing literature on the monetary value of genetic resources in agriculture, the value of AnGR in developing countries has been most widely investigated. Future research should focus on issues and genetic resources that have thus far been less studied or have not been studied at all. These include improving our knowledge of the value of PGR, obtaining value estimates for maintaining the genetic diversity in Europe and the United States, estimating the relative magnitude of use and non-use values and determining the value consumers place on genetic resources and diversity in agriculture.

Valuation information could guide decision-making and help define the focus of conservation. Determining the importance of local breeds for citizens might offer strong motivation for the conservation of genetic resources. As financial and time-related resources are often limited, it is not possible to conduct a primary valuation study in every decision-making context. The focus of future research should be on developing a diversified and large enough body of literature on the value of genetic resources that would serve as a base for benefit transfers. In benefit transfer value estimates for conserving certain genetic resources are transferred from one site to another while adjusting the estimates for differing conditions, for example, the income level or the availability of substitutes. More generalisable knowledge is essential for conducting benefit transfers, as current information on the value of genetic resources is fragmented and context-specific.

The requirements of transferring benefits should be taken into account in designing and reporting future studies (Loomis and Rosenberger 2006). Detailed reporting of the features of the original study related to the valued good, market area and population and welfare measures is central for benefit transfer. Furthermore, it is essential to address the previously identified gaps in knowledge to improve the premises of conducting benefit transfers in genetic resource valuation, and to target issues that are of particular relevance to policy-making (Loomis and Rosenberger 2006).

Studies more extensively covering the value of PGR, the value consumers place on genetic resources, and values in developed countries would significantly complement existing knowledge. Striving for a more complete database on the value of genetic resources in agriculture would be of great help to researchers and policy-makers alike.

Notes

1. Several studies provide a variety of approaches to assess the economic aspects of genetic resource conservation and information that can be included in decision-making, but they do not provide benefit estimates. These include several studies that have examined the indicators or determinants of crop diversity (e.g. Smale 1998; Benin et al. 2006; Gebremedhin et al. 2006; Van Dusen 2006). Brush and Meng (1998) have addressed the demand for specific plant varieties. For AnGR, Tano et al. (2003) have studied farmers' preferences for cattle traits. In developed countries, the focus has in many cases been on the benefits of animal improvement programmes (e.g. Ladd and Gibson 1978; Mitchell et al. 1982; Richards and Jeffrey 1995). Costs of genetic resource conservation have been presented, for example, by Smith (1984), Heisey et al. (1997), Koo et al. (2004), Virchow (2005) and Pattison et al. (2007).
2. The data used in the adjustments are from the IMF World Economic Outlook Database (October 2009), <http://www.imf.org/external/pubs/ft/weo/2009/02/weodata/index.aspx>.
3. Both GDP and CPI data were from the IMF World Economic Outlook Database (October 2009).
4. The non-normality of the distribution of value estimates requires the use of a non-parametric test.

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Appendix 1. Primary studies included in analysis.

Study	Authors and publication year	Study/data year	Country	Genetic resource	Species	Valuation method	Mean WTP/WTa ^a	No. of value estimates	Included in meta-analysis
1	Evenson (1998)	1971–1990	Indonesia	PGR	Rice	HP	NA	NA	No
2	Rao and Evenson (1998)	1977–1989?	India	PGR	Rice	Yield changes	NA	NA	No
3	Gollin and Evenson (1998a)	1965–1990	several	PGR	Rice	Increase in improved varieties	NA	NA	No
4	Gollin and Evenson (1998b)	1965–1986	India	PGR	Rice	HP	NA	NA	No
5	Cicia et al. (2003)	2000	Italy	AnGR	Horse	CV	47.1	1	Yes
6	Jabbar and Diedhiou (2003)	1993–1994	Nigeria	AnGR	Cattle	HP	NA	NA	No
7	Scarpa et al. (2003a)	2000	Mexico	AnGR	Pig	CE	21.2	7	Yes
8	Scarpa et al. (2003b)	2000	Kenya	AnGR	Cattle	CE	154.0	4	Yes
9	Scarpa et al. (2003b)	2000	Kenya	AnGR	Cattle	HP	114.4	3	Yes
10	Smale et al. (2003)	1999–2000	Mexico	PGR	Maize	Yield advantages	NA	NA	No
11	Drucker and Anderson (2004)	2000	Mexico	AnGR	Pig	CV	16.7	1	Yes
12	Birol et al. (2006a, b)	2002	Hungary	PGR	Several	CE, RP, combined SP and RP	1042.5	26	Yes
13	Birol and Villalba (2006)	2004	Mexico	PGR	Maize	CE	NA	NA	No
14	Hein and Gatzweiler (2006)	2004	Etiopia	PGR	Coffee	Avoided costs, yield increases	NA	NA	No
15	Makokha et al. (2007)	2002?	Kenya	AnGR	Cattle	CE	883.7	4	Yes
16	Ouma et al. (2007)	2004–2005	Kenya, Ethiopia	AnGR	Cattle	CE	28.8	8	Yes
17	Roessler et al. (2008)	2004	Vietnam	AnGR	Pig	CE	7.9	5	Yes
18	Omondi et al. (2008a)	2006	Kenya	AnGR	Goat	CE	61.3	8	Yes
19	Omondi et al. (2008b)	2006	Kenya	AnGR	Sheep	CE	35.5	4	Yes
20	Zander and Drucker (2008)	2003–2004	Ethiopia	AnGR	Cattle	CE	111.3	11	Yes
21	Zander and Drucker (2008)	2003–2005	Kenya	AnGR	Cattle	CE	151.4	9	Yes
22	Poudel and Johnsen (2009)	2003	Nepal	PGR	Rice	CV	0.2	2	Yes

Notes: WTP, willingness-to-pay; WTA, willingness-to-accept; PGR, plant genetic resources; AnGR, animal genetic resources; NA, not available; CV, contingent valuation; CE, choice experiments; HP, hedonic pricing/hedonic valuation; RP, revealed preference; SP, stated preference. ^aWTP/WTA is reported in 2008 international dollars.