

# Predicting future costs of High-Pathogenicity Avian Influenza epidemics: large versus small uncertainties

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## Abstract

Every five years, the Dutch government and the poultry sector agree on how the direct costs of epidemics in poultry, should they occur, will be shared. In the agreement for 2005–2009 the maximum amount to be paid by the poultry sector was set considerably higher than in the 1999–2004 agreement. This increase was caused mainly by the expected financial risks associated with High-Pathogenicity Avian Influenza (HPAI) epidemics. In this paper we focus on elucidating the uncertain and the less uncertain aspects of the HPAI financial risk problem. We distinguish between (1) the probability of an introduction of HPAI in the Netherlands, (2) the transmission potential of HPAI in the Netherlands, and (3) the costs and financing issues resulting from HPAI epidemics. We argue that whereas current understanding allows relatively precise answers to the question ‘If there is an epidemic, how many farms will be affected and what will be the direct costs?’, much larger uncertainties are associated with the questions ‘What is the chance of an HPAI epidemic in the Netherlands?’, ‘How large will be the long-term government share in the direct costs?’, and ‘How large will be the indirect costs?’.

*Additional keywords:* financial risk, risk analysis, modelling an epidemic

## Introduction

In the Netherlands, three partners are usually involved in the financing of the direct costs of livestock epidemics: (1) the European Union, (2) the Dutch government, and (3) the farmers. Farmer organizations and the Dutch government arrange the sharing of direct costs in the so-called veterinary funds. Such funds exist for pigs, cattle, poul-

try, and sheep and goats, the main livestock sectors in the Netherlands. Although they also cover costs of some other diseases, the funds' size is determined mainly by the expected financial risk of major livestock epidemics like Foot and Mouth Disease and High-Pathogenicity Avian Influenza (HPAI).

The direct costs of the 2003 epidemic of HPAI in the Netherlands amounted to 250 million euros, which covered the veterinary costs, consisting of the value of the culled herds, the organizational costs and the overhead costs. Of these direct costs 11.3 million euros were borne by the poultry sector, as this was the amount at which the sector's responsibility was maximized in the veterinary fund agreement for 1999–2004. This contribution corresponded to 4% of the total direct costs. The contributions of the Dutch government and the European Union were 63% and 33%, respectively. The indirect costs of the 2003 epidemic, such as costs due to business interruption, (temporarily) lower prices and lost export markets, have been estimated much higher than the direct costs (Tacken *et al.*, 2003). However, these costs are not part of the veterinary fund agreement and are fully borne by the poultry farmers and other chain participants involved. The same applies to the indirect costs incurred by other stakeholders, such as tourism, consumers, and, possibly, pig, beef and fish producers.

In the veterinary fund agreement for 2005–2009 the sector's maximum responsibility for direct costs is set at 30 million euros for the whole five-year period. The increase from 11.3 million to 30 million euros is caused mainly by the expected risk of HPAI epidemics. This risk was explored in a scenario analysis carried out by Meuwissen *et al.* (2005a, b) for the Ministry of Agriculture, Nature and Food Quality and the Product Boards for Livestock, Meat and Eggs, to inform the negotiations leading up to the new agreement. Eventually – based amongst other things on Koole *et al.* (2004) discussing the rather limited profitability of the poultry sector – the 30 million euros maximum sector contribution was changed and the Dutch government agreed to reduce the maximum responsibility of the poultry sector for the period 2005–2009 to 20 million euros.

Total financial consequences of epidemic outbreaks in a given area are the result of (1) the introduction of the virus into the area, (2) the subsequent spread of the virus from farm to farm, (3) the choice of intervention policy modulating direct costs, and (4) the interaction of the epidemic with the farm and regional economy, including price effects and indirect costs incurred by producers. Although the scenario analysis by Meuwissen *et al.* (2005a, b) does not include all these aspects, their study has been used as a basis for reviewing large and small uncertainties with respect to these issues as well as the distribution of the direct costs. The issue of indirect costs will only briefly be discussed.

## Probability of HPAI introduction in the Netherlands

### Background

HPAI viruses belong to the category of influenza A viruses. Although influenza A

viruses can infect many avian and mammalian species, their natural hosts and reservoir are generally considered to be free-living aquatic birds (Alexander, 2000). From time to time, inter-species transmission events cause severe outbreaks of influenza in chickens and turkeys. Up to now, inter-species transmission events leading to massive mortality have been limited to specific subtypes of the virus (H5 and H7). It appears that under certain circumstances these subtypes may transform from a relatively harmless state, in which they can multiply in the trachea and gastrointestinal tract only, to a state where they can multiply systemically.

Some researchers have suggested that outbreaks of HPAI may have become more prevalent over the last 15 years. Indeed, whereas only 9 outbreaks of HPAI have been described in the period 1959–1990, there have been more than 15 outbreaks of HPAI since (Alexander, 2000; Capua & Alexander, 2004; Lee *et al.*, 2005). This has given some credibility to the suggestion that the worldwide incidence of HPAI outbreaks has increased over the past 15 years. On the other hand, the total number of reported outbreaks remains fairly small, and it is quite conceivable that reporting bias is (partly) responsible for the observed increase. Alternatively, it is also conceivable that the number of introductions has remained (more or less) constant but that the consequences of a primary introduction have become much more serious (i.e., much larger subsequent outbreaks). All in all, the evidence that the risk of HPAI introduction in poultry has increased remains fragmentary. For an overview of the available evidence we refer to Koch & Elbers (2006). In our scenario study (Meuwissen *et al.*, 2005a, b) we considered a range of different values for the probability of introduction. In this paper we focus on a scenario in which on average one introduction occurs every five years in a poultry-dense area.

### The introduction of HPAI virus

In principle, introductions of HPAI viruses in poultry may occur via two routes. Firstly, it may be that pre-existing highly pathogenic viruses in the aquatic reservoir are directly introduced into poultry. Secondly, it may be that viruses of low pathogenicity (LPAI) are introduced into poultry where they subsequently transform into a state of high pathogenicity.

How long it takes before a virus of low pathogenicity transforms into a highly pathogenic one is unknown. The available data from previous epidemics suggest that the time to transform may vary highly. An example of a virus of low pathogenicity that circulated for considerable time before transformation took place is the virus H5N2 in chickens in Pennsylvania in 1983. The outbreak started in April and caused only limited mortality. It took until October of the same year before the virus had transformed into a state of high pathogenicity (Alexander, 2000). In many other cases, however, the virus of low pathogenicity circulated for a relatively short time, or could not be identified at all. An example of a high-pathogenicity outbreak is presented by the outbreak of H7N7 in the Netherlands in 2003. In this case no virus of low pathogenicity was found.

The risk of an introduction of influenza viruses from the aquatic reservoir into poultry is not well understood. At present the following aspects are often implicated

as possible risk factors for the introduction of HPAI into poultry:

- Outdoor housing;
- Close proximity of poultry to aquatic birds;
- A high local farm density;
- Production systems with a continuous supply and removal of birds.

Although these factors intuitively make sense, there is surprisingly little convincing evidence. In part this is due to the difficulties of performing adequate epidemiological studies during a calamity.

Due to a scarcity of reliable quantitative evidence, it is not possible at present to estimate the risk of introduction of HPAI in the Netherlands with any useful precision. In order to explore the financial risk due to future HPAI epidemics, one therefore needs to resort to investigating a number of different scenarios, each corresponding to a different assumed risk of introduction of HPAI.

## Modelling approach

### Modelling an epidemic

Owing to the large number of farms that were affected in the 2003 epidemic (Stegeman *et al.*, 2004), many data from that epidemic are available that yield powerful information for the calibration of mathematical models describing the between-farm transmission of HPAI in the Netherlands. Such models describe the possible epidemic outcomes that may result, *given* that an introduction of the virus has taken place. The availability of such a calibrated model description enables us to examine the theoretical efficacy of alternative intervention strategies as well as other ‘what-if’ questions.

The modelling approach was as follows. A mathematical model was used to describe the between-farm transmission, focusing on the transmission that remains after the implementation of intervention measures required by EU directives (‘EU strategy’), i.e., culling the infected and contact farms and establishing surveillance (3 km) and protection (10 km) zones around such farms. The model consists of a ‘transmission kernel’ (see e.g. Keeling *et al.*, 2001), defined as the probability of virus transmission between an infected and a susceptible farm as a function of the distance between these two farms. This transmission kernel can be estimated from epidemic data using Maximum-Likelihood estimation as explained by Ferguson *et al.* (2001). Using the estimated transmission kernel and the location data for all poultry farms in the Netherlands, we simulated the spatial propagation of HPAI epidemics. The calculations involved many realizations for each given scenario, leading to a sample of the distribution of epidemic outcomes (Figures 1–3). In each of the realizations the epidemic was started by assigning the first infection to a different farm. The numbers of realizations used were 150 in Figures 1 and 3, and 850 in Figure 2.

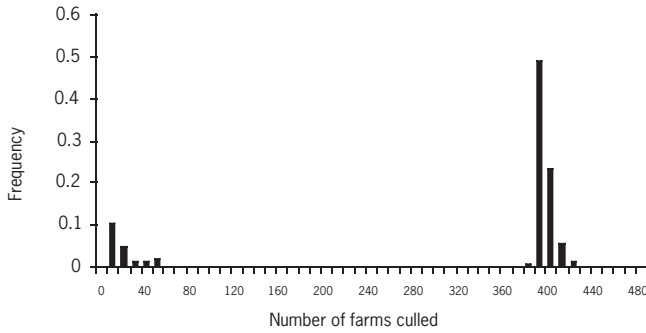


Figure 1. Frequency distribution of the modelled size of the HPAI outbreak in terms of total number of culled farms in the Gelderland Valley, using data from the 2003 epidemic. Intervention measures applied as required by EU directives.

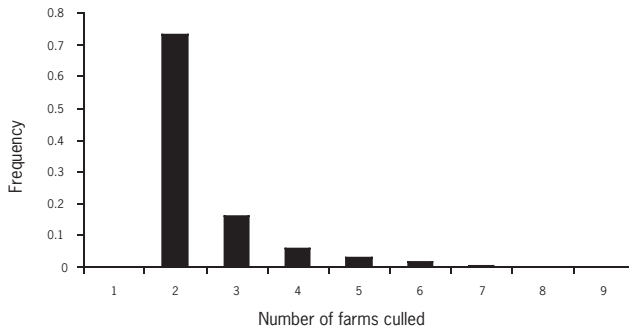


Figure 2. Frequency distribution of the modelled size of the HPAI outbreak in terms of total number of culled farms in the remainder of the Netherlands, using data from the 2003 epidemic. Intervention measures applied as required by the EU directives.

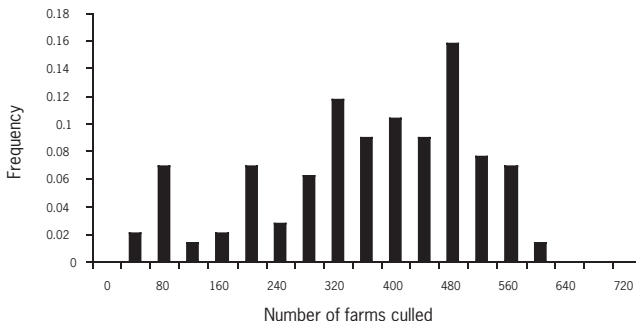


Figure 3. Frequency distribution of the modelled size of the HPAI outbreak in terms of total number of culled farms in the Gelderland Valley, using data from the 2003 epidemic. Interventions according to the EU strategy plus culling in a radius of 1 km around the affected farms.

## Modelling the costs

In order to simulate the 2005–2009 direct costs for the Netherlands as a whole we first transformed the epidemiological data for each region and the control strategy into economic parameters. Next, a Monte Carlo simulation model (@Risk in Excel; Anon., 2002) was developed with essentially three inputs: (1) the number of HPAI epidemics in the Netherlands during a five-year period, (2) the region(s) of occurrence, and (3) the relevant cost distributions. In the Monte Carlo simulation model a Poisson distribution reflects the uncertainty about the number of epidemics. The region in which an epidemic occurs is simulated by a discrete probability distribution. Direct cost data are reflected by cumulative probability distributions with parameters covering the full cost distributions as derived from the epidemiological data. Results are based on 1000 iterations.

## Transmission potential of HPAI in the Netherlands

The risk of between-farm transmission of a virus like HPAI is best measured by the basic reproduction number,  $R_0$ , a central epidemiological parameter that quantifies the potential for transmission (Anderson & May, 1991).  $R_0$  is defined mathematically as the expected number of secondary infections (i.e., secondary ‘infected farms’ in the present context) caused by one primary infection (i.e., primary ‘infected farm’) throughout its infectious period in a naïve host population. In our context ‘a naïve host population’ refers to a population of poultry farms without a (recent) history of (highly pathogenic) AI infections. In our model as described above, a local  $R_0$  can simply be calculated for each particular farm by totalling the probabilities of transmission to all other farms (as determined by the transmission kernel).

The transmission dynamics of any infectious agent exhibits a profound change of character as a function of the value of  $R_0$ . If each case of infection (infected farm in our context) generates on average at least one new case of infection (i.e.,  $R_0 > 1$ ), introductions of the infection will lead either to large outbreaks or to outbreaks that are small because they are terminated early simply by chance. If  $R_0 < 1$ , the transmission chain will never be able to maintain itself and outbreaks are always small.

We note that because of this ‘threshold behaviour’ around the threshold value  $R_0 = 1$ , the impact of interventions in disease transmission is hardly ever proportional to the invested intervention effort. For example, if  $R_0$  can be reduced to values below 1 by a small extra intervention effort, this small extra effort has a very large impact. In contrast, a large control effort that fails to achieve such a reduction will have a much smaller relative impact.

A very important epidemiological determinant that can be estimated directly from agricultural census data is the local farm density. To a large extent, this quantity determines the local  $R_0$  described above. This local transmission potential increases with increasing local farm density. Given the threshold behaviour of the transmission process, two types of areas can be distinguished. An area of low risk, with a (relatively) low farm density, where  $R_0 < 1$  and thus not large enough to cause sustained trans-

mission, and an area of high risk, with a high farm density, where  $R_0 > 1$  so that additional interventions are required to achieve epidemic control.

By calculating the local  $R_0$  for all farms in the Netherlands, we identified the Gelderland Valley (an area in the Gelderland province) as the most important high-risk area in the Netherlands. Figure 1 shows the model results for this area under the 'EU strategy' of intervention described above. Here we focus on the distribution of outbreak size, where we define outbreak size as the total number of culled farms throughout the epidemic. The distribution of outbreak size (Figure 1) consists of two separate parts, one part with relatively small outbreak sizes that correspond to outbreaks that, by chance, terminated relatively early, and a second part with large sizes corresponding to large epidemics. The fact that under EU intervention policy there is a probability that large epidemics may occur confirms that the Gelderland Valley is a high-risk area. A second (smaller) high-risk area is located in the south of the Netherlands. Both areas were heavily affected during the 2003 epidemic. All outbreak sizes modelled for the remainder of the Netherlands (Figure 2) are small, indicating the low-risk character of that part of the country.

The outbreak size distribution in the Gelderland Valley for a more aggressive intervention strategy is presented in Figure 3. This aggressive strategy consisted of the 'EU strategy' combined with the additional measure – initiated after a high-risk period assumed to last 21 days – of pre-emptive culling of all farms within a 1-km radius around the infected farms. The results illustrate that because of a high farm density in this area even strategies that include pre-emptive culling are not able to terminate the epidemic without having to cull in a large part of the area. On the other hand, we did find that pre-emptive culling leads to a reduction of the expected length of the epidemic (Meuwissen *et al.*, 2005a, b).

With respect to the transmission potential of HPAI in the Netherlands we arrive at the following conclusions. Owing to the availability of the 2003-epidemic data, a theoretical framework is available in which 'what-if' questions on between-farm HPAI transmission in the Netherlands can be addressed, *given* that an introduction of the virus has taken place. Analyses within this framework suggest that highly pathogenic AI viruses spread rapidly in two defined poultry-dense areas in the Netherlands, and that current options for control measures are unlikely to be able to halt an ongoing epidemic in these two areas. However, the more pre-emptive culling is applied, the shorter the expected duration of the epidemic.

## Costs and financing of HPAI epidemics in the Netherlands

Direct costs of livestock epidemics refer to the veterinary costs directly related to the control of an epidemic, i.e., the value of culled animals, and organizational and overhead costs. These types of costs are fairly straightforward to assess. For the 2003-epidemic of HPAI, during which 30 million animals were killed, direct costs amounted to 250 million euros, or 8 euros per animal. Transferring this amount to the scenarios for the Gelderland Valley presented above, results in direct costs of 82 million euros in case of additional culling within a radius of 1 km around infected farms and

Table 1. Simulated direct costs of HPAI epidemics using two control strategies, for two regions in the Netherlands.

Region	EU strategy			EU strategy + culling in a 1-km radius		
	Average	Minimum	Maximum	Average	Minimum	Maximum
	----- (€ × 10 <sup>6</sup> ) -----					
Gelderland Valley	76	0.2	100	82	5	144
Remainder of the Netherlands	0.4	0.2	2.4	1	0.2	9.4

Table 2. Simulated distribution of average and maximum direct costs of HPAI epidemics in the Netherlands, and probability of payment, in two scenarios, over the period 2005–2009.

Contributors	Default scenario			More optimistic scenario <sup>I</sup>		
	Direct costs		Probability of payment	Direct costs		Probability of payment
	Average	Maximum		Average	Maximum	
	----- (€ × 10 <sup>6</sup> ) -----			----- (€ × 10 <sup>6</sup> ) -----		
Dutch poultry farmers	18	30	0.63	10	30	0.39
Dutch government	34	430	0.56	6	145	0.27
European Union	28	248	0.63	9	94	0.39
Total 2005–2009	80	708	–	25	269	–

<sup>I</sup> As the default scenario, but with a reduced number of epidemics (1 every 10 years) and reduced costs per animal (5 instead of € 8).

in 76 million euros if the EU strategy is strictly applied. These are average values. Table 1 also lists the minimum and maximum costs, as well as the (much lower) costs in the 'remainder' (excluding the second high-risk area mentioned above) of the Netherlands.

Indirect costs are much more difficult to assess. This even holds for relatively straightforward aspects such as business interruption. Losses due to business interruption depend on uncertain factors of, for instance, farmers finding another job. Also losses due to price effects depend on many uncertain aspects, such as the response of other countries. Countries free from HPAI may induce short-term or longer-term export limitations or they may even expand their own production capacity, thereby permanently reducing the export opportunities for the country facing HPAI. Indirect costs are not compensated by governments. In general, they are considered to be too



complicated for any risk-financing (e.g. insurance) scheme.

In the 2005–2009 scenario analysis of the direct costs, the following default scenario was defined:

1. On average one HPAI introduction every five years, occurring either in the Gelderland Valley (96%) or in the high-risk area in the south of the Netherlands (4%);
2. Additional culling within 1 km from infected farms controls epidemics;
3. Direct costs include 8 euros per animal killed.

Table 2 presents the results for the default scenario and for a more optimistic scenario (i.e., with fewer epidemics occurring and with lower costs per animal). Average 2005–2009 costs are 80 million euros in the default scenario and 25 million euros in the more optimistic scenario. Maximum costs are estimated at 708 million euros and 269 million euros in the default and the more optimistic scenario, respectively.

With respect to the distribution of the 2005–2009 costs, both scenarios assume an EU-share of 35% and a 'Dutch share' of 65%. Dutch poultry farmers contribute up to a maximum of 30 million euros. Table 1 shows that the Dutch government together with the European Union pays on average the largest part of the costs in the default scenario as well as in the more optimistic scenario. In the default scenario the European Union pays on average 28 million euros (i.e., 35%) of the direct costs of HPAI epidemics in the Netherlands during the period 2005–2009. The probability of such a payment is 0.63. For the Dutch government the probability of having to pay is somewhat less (0.56) but the average contribution is higher (34 million euros, i.e., 42%). On the other hand, there is a relatively small chance that the Dutch government does not have to make any 'poultry disease related payments' in the 2005–2009 period. Probabilities are only 0.07 in the default scenario (i.e., 0.63–0.56) and 0.11 (i.e., 0.39–0.27) in the more optimistic situation (Table 2).

In case of a maximum farmer contribution of 20 million euros (not shown in Table 2), the average farmer contribution in the default scenario decreases from 18 million to 12 million euros, whereas the chance for the Dutch government of becoming financially involved increases from 0.56 to 0.58. The probability and size of payments for the European Union remain 0.63 and 28 million euros, respectively. Such a large involvement for both the Dutch government and the European Union is unlikely to persist in the future.

As to the cost issue of HPAI epidemics in the Netherlands we arrive at the following conclusions. The less uncertain aspects relate to the size of the direct costs and the short-term distribution of these costs among European Union, Dutch government and poultry farmers. The more uncertain aspects are the longer-term financial participation of the Dutch government and the European Union in the sharing of costs and the size of the indirect costs.

## Concluding remarks

In this paper we have argued that, on the one hand, some of the determinants of the

financial risk resulting from HPAI epidemics are very uncertain. Specifically, the probability of a primary introduction of HPAI in poultry, its long-term economic effects and the long-term distribution of costs cannot be determined with much precision. On the other hand, the availability of a calibrated model description of between-farm transmission enables us to calculate probability distributions of size and duration of an epidemic that is likely to ensue once HPAI has been introduced into a poultry-dense area. Based on these distributions it is possible to calculate a probability distribution of direct economic cost associated with such an epidemic.

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