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Review

European biodiversity assessments in livestock science: A review of research characteristics and indicators

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ABSTRACT

Developments in agriculture are a main driver for biodiversity loss, in which livestock play a major role through pastures and feed crop cultivation. Addressing biodiversity loss is challenging due to the broad definition of and the multitude of indicators for biodiversity. We reviewed scientific literature assessing effects of livestock on biodiversity in Europe, to provide an overview of general characteristics of these studies and their indicators for biodiversity. The search was performed in SCOPUS and Web of Science and yielded 857 records after deduplication, which was narrowed down to 131 articles that assessed biodiversity impacts of livestock in Europe. Analysis of these articles focused on general characteristics of the research (i.e. context, scale, species, function of livestock, approach), indicators used, and the general conclusion regarding the impact of livestock on biodiversity. The majority of articles studied biodiversity in France, UK, Italy, Germany and Spain; and studied the direct impact of grazing cattle and sheep on biodiversity at field scale. Indirect impacts of livestock on biodiversity through feed production were assessed in few studies. In about one third of the studies, the function of livestock was not related to food production, but to conservation of open landscapes through grazing. We found a large variety of indicators used to assess the impact of livestock on biodiversity. The indicators were divided in seven clusters: 1) DNA, breeds, populations, 2) abundance and richness, 3) traditional diversity indices, 4) novel diversity indices, 5) composition and function, 6) structure and habitats, and 7) qualitative scoring systems. The majority of studies included the indicators abundance and richness, although studies differed in the plant or animal species studied. Indicators used differed across scales and between functions of livestock. Studies with a conservation function of livestock more often used indicators from clusters 5 and 6 than studies with a food production function. A positive impact of livestock on biodiversity was often found in studies with a conservation function, whereas a negative impact of more intensive livestock was often found in studies with a food production function. The identified indicators for biodiversity were connected to different assumptions and values, and therefore answer different questions and present different conclusions regarding the state of biodiversity. This review provides insight in biodiversity assessments of livestock across scales and purposes; highlights that few studies linked livestock to their indirect impacts on biodiversity; and stresses that one should be critical about the indicators used for biodiversity.

1. Introduction

Biodiversity is vital to ecological functioning, the provision of ecosystem services such as the production of food, soil fertility, pollination and climate regulation, and human wellbeing (Kremen, 2005; Millennium Ecosystem Assessment, 2005). Human activities, including agriculture, contribute to changes in ecosystems and loss of biodiversity (Millennium Ecosystem Assessment, 2005). Current losses in biodiversity are considered as critical and could threaten the Earth system functioning and its adaptive capacity (Steffen et al., 2015).

Overexploitation of habitats and developments in agriculture are considered as main drivers for biodiversity loss (Kleijn et al., 2009; Maxwell et al., 2016). Of the losses in terrestrial biodiversity caused by European agriculture, 76% is estimated to be caused by livestock (Leip et al., 2015). At the same time, traditional livestock systems are acknowledged to play an important role in conservation of biodiversity (Herzog et al., 2012; LEAP, 2015). Livestock, therefore, is a main driver of biodiversity loss, but can also be used to conserve or restore biodiversity (Herzog et al., 2012; LEAP, 2015).

The European Union has launched and supported several international (i.e. Aichi, SDGs) and own initiatives to reverse the trend in biodiversity loss, such as the Birds Directive and Habitat Directive. The

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EU reinforced the commitment releasing the EU Biodiversity Strategy to halt the loss of biodiversity by 2020 (European Commission, 2011). Among the different targets, the strategy sets out to increase the contribution of agriculture to maintain and enhance biodiversity (i.e. Target 3). Within European agriculture, biodiversity is addressed in the Common Agricultural Policy (CAP). So-called greening measures of the CAP aim to increase biodiversity within conventional agriculture, and rural development programmes support traditional practices and agri-environment measures (EC, 2017). Despite numerous initiatives to conserve biodiversity on farmland, however, biodiversity continues to decline (EEA, 2018; Kleijn et al., 2011). The EU is currently preparing the Biodiversity Strategy 2030. This calls for European directions and strategies to enhance biodiversity.

Although the concept of biodiversity is well described and accepted, the concept is broad and aspects of biodiversity are valued differently among stakeholders (Duelli and Obrist, 2003). In addition, addressing biodiversity loss is challenging because effectiveness of measures is context-specific (Kleijn et al., 2011), and is further complicated by the multitude of indicators that is used for biodiversity across studies and scales (Bockstaller et al., 2011; Duelli and Obrist, 2003; LEAP, 2015). For instance, at a national scale, population data on the number of bird and butterfly species (i.e. richness) and individuals per species (i.e. abundance) are collected. These population statistics are used to inform policy about trends in biodiversity (EEA, 2018). However, these measurements are not available for all species groups, are labour-intensive to collect, and are difficult to link directly with management practices and thus agricultural policy. To assess impacts of management practices or agro-environmental measures on biodiversity, many other indicators are used, which each reflect some measure of diversity or habitat quality.

Thus, to monitor biodiversity, many indicators are used that each give a partial picture of biodiversity. The chosen indicator for biodiversity will likely be linked to the study objective. The study objectives, however, may not align with policy aims (Kleijn et al., 2011). There is a need for a comprehensive understanding of used indicators, to identify which can be used to monitor biodiversity targets at different scales (CBD, 2019). This paper aimed to review scientific literature assessing effects of livestock on biodiversity in Europe, with a focus on general research characteristics and the indicators used for biodiversity. Insights into the heterogeneity of research and existing biodiversity assessment methods in relation to livestock can be valuable to identify hotspots and gaps in livestock research, and to reflect on the implications of indicator choice for policy making.

2. Material and methods

We conducted a systematic review of scientific literature about impacts of livestock on biodiversity in Europe, and assessed general characteristics of the studies, biodiversity indicators used, and general conclusions. The literature search was performed using keywords and Boolean operators. First, several search queries were evaluated in SCOPUS to ensure inclusion of relevant papers. The final search for research articles that assessed impacts of livestock on biodiversity focused on the aspects livestock, agriculture and biodiversity assessment and was restricted to research articles from peer-reviewed scientific journals in English (exact queries in Supplementary Material S1). The search was performed in SCOPUS and Web of Science on 18-09-2017. The search yielded 677 records in SCOPUS and 577 records in Web of Science. These records were exported into EndNote. Subsequently, duplicate records were systematically removed. After deduplication, 857 records remained.

The remaining records were narrowed down to relevant articles based on the following selection criteria. Articles were excluded if they did not measure, model or test biodiversity, when the system described in the article did not involve livestock, or when the study was not conducted in Europe, unless studies were at continental or global scale and included Europe. These were applied in two rounds, first based on titles and abstracts and subsequently looking at the whole article. Based on these selection criteria, the 857 records were narrowed down to 145 articles to be downloaded for analysis based on titles and abstracts. Looking at the whole articles, this was narrowed down to 131 articles to be included in the analysis.

Analysis of the articles focused on the general characteristics of the research, indicators used to assess the impact of livestock on biodiversity, and the general conclusion regarding the impact of livestock on biodiversity. To develop an overview of the studies included, several general characteristics were coded, including year of publication, context, scale of focus of the study, livestock species, function, and approach of the research. The context of the study referred to the country in which the assessment was based, unless this was at continental or global scale. The categories for scale of focus of the study were revised in response to the included studies, which resulted in five scales: genetic scale, field element scale (e.g. river margins, swards within grassland), field scale (e.g. grazed versus not grazed fields), farm scale (in- or excluding off-farm inputs), and landscape or larger scale (anything beyond the level of the farm, from region to country to global level). Scale refers to the focus of the study, not to the scale of biodiversity measurements. For example, a study about differences between organic and conventional dairy farms (farm scale focus) may still only look at plant diversity in plots within the grassland. Livestock species studied were categorised as cattle, goat, sheep, horse, chicken, pig, other, and general livestock. In case of general livestock, the research had no emphasis on particular species and used a method of genetic biodiversity that could be applied to any livestock species, used grazing intensity only, or focussed on multiple species. Function referred to the fact that livestock can be farmed for different purposes and can fulfil different functions (e.g. food production, conservation, insurance). In this review, three categories of functions were distinguished based on the functions encountered in the reviewed articles: food production; conservation (i.e. studies about habitat restoration, conservation and land abandonment); and mixed (i.e. food production and conservation such as grazing in a marginal area). In some cases, functions were not applicable. The biodiversity assessment approach used in a research was categorized as measured (in fieldwork and/ or subsequent statistical approaches), modelled, or based on a qualitative scoring system. Additionally, articles with a measured approach were checked for the use of comparisons of treatments or changes over time, assessments of species composition (ordination techniques), and other statistical approaches (regression, factor analysis).

To provide a systematic overview of indicators used to assess the impact of livestock on biodiversity, indicators used in research were listed. Background information on the indicators was gathered from the papers and additional literature. Finally, the general findings of each study with respect to the impact of livestock on biodiversity were evaluated. Based on the abstract and conclusions, the impact of (more intensive) livestock on biodiversity was classified as positive, negative, both positive and negative, neutral or not applicable. Depending on the study, for example, this could be a comparison of livestock versus no livestock (such as abandonment versus grazing), or conventional versus organic livestock keeping (i.e. conventional was assumed to be more intensive than organic). In case of assessments of genetic biodiversity, the study's conclusion regarding the current biodiversity status of the breed or species was considered to be negative, positive, or neutral based on the interpretation of the article.

Further integration of findings of the studies was difficult, due to the huge variation in study design and biodiversity indicators. However, encountered similar findings were aggregated and described, to highlight aligned conclusions and to illustrate lack of consistency of effects between indicators and species groups.

3. Results

3.1. General characteristics

The literature search yielded 131 articles that assessed the impact of livestock on biodiversity (a list of included studies and their characteristics and indicator cluster use can be found in Supplementary Material S2). The majority of articles studied biodiversity in France, UK, Italy, Germany, and Spain. Not all articles focussed on a specific country; some studied impacts of livestock on European (n = 4) or global (n = 4) biodiversity. The impact of livestock was in the majority of studies assessed at the field scale (n = 72), followed by landscape (n = 22) and farm scale (n = 19). A limited number of studies focussed on genetic scale (n = 12) and the scale of field elements (n = 6).

The majority of studies considered the impact of cattle and sheep on biodiversity (Fig. 1). At field scale, all studies focussed on the impact of grazing, from ruminants, horses and undefined species. At farm scale, the majority of the studies focussed on cattle. Studies on chicken and pigs were limited in number.

The function of livestock in the included studies was divided between food production (34%), conservation (36%), and mixed (28%) (2% not applicable; n = 3). Studies in France, UK, Germany and Ireland mostly assessed biodiversity in relation to food production, whereas studies in Italy, Spain and Finland mostly assessed biodiversity in relation to conservation (Table 1a). In studies focussing on cattle, pigs and poultry, the main function was food, whereas studies that focussed on sheep or goat either had a conservation or mixed function, but were never classified as a food production function alone (Table 1b).

The majority of the studies assessed the impact of livestock on biodiversity using measured data (n = 109), followed by modelling (n = 15) and a qualitative scoring system (n = 7). Across scales, measured data was the only approach used in studies at genetic and field element scale, and used in 97% of the studies at field scale. Farm scale studies showed the greatest variety in approaches, being equally likely to be measured, modelled, or qualitatively scored. At landscape scale, a third of the studies were modelled, the rest used measured data.

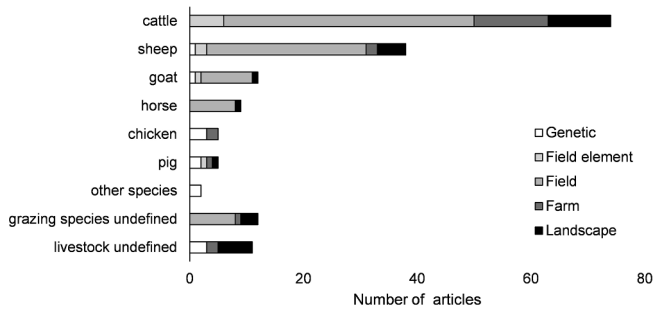

Fig. 1. Frequency with which livestock species were assessed at different scales of analysis. NB: 29 out of 131 studies included multiple species.

Table 1a
Percentage of studies with a food production, conservation or mixed function per country.[1]

	N	Food production	Conservation	Mixed
N		*44*	*47*	*37*
Country				
France	*20*	55	20	25
UK	*18*	44	33	22
Italy[2]	*16*	19	50	31
Spain	*11*	–	55	46
Germany	*11*	64	27	9
Ireland	*7*	86	–	14
Finland	*6*	–	100	–

[1] Table only includes countries with more than five articles (n = 89).
[2] Excluding one study classified as not applicable.

Table 1b
Percentage of studies with a food production, conservation or mixed function per livestock species group.[1]

	N	Food production	Conservation	Mixed
N		*44*	*47*	*37*
Species				
Cattle	*50*	50	34	16
Sheep and goat	*19*	–	58	42
Pigs and poultry	*7*	71	29	–

[1] Table only includes studies that focussed on one specified livestock species (n = 76).

3.2. Indicators for biodiversity

There are many indicators used in literature to measure biodiversity. Three main levels emerge from the general definition of biodiversity: genes, species and ecosystems (CBD, 1992). Therefore, we aimed to cluster the indicators around genetic, species, and landscape diversity. In total, we identified seven clusters of indicators across levels of biodiversity (Fig. 2). Indicators related to DNA, breeds and populations (i.e. genetic diversity) were clustered together (cluster 1). At species level, indicators were subdivided in four clusters because of the large number of studies reporting on species diversity and the different nature of indicators used. These cluster were: a cluster including species abundance (i.e. the number of individuals from a species) and species richness (i.e. the number of species) (cluster 2); clusters including traditional (cluster 3) and novel (cluster 4) diversity indices derived from abundance and richness; and a cluster on species composition and ecological functioning (cluster 5). At a landscape level, indicators addressed landscape diversity and related to spatial structure and habitats (cluster 6). The last cluster comprised qualitative scoring systems (cluster 7), that were based on indicators from genetic, species, and landscape diversity and additionally included management aspects that influence biodiversity. A more detailed description of the clusters and the indicators used within the clusters is given in the following sections.

Indicators used in the different studies varied, making some indicators and clusters more used and represented than others. An overview of the frequency and percentage of articles using indicators per cluster is given in Table 2. In 9% of the articles, indicators related to genetic biodiversity (i.e. DNA, breeds and populations (cluster 1)) were used. Species diversity related indicators (clusters 2–5) were used in 83% of the articles, whereas landscape diversity related indicators were used in 24% of the studies (cluster 6). Qualitative scoring systems were used in seven articles (5%). Of the indicators used to assess species diversity, indicators from cluster 2 'abundance and richness' (73% of all articles) and cluster 5 'composition and function' (53%) were more often used than from cluster 3 'traditional diversity indices' (30%) and cluster 4 'novel diversity indices' (9%).

A comparison of indicator clusters across scales shows that indicators for genetic diversity (DNA, breeds, populations; cluster 1) were only included in articles at genetic scale, and were the only indicators that were used at this scale. Indicators within the cluster abundance and richness (cluster 2) were used from field element to landscape scale, and were used in all studies at field element and nearly all studies at field scale. Novel diversity indices (cluster 4) were mainly used in studies at farm scale and landscape scale. Composition and function related indicators (cluster 5), like in cluster 2, were used from element to landscape scale, and were most commonly used at field element and field scale. Indicators for structure and habitats (cluster 6) were used from field to landscape scale. Finally, qualitative scoring systems (cluster 7) were mainly used at farm scale.

Irrespective of the function, the majority of studies included

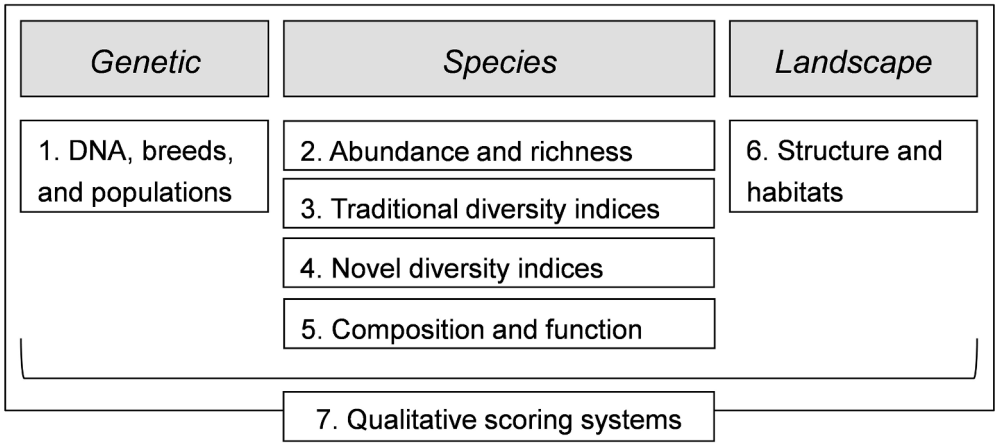

Fig. 2. Schematic representation of clusters of indicators for biodiversity.

indicators related to abundance and richness (cluster 2) (Table 3). In particular, conservation and mixed function studies commonly used indicators for abundance and richness, 85% and 87% respectively. Moreover, these studies commonly included indicators related to composition and function, structure and habitats and traditional diversity indices. In addition, conservation and mixed function studies more often combined indicators from multiple indicator clusters. While studies with a conservation and mixed function assessed indicators from on average 2.5 and 2.2 clusters, respectively, studies with a food production function used indicators from 1.5 clusters.

3.3. Indicator clusters

Detailed characteristics of the seven indicator clusters are described in the following sections. Which indicators were used within each cluster can be found in Supplementary Material S3.

3.3.1. Cluster 1: DNA, breeds, and populations

Twelve out of 131 studies used indicators that related to this cluster on genetic diversity. Half of these studies used microsatellites and/or single nucleotide polymorphisms as indicators for genetic diversity. Microsatellites are segments of DNA in which a short nucleotide sequence (1–6 nucleotides) is repeated several times, with alleles differing in the number of repeats of the sequence (Queller et al., 1993). The different alleles can be used to assess kinship. Five studies focussed on the number of breeding males and females of a species, its effective population size and inbreeding rate. The other study used the number of breeds or strains as an indicator for genetic biodiversity.

3.3.2. Cluster 2: Abundance and richness

The most commonly used indicators for biodiversity were species abundance and species richness (S). Abundance refers to the number of individuals of a certain species (or the (relative) area covered by a certain species), whereas richness refers to the number of species (i.e. Σs_i, where s_i is the ith species). Both indicators were used in 60% of the articles (n = 78), of which 75% articles reported both richness and abundance.

The species whose abundance or richness were assessed differed

Table 2
Frequency and percentage of articles that used indicators per indicator cluster; and percentage of articles at each scale that used indicators of each cluster. NB: many articles used multiple biodiversity indicators from different clusters.

Indicator clusters	N	%	Scale				
			Genetic (N = 12)	Field element (N = 6)	Field (N = 72)	Farm (N = 19)	Landscape (N = 22)
1. DNA, breeds, populations	12	9	100	–	–	–	–
2. Abundance and richness	96	73	–	100	96	37	64
3. Traditional diversity indices	39	30	–	17	44	5	23
4. Novel diversity indices	12	9	–	–	6	26	14
5. Composition and function	70	53	–	67	74	21	41
6. Structure and habitats	32	24	–	–	25	16	50
7. Qualitative scoring systems	7	5	–	–	1	32	–

Table 3
Percentage of studies of each function that used indicators from each cluster. NB: articles used multiple indicators for biodiversity from different clusters.

Function (N) Indicator clusters	Food production (44) %	Conservation (47) %	Mixed (37) %
1. DNA, breeds, populations	9	11	–
2. Abundance and richness	55	85	87
3. Traditional diversity indices	14	43	35
4. Novel diversity indices	16	6	5
5. Composition and function	25	72	68
6. Structure and habitats	14	36	24
7. Qualitative scoring systems	14	–	3

between studies. Plants were assessed more often than animals (68% vs 49% of studies that assessed abundance; 83% vs 37% of studies that assessed richness). Within plants, when a subset was explicitly mentioned, mainly vascular plants were measured. Within animals, invertebrates were more often studied than vertebrates. Beetles (*Coleoptera*) and butterflies and moths (*Lepidoptera*) were the most common invertebrates studied. Even within these categories, however, different subgroups were studied. For example, studies that assessed beetle abundance and richness focussed on beetles, ground beetles (family *Carabidae*) or dung beetles (superfamily *Scarabaeoidea*). Regarding vertebrates, mainly (specific) birds were assessed. Some authors argued that they used abundance and richness of vascular plants because these were representative for changes in other species groups (Klimek et al., 2014), whereas others stated these indicators were relatively easy to measure or that this data was available (Mueller et al., 2014).

Several studies specifically focused on a species of interest. For example, multiple studies focussed on a specific bird that was considered of high conservation importance, such as the griffon vulture in Spanish uplands and the hen harrier in the UK. Other studies focussed on red data book/red list species, endemic species or species that are typical for the habitat, and rare species.

3.3.3. Cluster 3: Traditional diversity indices

Cluster 3 focuses on traditional diversity indices that combine abundance and richness aspects into one diversity score (Heip et al., 1998). In 39 articles, traditional diversity indices were used. The Shannon index was the most commonly used diversity index, which was used in 66% of studies that used traditional diversity indices. The Shannon index (H′) is computed as:

$$H' = -\sum_{i=1}^{S} p_i \ln(p_i)$$

in which S is the total number of species (i.e. richness) in the community or sample, and p_i is the proportion of S made up of the *i*th species (i.e. relative abundance). How the Shannon index relates to richness and abundance is illustrated in Box 1. The Shannon index was mostly based on plants species (69%), and sometimes on animals (23%) or both plant and animal species (8%). Other studies reported using Simpson diversity index and Pielou's evenness index. Pielou's evenness index scales the Shannon Index from 0 to 1 (H'/H'_{max}), with 1 expressing that all species in the community are equally abundant. In addition, the exponent of the Shannon Index was used as diversity index and referred to as 'true' diversity because its value does not depend on the functional form of the index (Jost, 2006) (see Box 1). Almost half of the studies that used traditional diversity indices (n = 19) also included a measure of (dis)similarity to assess the degree to which samples/communities share the same species (see Supplementary Material S3for specific indicators).

Box 1

The Shannon index depends on species richness and the relative abundance of species. Relative abundance of species is a major determinant in the final score. For example, a sample with some, but equally represented, species results in a higher Shannon Index than a sample with twice the species, with one dominant species that has a relative presence of 50% and otherwise equally abundant species (Fig. box 1; left panel). An even distribution of species is generally favoured by ecologists, because it suggests a more robust ecosystem functioning, whereas the sample with higher richness is generally favoured by conservationists, because these intrinsically value the existence of rare species (Duelli and Obrist, 2003). Thus, the Shannon index may be a more relevant indicator for ecologists, whereas species richness may be more relevant for conservationists. Moreover, the Shannon index has been criticized for its unintuitive interpretation: a doubling of equally abundant species does result in a doubling of the index (Jost, 2006). It has been proposed to transform the Shannon index and other diversity indices to a ratio scale, to reflect the 'true' diversity' of species (Fig. box 1; right panel; Jost, 2006).

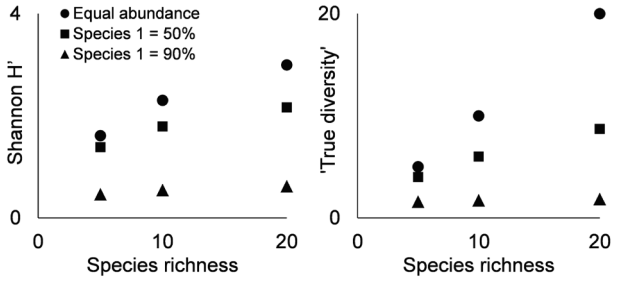

Fig. Box 1. Comparison of Shannon Index (H′; left panel) and 'true diversity' (exp(H′); right panel) for different species richness and relative abundance of species. Species were equally abundant, or had one dominant species with a relative abundance of 50% or 90%, with otherwise equally abundant species.

3.3.4. Cluster 4: Novel diversity indices

Novel diversity indices based on abundance and richness were used in 12 studies. Three indices were each used in three articles, these were the mean species abundance (MSA), potentially disappeared fraction (PDF) and multidiversity. The MSA and PDF modelled biodiversity loss linked to agricultural land use, compared with a reference situation. Multidiversity scores, in contrast, were computed from sampled data.

The MSA expresses the relative abundance of originally occurring species compared with the undisturbed ecosystem (Alkemade et al., 2009). The concept was only used at landscape scale (and beyond) to assess biodiversity impacts of grazing on natural rangelands (Alkemade et al., 2009), of a policy reform and agricultural land abandonment in the EU (Renwick et al., 2013) and of economic sectors in the Netherlands (Wilting and van Oorschot, 2017).

The PDF expresses the relative change in vascular plant species richness compared with the semi-natural woodland that would arise without human interference (Battini et al., 2016; Guerci et al., 2013). The method was used at farm scale only, in life cycle assessments of dairy production, expressing the impact of producing one kg milk on biodiversity. The PDF is computed using characterisation factors that express the relative richness loss for different agricultural practices (organic/intensive/less intensive) and land uses (De Schryver et al., 2010). One study applied a biodiversity weighting factor based on absolute species richness, irreplaceability and vulnerability of species in the calculation (Mueller et al., 2014).

Multidiversity is a metric based on the relative richness of multiple taxonomic groups (Allan et al., 2014). For each group, the proportion of species relative to the maximum observed number of species is calculated, after which the average proportion is computed across taxonomic groups. Multidiversity was used at field scale only. All three studies used multidiversity to combine their measurements into one score. One of these studies assessed multidiversity in relation to an indicator of land use intensity (Manning et al., 2015), as was done by Allan et al. (2014). This land use intensity was computed by aggregating the relative intensity of grazing (LU per year), mowing (cuts per year) and fertilisation (kg N per ha) compared to their respective means in the dataset.

Three studies in our search applied novel diversity indices that were only encountered once in this review. One study modelled a field-scale indicator of floristic diversity based on soil fertility and biomass utilization rate (% biomass removed by cutting and grazing; (Jouven and

Baumont, 2008)). Another study, using a life cycle approach, modelled the potential aquatic biodiversity loss (ABL) and reduction of potential terrestrial biodiversity (Tendall and Gaillard, 2015) with a method similar to the PDF. Finally, one study used an Auchenorrhyncha Quality Index to rank habitat quality based on the abundance and diversity of *Auchenorrhyncha* (i.e. a suborder including leafhoppers); and an arthropod-based biological soil-quality index that was assumed to relate with the number of microarthropod functional groups (Primi et al., 2016). Together, these indicators provided insight in above- and below-ground biodiversity. Both indices in this study were, like multidiversity, computed after sampling (i.e. not modelled).

3.3.5. Cluster 5: Composition and function

In total, 70 articles used indicators related to community composition and function to assess impacts on biodiversity. In 58 studies an ordination technique such as (canonical) correspondence analysis or nonmetric dimensional scaling was used to assess changes in community composition and ecological function (e.g. (Barbaro et al., 2004; Bucher et al., 2016)). These techniques often resulted in two-dimensional scatter plots depicting whether communities were similar (i.e. scatter plots of different communities overlapping), or different (i.e. separate non-overlapping scatter plots); and were first classified as an approach, rather than recognised as an indicator. However, for the sake of giving an overview of indicators for biodiversity, we felt that the method, being widely used to assess species communities and giving other information than the other indicators, should not be ignored. Features that were used in these ordination analyses included Ellenberg indices for ecological niche (e.g. (Bucher et al., 2016)), functional traits of plants (e.g. (Koch et al., 2017)), functional diversity of beetles and biological forms of micro-arthropods and aquatic macro-vertebrates (e.g. (Primi et al., 2016)).

Of the 12 articles that did not use ordination techniques, six categorised bird species based on traits. These used indicators such as 'Community Specialisation Index', 'Community Trophic Index' and 'Farmland Bird Index' or 'Grassland Specialisation Index'; or grouped farmland species and generalist species; species negatively or positively affected by abandonment and encroachment (i.e. winner and loses species); or species based on whether they potentially used the habitat for foraging and/or breeding (e.g. (Teillard et al., 2015)). Moreover, four studies clustered plants based on traits, based on tree versus shrub, woody versus grass, annuals versus perennials, and woody, riparian and sclerophyllous plant species (e.g. (Dostálek and Frantík, 2012)). One study assessed changes in plant composition by changes in percentage coverage of socio-ecological species groups (Schrautzer et al., 2016) and one study derived several biological water quality indicators compiled from the presence of different taxonomic groups in rivers (McMahon et al., 2012).

3.3.6. Cluster 6: Structure and habitats

Indicators related to the spatial structure of plants and habitats were used in 32 studies. To assess vegetation structure, 22 studies measured coverage by different height classes or plant categories. Commonly used indicators were mean vegetation height, or height of swards, herbaceous plants, shrubs and trees, or the canopy. Also the proportion of coverage of different vegetation types and bare ground, as well as the amount of dead material or litter were frequently evaluated.

Regarding habitats, 10 studies assessed richness, (relative) abundance, and Shannon index for land cover or land use types, as well as arable land to grassland ratio (e.g. (Teillard et al., 2015)). The use of abundance or a traditional diversity index applied to habitat types was scored as indicator of structure and habitats, because it does not focus on species diversity but on landscape diversity. For linear elements, such as rivers and hedgerows, indicators were either expressed as percentage of total area or length of the linear elements per ha.

Spatial organisation of the landscape was explicitly assessed in six studies, using patch size of arable land and grassland, grassland connectivity, effective mesh size, bordering habitats, and a distinction between edge and core area. For example, abandonment resulted in an increase in number of patches of pasture, but a reduction in total pasture area and a larger reduction of core area (Garbarino et al., 2014).

3.3.7. Cluster 7: Qualitative scoring systems

Seven studies used a qualitative scoring system to compare biodiversity between sites or over time, using one score. In all cases, a new scoring system was presented (summarized in Supplementary Material S3). The associations between indicators included in the scoring system and biodiversity were generally substantiated by literature, and in some cases determined by stakeholder and experts. The scoring systems based their final score on indicators from the other clusters – although the studies were only scored as 'cluster 7', because these sub-scores per indicator were not used as indicators themselves – in combination with management factors. Most scoring systems focussed on grassland, including management aspects such as grazing, mowing and fertiliser intensity. More specifically, recurring attributes were grazing intensity or pattern, date of first cut, and kg of fertiliser (N and P) application. Other recurring attributes were the presence or relative abundance of habitats – especially high-nature-value areas –, landscape elements and management techniques. Cropland was included as an indicator in terms of diversity of cultivated crops, and breeds as presence of and number of native breeds.

3.4. General conclusion regarding the impact of livestock on biodiversity

The general impact of (more intensive) livestock on biodiversity was classified as negative in 36% of studies, positive in 21% of studies, both positive and negative in 15% of studies, and not applicable or neutral in 26% of studies. Opposing patterns could be seen between food production and conservation functions. While studies in which livestock had a food production function found the impact of more intensive farming to be mostly negative, and never found it to be only positive, studies with a conservation function found the impact of livestock to be positive for biodiversity in almost half of the cases (Table 4). A positive impact of livestock on biodiversity was often found in studies that compared abandonment or no grazing with restoration or continuation of extensive grazing in e.g. heathlands and wetlands, whereas negative impacts of livestock were generally related to higher intensities, e.g. comparing organic and conventional farming.

Most similarities in studies were seen at field level, where all studies focussed on grazing. Regarding abundance and richness, studies concluded that grazing increased (Bucher et al., 2016; Gachet et al., 2009; Takala et al., 2012) plant species richness, but not in case of orchids (Catorci et al., 2013) and endangered plant species (Bucher et al., 2016). Moreover, grazing negatively affected abundance and richness of butterflies and moths (Kruse et al., 2016; Potts et al., 2009; Rickert et al., 2012; Schtickzelle et al., 2007) and small mammals (Amar et al., 2011; Ważna et al., 2016). Richness, abundance and diversity of beetles seemed to be greatest at intermediate grazing intensities (García et al., 2009; Kaltsas et al., 2013; Negro et al., 2011), though not always

Table 4
Percentage of studies with a farming, conservation or mixed function that find a certain effect of livestock.

N	*N*	Farming *44*	Conservation *47*	Mixed *37*
Effect of livestock				
Negative	47	61	13	38
Positive	28	–	49	14
Both positive and negative	19	11	17	16
Neutral	3	2	4	–
NA	34	25	17	32

[4]Studies with function classified as 'not applicable' were excluded (n = 3).

(Negro et al., 2007), and the impact of grazing differed across beetle species (Dennis et al., 1997). Also, grazing was found to change species composition (Burnside et al., 2007; Catorci et al., 2014; Farris et al., 2010; Marrs et al., 2007), to create structural diversity (Dennis et al., 1997; Ravetto Enri et al., 2017), and to stall plant succession and encroachment (Aptroot et al., 2007; Ascoli et al., 2013; Pollock et al., 2013; Tocco et al., 2013). Studies on abandonment and restoration of biodiversity through grazing observed that restoration did not yield as high biodiversity as before abandonment (Pöyry et al., 2005; Pykälä, 2005), and that endemic groups disappear with abandonment (Farris et al., 2010). Organic fields had a greater biodiversity than conventional ones (Hutton and Giller, 2003; Petersen et al., 2006; Power et al., 2013). Despite these seemingly aligned conclusions, further quantification of effects is not straightforward due to different study designs (for further illustration of this difficulty, see example in Supplement S4).

At farming system level, studies had various topics, of which two were recurrent. Studies on organic versus conventional dairy farms, similar to field level, concluded that organic farms had a greater biodiversity than conventional farms based on qualitative scoring systems (Del Prado et al., 2011; Haas et al., 2001; Schader et al., 2014). However, this finding was controversial when the total land use per unit milk was assessed using the indicator PDF: One study found that biodiversity loss per unit milk was lower for more intensive systems with a smaller land use per unit milk, despite a greater negative impact per unit area (Battini et al., 2016), the others had a smaller impact of organic systems, despite a larger land use per unit milk (Guerci et al., 2013; Mueller et al., 2014). Three studies focussed on ammonia emissions from pig and poultry farms, which reduced richness (Pitcairn et al., 2002) and changed composition (Frati et al., 2007; Von Bobrutzki et al., 2012) of plant species.

At landscape or larger scale, little similarity in topics was encountered, except for studies that assessed impacts of abandonment over time. Abandonment after grazing resulted in fragmentation of grassland and encroachment over time (Garbarino et al., 2014; Hannus and Von Numers, 2010; Herrando et al., 2014; Sirami et al., 2010). In the opposite direction, a change from extensive pastoralism towards intensive herding threatened biodiversity (Fonderflick et al., 2010).

4. Discussion

This paper aimed to review scientific literature assessing effects of livestock on biodiversity in Europe, with a focus on general characteristics and the indicators used for biodiversity.

Regarding general characteristics, the focus of most papers was on the direct impacts of grazing livestock on biodiversity at field scale, whereas indirect impacts of feed production were rarely studied. The few studies on pigs and poultry at farm level focused on direct impacts of ammonia emissions to the local environment (Frati et al., 2007; Pitcairn et al., 2002; Von Bobrutzki et al., 2012). There seems to be a gap regarding the linking of livestock to their indirect impacts on biodiversity, such as through feed and water use. A reason for this may be that it is complicated to find a common unit for biodiversity that could take these indirect effects into account (Winter et al., 2017). Of the losses in terrestrial biodiversity caused by European agriculture (based on MSA), 76% was estimated to be caused by livestock, mainly through feed production (Leip et al. 2015). Hence, of the indirect effects, externalisation of feed production and origin of feeds is of utmost importance to properly account for the impact of livestock on biodiversity.

In some studies, indirect impacts on biodiversity due to feed production were taken into account (Battini et al., 2016; Guerci et al., 2013; Mueller et al., 2014). These studies focused on dairy farms and analysed impacts on biodiversity using the PDF in a life cycle approach, i.e. studying the impact of milk production on relative plant species richness along the production chain. For animal production purposes, a life cycle approach on biodiversity impact is relevant for two reasons: 1) it includes the indirect impacts on biodiversity through land use for feed production, and 2) it expresses the biodiversity impact per unit of animal product. By doing so, both the total land use and the impact on biodiversity on this land are accounted for. This can provide insight in the discussion of land sharing, where production is more extensive to allow for more biodiversity within agriculture, and land sparing, where intensive production spares land for alternative use such as nature conservation (e.g. (Tuomisto et al., 2012)). However, using the PDF as sole indicator for biodiversity has limitations (Knudsen et al., 2017). First, the method focuses on local plant species richness, and does not provide information about the total plant species richness. As such, a landscape of only mixed pasture would have a better biodiversity score than a landscape that includes a mixture of pasture and natural forest – because the latter has a lower expected plant species richness – whereas a combination of both biomes would result in the largest total number of species. Second, the indicator does not include other taxa than plants, whereas biodiversity impacts may differ between taxa (Manning et al., 2015). Third, the PDF does not account for specific biodiversity that may be considered to have greater value, such as rare species or habitats. Finally, in the life cycle approach, a large biodiversity loss in one area can be compensated by a limited impact on other areas along the product chain. Despite these limitations, the PDF and life cycle approach can be relevant to make the indirect impact of livestock through feed production explicit. Also, it would enable a comparison of biodiversity impacts of different livestock species and production systems.

Conservation or restoration of open landscapes, as opposed to food production, was the main function of livestock in a third of the studies. In case of a conservation function, where food production is less or not relevant, a life cycle approach is unlikely to be a suitable tool, and the degree to which a landscape and its biodiversity and ecosystem services can be conserved may be more relevant. Duelli and Obrist (2003) argued that biodiversity indicators should be linked with one of three value systems for biodiversity: conservation, ecology, or biological control. Similarly, Kleijn et al. (2011) argued that different biodiversity conservation objectives, based on intrinsic values versus ecosystem services of biodiversity, require different evaluation approaches. In this review, studies with different functions of livestock used different indicators. Studies with a conservation function had a higher relative use of indicators from clusters ‘traditional diversity indices’ (43% vs 14%), ‘composition and function’ (72% vs 25%) and ‘structure and habitats’ (36% vs 14%) than studies with a farming function. In case of a conservation goal, indices for community composition can reflect the similarity or distance from the target community that one wishes to conserve. For example, the MSA is an indicator that only accounts for abundance of biodiversity that is part of the reference ecosystem that one wishes to conserve. Currently, however, this reference value is a pristine ecosystem without human interference, which does not take the biodiversity of anthropogenic origin, such as semi-natural grasslands, into account (Renwick et al., 2013).

A large variety of indicators for biodiversity was used in the reviewed literature. These indicators were grouped in genetic, species and landscape diversity, following the general definition of biodiversity (CBD, 1992), and structured in seven clusters to allow for subgroups of indicators for species diversity. Although clusters of biodiversity indicators have also been made in previous studies, we considered previous clusters provided limited insight in the diversity of indicators. The Pressure-State-Response indicator framework, for example, focuses on indicators for the state of biodiversity, as well as on pressures and responses that could negatively or positively affect this state (LEAP, 2015). However, relations between pressure indicators and state indicators are often not linear (Kleijn et al., 2011, 2009). Grazing, for example, may be a pressure at high intensity, but a response to improve the state of biodiversity at low intensity. This makes the framework difficult to work with, in the context of livestock and biodiversity. Moreover, the actual biodiversity is only reflected in the state of biodiversity, and we, therefore, with the exception of management factors

in qualitative scoring systems, only focused on state indicators for biodiversity. Bockstaller et al. (2011) clustered indicators based on their approach being simple, predicted (using models), or measured. An indicator such as 'richness', however, could both be measured or modelled, and would in both cases convey information on the number of species. Therefore, in this paper we distinguished the indicator and approach (modelled vs. measured) as separate aspects. The different indicator clusters provided more detailed insight in use of indicators across scales and functions.

The broad variety of indicators for biodiversity and their underlying assumptions obstructs easy comprehension of their meaning. However, it is of utmost important to understand what indicators are used and what these indicate, before any conclusion about biodiversity is drawn from its (relative) value. The Shannon index has been used at two different levels: for species diversity and landscape diversity. For species diversity, the Shannon index is difficult to interpret because different species richness and abundance data can result in similar values, and the value does not increase linearly (Box 1) (Jost, 2006). For landscape diversity, the Shannon index based on land cover types was used in a qualitative scoring system and a higher value was assumed to be better for biodiversity (Müller-Lindenlauf et al., 2010). However, this application can lead to counter-intuitive results: an extensive farm with only grassland will have a lower Shannon index for habitats than a more intensive farm with 80% intensive grassland and 20% cropland; and could therefore be concluded to have a lower biodiversity. Thus, the interpretation of an indicator may already be complex, and application of the indicator at a different level conveys very different information which requires a different interpretation.

Moreover, some indicators have been encountered only few times in the review, but may have a larger impact on policy or the field of livestock than others. Mean species abundance was only used in three of the reviewed articles, but has been used for impact assessments of biodiversity at European and global scale (Leip et al., 2015; Westhoek et al., 2011). Potentially disappeared fraction was used in three of the reviewed articles, but is a main indicator for biodiversity in the field of life cycle analysis (Knudsen et al., 2017). Both indicators, however, have different underlying assumptions that could lead to opposite conclusions (Box 2). A policy that aims for pristine nature conservation may use an existing MSA, and would lead to different conclusions and actions for biodiversity conservation than a policy that seeks to conserve pollination or rare species in agricultural landscapes – that would use different indicators. Therefore, it is important to understand the assumptions underlying indicators, and to reflect whether these match the biodiversity target. Clear biodiversity targets and incentives are needed to select the relevant indicators and to move forward.

Box 2

The potentially disappeared fraction (PDF) and mean species abundance (MSA) are both indicators that express biodiversity compared with a reference situation. The PDF shows the plant species richness relative to the reference situation (De Schryver et al., 2010); the MSA shows the average abundance of originally occurring species relative to the reference situation (Alkemade et al., 2009). However, the two indicators can reach opposite conclusions regarding biodiversity impact due to their different assumptions. The MSA ranges from 100 to 0% of the abundance of originally occurring species and ignores other species (Alkemade et al., 2009), whereas characterisation factors for the PDF not only range from 0 to 1 (i.e. 100% damage) but could also be negative, when the number of plant species increased. For example, mixed pasture has a higher potential species richness than the reference situation (Knudsen et al., 2017). These assumptions can result in opposite conclusions. For example, if the species composition would change completely to the same number of different species, the MSA would be 0% (i.e. no abundance of original species), whereas the PDF would remain unchanged (i.e. the same number of species as the reference situation). When the aim is to preserve the originally occurring species (e.g. in case of converting nature into agricultural land), the MSA could therefore make more sense than the PDF. However, the reference value should be adjusted to the habitat that is aimed to be preserved: as emphasized by Renwick et al. (2013), biodiversity of anthropogenic origin, such as semi-natural grassland, is not explicitly accounted for. The PDF, on the other hand, gives information about total richness, including novel and old species, but does not take into account whether these species were endemic/ originally occurring. Species that would replace original species in case of agriculture would be accounted for in the PDF. Therefore, PDF may be the more sensible to compare potential plant species richness between different agricultural land uses. Neither of the two methods account for an increase in total richness or abundance in case of multiple habitat types. For example, having a mixture of naturally occurring forest and extensive grassland could result in a greater total diversity in reality, but would not improve the MSA or PDF value compared with having only the habitat with the better biodiversity value according to the indicator.

Deriving conclusions from the body of reviewed literature are not straightforward, due to different study objectives, study designs and indicators used. Results on impacts of livestock on biodiversity seem to be in line with the intermediate disturbance hypothesis (IDH). The IDH, albeit controversial (Fox, 2013), implies that local diversity is greatest when disturbance is neither absent nor too frequent, i.e. in this case at intermediate grazing intensities (Connell, 1978; Kaltsas et al., 2013). Another clear finding is that different species respond differently to presence of livestock, which fits with the concept of winner and loser species (Phalan et al., 2011). As a result, an improvement in one species or species group is likely to come at the cost of another. This is relevant for policy to take into account, because it implies one has to select at some point which biodiversity targets to address.

In conclusion, many different indicators were used to assess impacts of livestock on biodiversity across scales and purposes. In case of a food production purpose, indirect impacts of livestock through feed production were not often assessed, and different indicators were used compared with a conservation purpose. The various indicators and purposes made it difficult to aggregate and draw conclusions from the reviewed research. As such, the state of biodiversity and impacts of livestock on biodiversity are difficult to evaluate. It is important to realise how all identified indicators can be useful depending on the target for biodiversity, but at the same time that different indicators measure different aspects of biodiversity, are connected to different assumptions and values, and yield different conclusions. Policy would benefit from more streamlining between biodiversity targets and biodiversity indicators.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

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