



DEPARTMENT OF LIVESTOCK DEVELOPMENT
MINISTRY OF AGRICULTURE AND COOPERATIVES
BANGKOK, THAILAND.

Excerpts from a joint FAO/DLD study by Marius Gilbert, Jan Slingenbergh, Hans Wagner, Wantanee Kalpravidh, Sith Premashthira and Prasit Chaitaweesub

(publication in preparation; pls direct any queries to Dr. Marius Gilbert, Biological Control and Spatial Ecology, Free University of Brussels, mgilbert@ulb.ac.be)

End September 2004, the Government of Thailand launched a nationwide survey, termed *x-ray survey*, to detect and possibly remove HPAI from the country. The beginning of this survey showed a rise in the number of outbreaks reported weekly, and thus it became a major issue to determine whether this rise could be ascribed to the increased surveillance intensity or whether it reflected a true upsurge of HPAI across the country. This called for a detailed geospatial analysis of the distribution of the 2nd wave outbreaks, in particular in relation to the distribution of different poultry husbandry systems and species.

The data on HPAI outbreaks comprised all lab confirmed outbreaks recorded from the start of the 2nd wave on 3 July till 8 November 2004. Most clinical outbreaks were recorded in chickens (Fig. 1), with 64 percent of total outbreaks. Ducks were second with 28 percent of the recorded outbreaks.

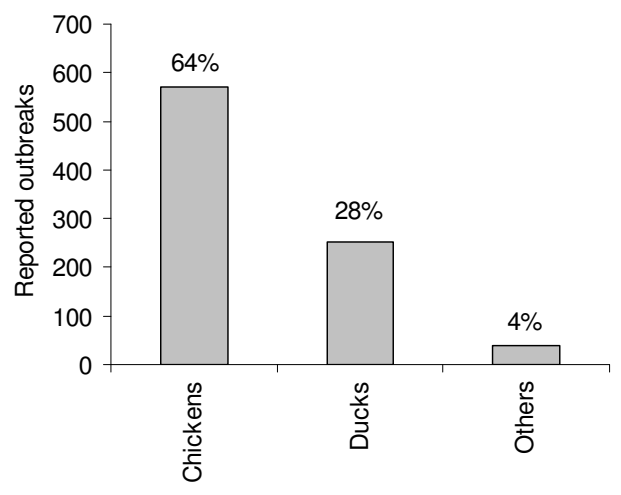


Figure 1 Distribution of 2nd wave HPAI outbreaks by poultry species

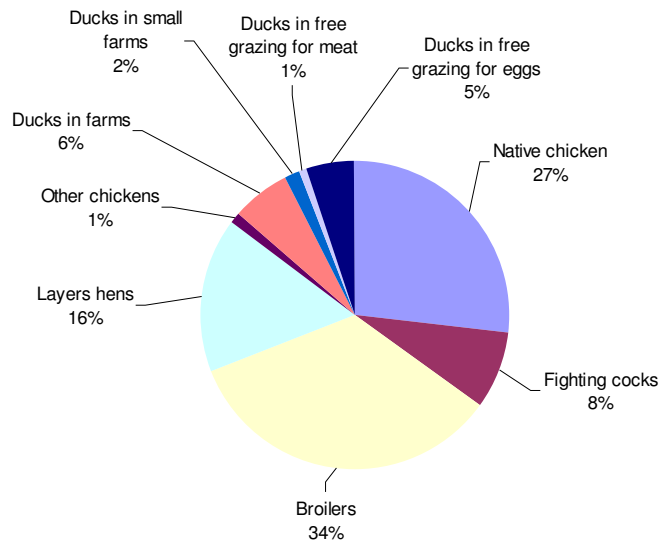


Figure 2 Relative proportions of poultry husbandry categories (as per DLD statistics end October 2004)

The distribution of outbreaks in poultry categories does not reflect their respective abundance, as illustrated in Fig. 2. Duck represent 13 percent of all overall poultry and yet a significant proportion (28 percent) of the total outbreaks.

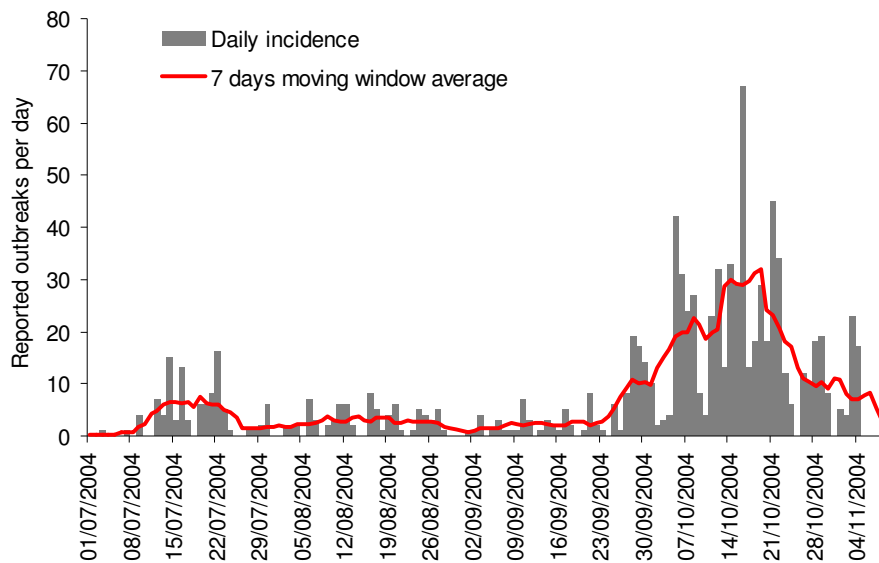


Figure 3 Distribution of 2nd wave HPAI outbreaks by date in Thailand

The time series of reported outbreaks during the second wave is presented in Fig. 3. The rise in outbreaks reflects the increased surveillance intensity. However, looking closer at the exact dates of and the way the x-ray survey was implemented leads to a slightly different interpretation. The x-ray survey was decided upon by the Thai Government on 28

September. The survey involved the initial training of several hundreds of thousands of volunteers to search for evidence of HPAI presence. All participants were instructed how to best protect themselves and prevent any exposure to the HPAI virus. So clearly, it took some time before the survey was fully in place.

From Fig. 3, it appears that the number of reported outbreaks was already on the increase end September when the effect of increased surveillance could not yet be observed. Since only a fraction of the total domestic poultry populations were affected by HPAI, the subsequent decrease in reported incidence starting from mid-October probably reflects the effect of the x-ray survey, a break in transmission, rather than through exhausting the number of susceptible birds.

Fig. 3 also suggests that there is periodicity in the HPAI records relating to the working days of the week, suggesting that these data should be grouped by week as per Fig. 4, which shows the temporal dynamics in chicken and duck outbreaks separately. There is no clear evidence of a time-lag between the temporal distribution of the two species group outbreaks, indicating that the rise and fall in HPAI affected ducks and chickens simultaneously.

The 2nd wave dynamics suggest that further data analyses should be split: the first from 3 July to 24 September (termed Period I in the rest of this report), followed by the 2nd flare-up phase from 25 September onward (termed Period II).

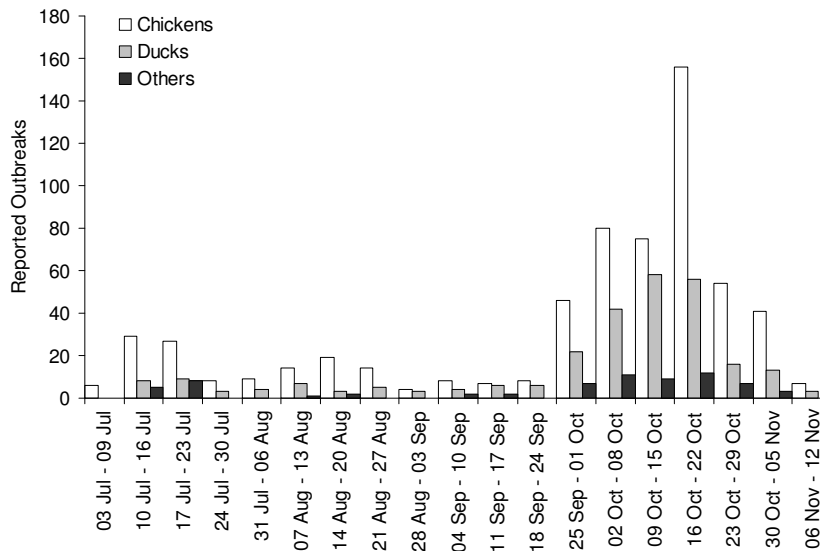


Figure 4 Weekly distribution of HPAI outbreaks by bird species group

Fig. 5 shows the spatial distribution of recorded outbreaks of all outbreaks (left column), chicken outbreaks (middle column), and duck outbreaks (right column) for the whole period (top), period I (middle) and period II (bottom). These distributions reveal no apparent difference in pattern of outbreaks in ducks or chickens (maps look identical along the horizontal axis), but there was a marked difference between the first and the second period, with the first being more concentrated in central Thailand and more scattered and extending also into the eastern part of the country during the second period.

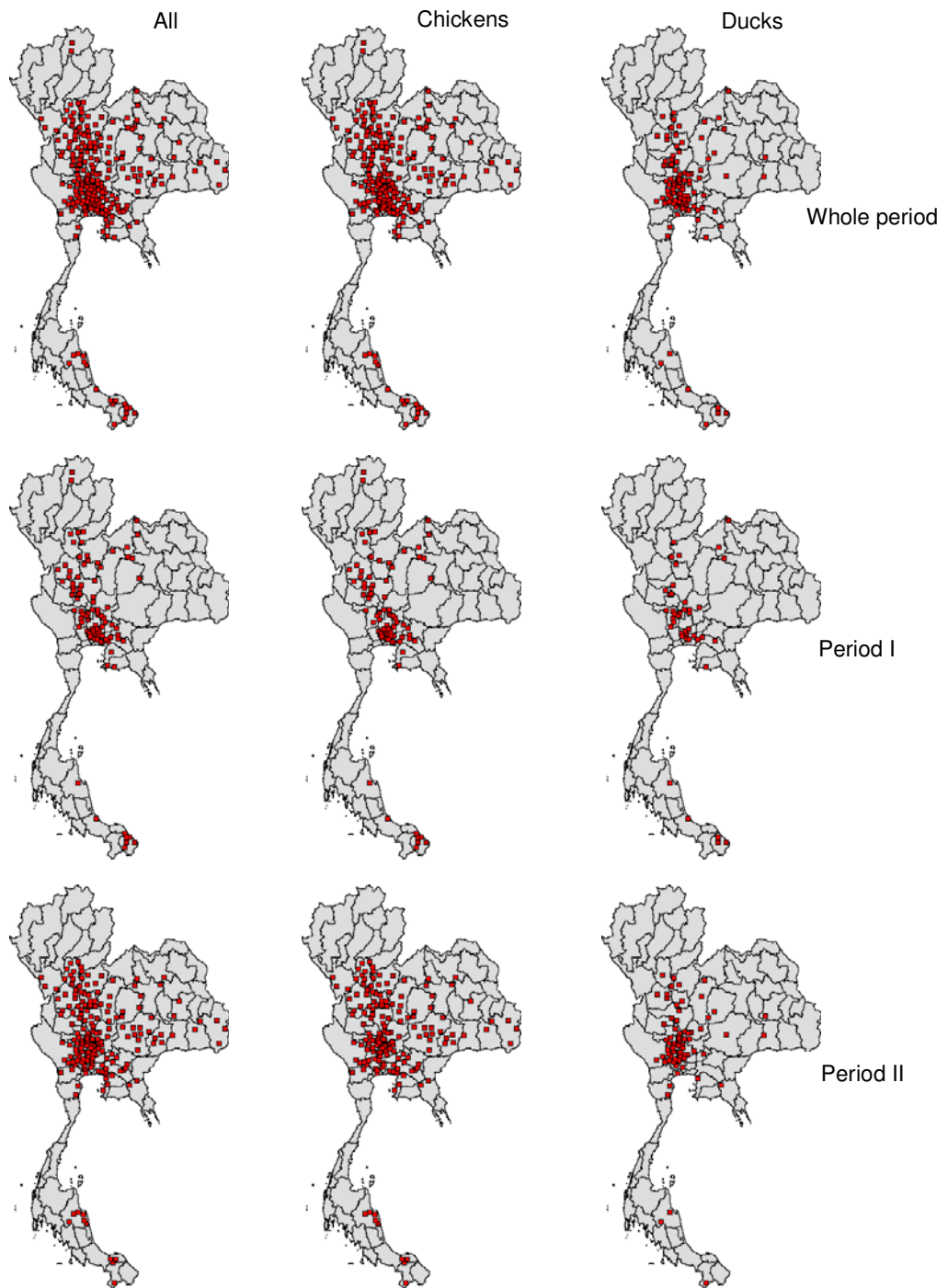


Figure 5 Spatial distribution of HPAI outbreaks by species group and periods

Fig. 6A shows the frequency distribution of outbreaks by province for chickens and ducks. Chicken outbreaks appeared to be much more widely distributed across the country, whereas duck outbreaks are very much concentrated in Suphanburi, counting for nearly 43 percent of all duck outbreaks. The geographical location of Suphanburi is shown in Fig 11.

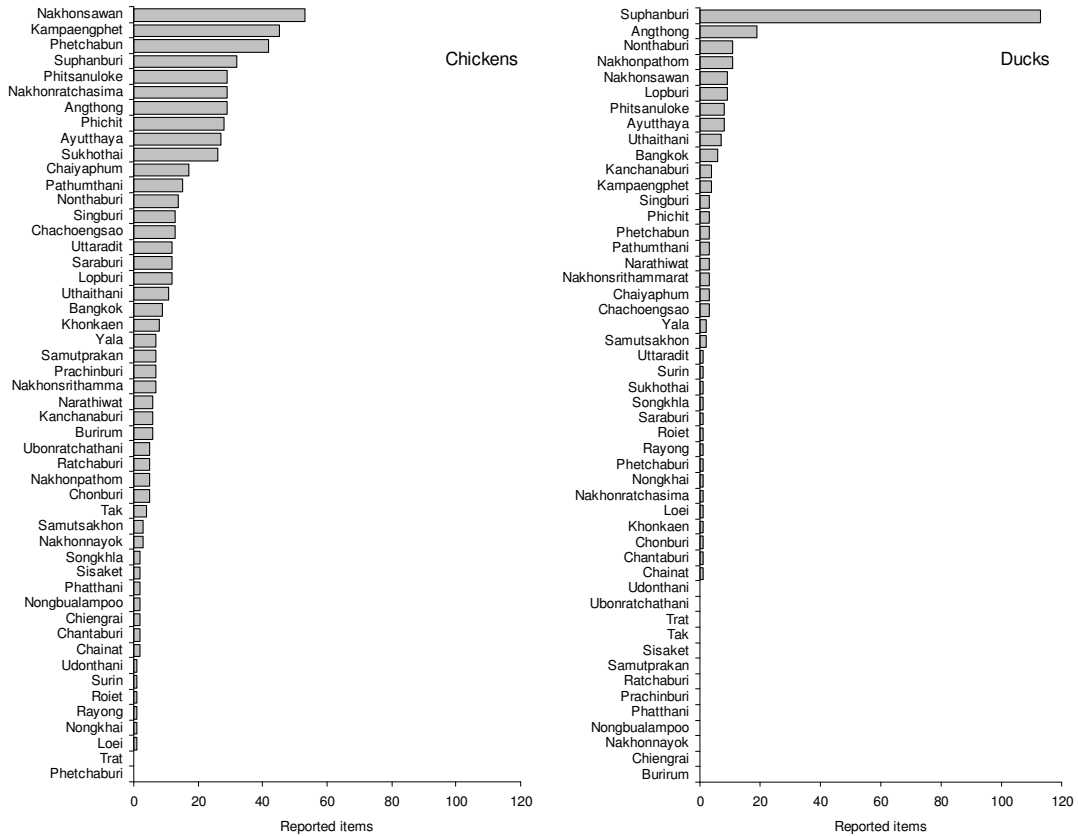


Figure 6A Distribution of outbreaks reported by province

The distribution of poultry species as illustrated in Fig. 7 shows that outbreaks of the first period (Fig. 5) concentrated in the duck areas, particularly the free grazing ducks areas. This pattern persists during the second period but with more outbreaks distributed in the eastern part of the country where we find high densities of native chickens.

The strong association between HPAI outbreaks and ducks is further highlighted in Fig. 8 where chicken outbreaks are depicted against a duck distribution background, showing a very good match, particularly against the free ranging duck distribution. The opposite is true for the duck outbreaks – chicken background. The implication is that ducks may play a role in generating chicken outbreaks but not the other way round.

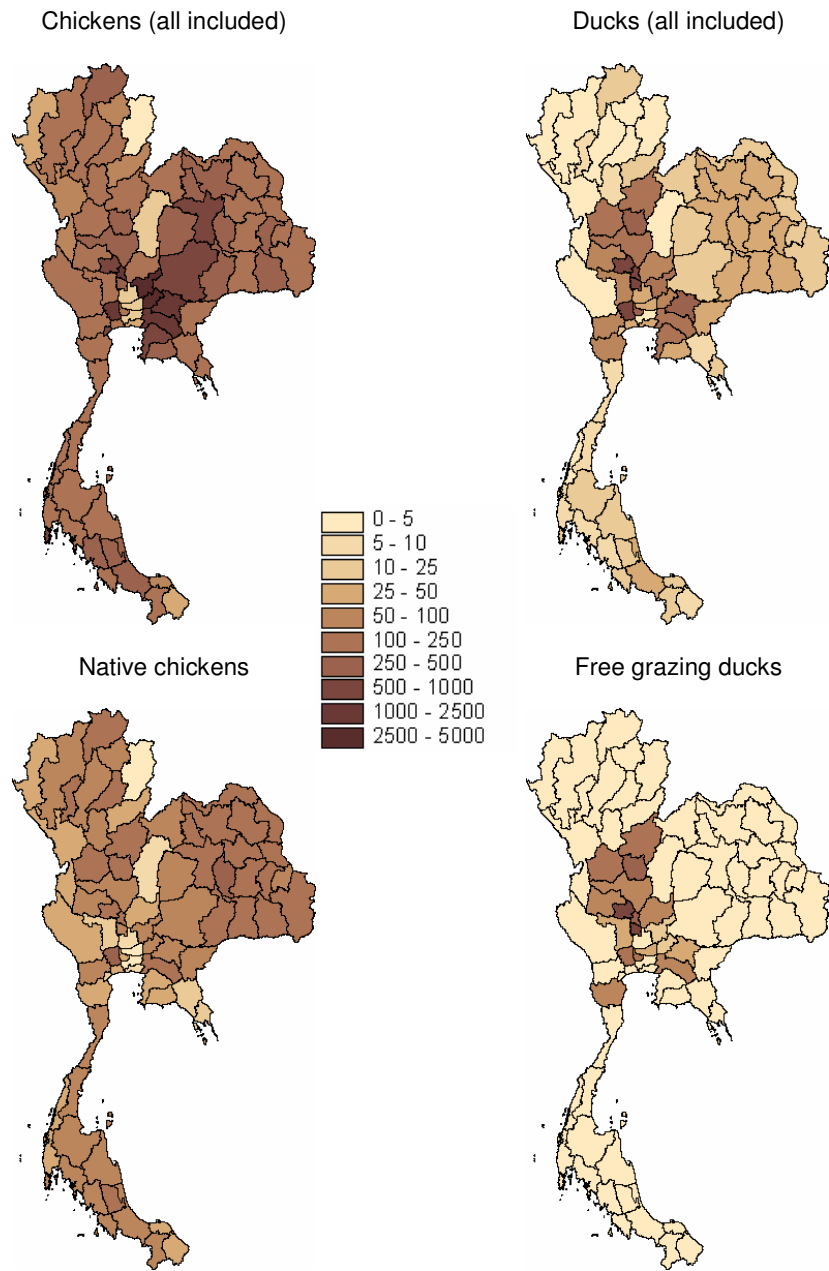


Figure 7 Spatial distribution of poultry by species (sub-) group and by province (birds per km²)

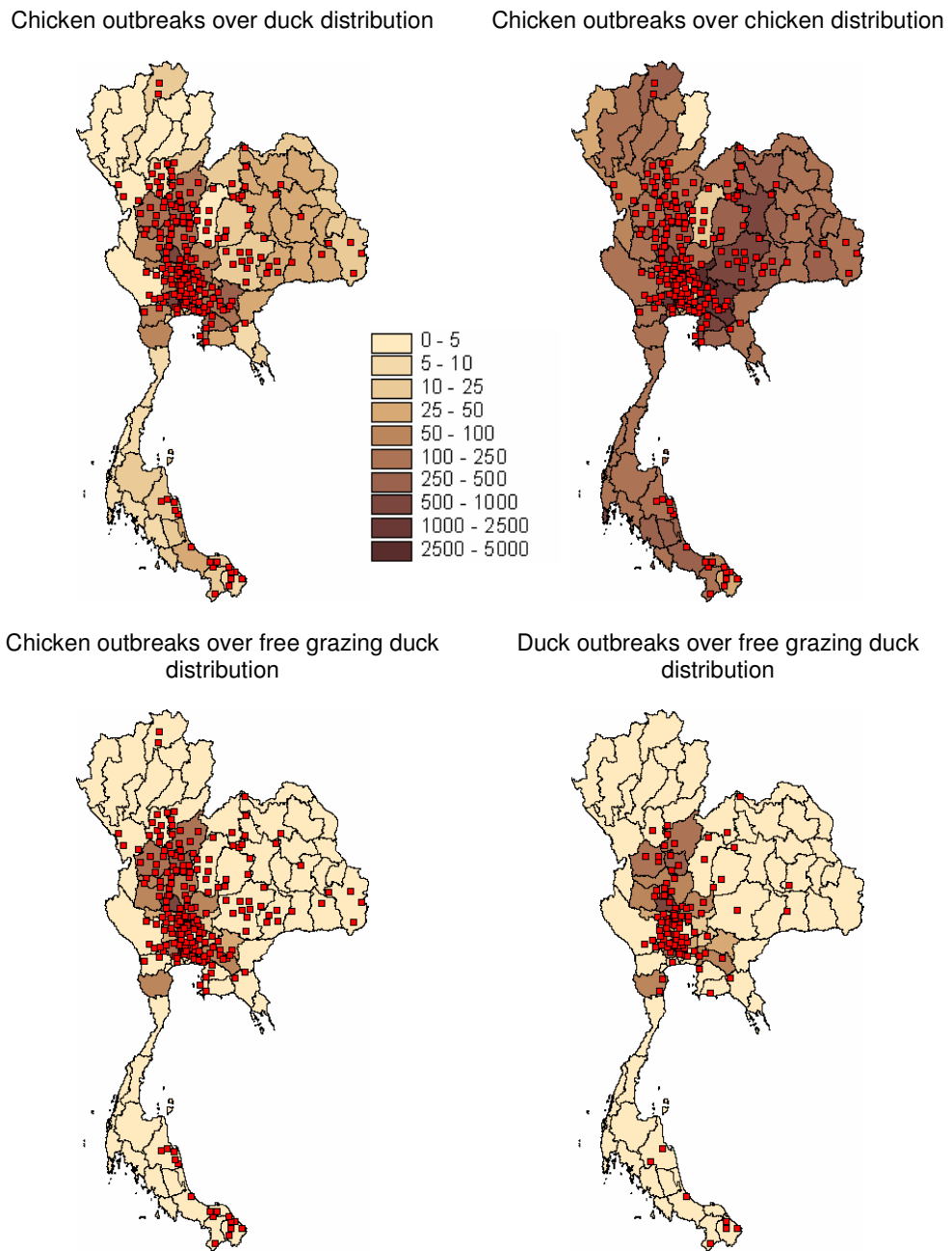


Figure 8 Distribution of HPAI outbreaks over chickens and ducks (birds / km²)

The association between the number of HPAI outbreaks in all poultry, chickens and ducks, for two time periods, and poultry density, husbandry and human population data was explored using multiple regressions carried out at province and district levels. The log-transformed number of outbreaks was taken as the dependent variable tested against log-transformed counts of animals or people. Furthermore, data at the district level were

reclassified for outbreak presence or absence and these data were entered in the logistic multiple regressions in order to determine the variables responsible for the presence/absence of HPAI.

The variables considered:

- Chickens number (natives not fighting. cocks): Cn
- Chickens fighting cocks: Cfc
- Chicken broilers: Cbr
- Chicken layers: Cly
- Chicken others: Cot
- Chicken Totals: Ct

- Ducks in farms: Df
- Ducks in small farms: Dsf
- Ducks in free grazing (eggs and meat): Dfgt
- Ducks Total: Dt

- Birds Geese: Bge
- Birds Quails: Bqu
- Birds Ostrichs: Bos
- Birds Pet Birds: Bpb
- Birds others: Bot
- Birds Swallows: Bsw

- People total: Hpop

Variables were included in the model adopting two different approaches: (i) stepwise (variables are entered step-by-step in the model) and (ii) backward removal (all variables are entered at first, then non-significant variables are removed until all variables are significant at the $p = 0.01$ level). Only variables showing up as significant in both approaches were maintained in the model. The results, as summarised in Table 1 indicate a fairly strong consistency for the province versus district level, for the two poultry species groups, as well as for the two different time periods.

A very strong positive association, significant in all cases, is found first with the number of free grazing ducks, whereas a strong negative association, shown in bold, appears for the density of native chickens (significant in all cases except period II for chicken outbreaks). In addition, we find frequently a positive association with duck totals and human population density. A few additional variables such as the number of geese and quails are found significant but only at the district scale, and with a low significance level (close to 0.01).

Table 1. Summary results of the multiple regression analyses of log-transformed HPAI outbreaks counts and livestock and human population data.

Model	Variables	R ²
Province level		
All outbreaks	Dfgt, Cn , Dt, Area	0.569
Chicken - whole period	Dfgt, Cn , Area	0.513
Chicken – period I	Dfgt, Cn , Hpop	0.447
Chickens – period II	Dfgt	0.219
Ducks – whole period	Dfgt, Cn , Dt,	0.472
Ducks – period I	Dfgt, Cn	0.297
Ducks – period II	Dfgt, Cn	0.309
District level: multiple regressions		
All outbreaks	Dfgt, Cn , Dt, Hpop, Bge	0.265
Chicken - whole period	Dfgt, Cn , Dt, Hpop, Bge	0.200
Chicken – period I	Dfgt, Cn , Dt	0.089
Chickens – period II	Dfgt, Cn , Dt, Hpop, Bge	0.158
Ducks – whole period	Dfgt, Cn , Dt, Bge , Bqu	0.204
Ducks – period I	Dfgt, Cn , Dt, Bqu	0.091
Ducks – period II	Dfgt, Cn , Dt, Bge , Bqu	0.173
District level: multiple logistic regressions (presence / absence)		Pseudo-R²
All outbreaks	Dfgt, Cn , Dt, Hpop	0.304
Chicken - whole period	Dfgt, Cn , Dt, Hpop	0.245
Chicken – period I	Dfgt, Cn , Bge	0.188
Chickens – period II	Dfgt, Cn , Dt, Hpop	0.158
Ducks – whole period	Dfgt, Cn , Dt, Hpop	0.302
Ducks – period I	Dfgt, Cn , Bot	0.215
Ducks – period II	Dfgt, Cn , Hpop, Df	0.352

More detailed models for total outbreaks, chicken and duck outbreaks are presented in Table 2. The parameter details of the multiple regression models indicate a less pronounced effect of Dfgt than suggested by its omni-presence in the regressions but Dfgt produces the strongest correlation with the log-transformed outbreak number in bi-variate analysis (respectively $r = 0.395$; $r = 0.343$, $r = 0.342$ for all outbreaks, chicken outbreaks and duck outbreaks). Dfgt significance becomes altered somewhat when the log-transformed counts of native chickens is entered in the model. Given that native chickens are distributed in areas where free grazing ducks are in low number (Fig. 7), these two factors basically reflect the same spatial pattern, i.e. outbreaks are the most abundant in free grazing duck areas where native chicken numbers are low.

Human population density appears as a frequent factor positively associated to outbreak numbers or to HPAI presence. Human population is generally a good surrogate estimate for the risk associated to movement of infected animals, i.e. markets and consumption areas distributed in highly populated areas.

The analysis was carried using the subset of districts distributed in Southern Thailand only to check if the outbreaks distributed in the South could be associated to fighting cocks densities, but the results were consistent with the nationwide analysis, in that only Dfgt and Hpop came out as significant variables.

The predicted and observed distributions for chickens and ducks outbreaks, ensuing from Table 2 equations are presented in Fig. 9. The results indicate that HPAI virus

circulation in ducks may in fact have been relatively widespread, albeit at a rather low level, not very visible (but see discussion). It also shows some provinces with very high deviations from the model prediction such as Suphanburi in duck outbreaks.

Table 2. Multiple regression parameters of log-transformed number of HPAI outbreaks at the province level. Also the poultry variables are log-transformed

Variable	Parameter	t	p
All outbreaks: F = 23.46; p < 0.001; R ² = 0.569			
Dfgt	0.106	2.68	0.0091
Cn	-0.705	-6.66	< 0.001
Dt	0.513	4.38	< 0.001
Area	5.69 10 ⁻⁵	4.24	< 0.001
Constant	1.201	-	-
Chicken outbreaks: F = 18.69; p < 0.001; R ² = 0.447			
Dfgt	0.0890	2.30	0.024
Cn	-0.626	-6.05	< 0.001
Dt	0.452	3.95	< 0.001
Area	5.494 10 ⁻⁵	4.17	< 0.001
Constant	1.201	-	-
Duck outbreaks: F = 18.91; p < 0.001; R ² = 0.472			
Dfgt	0.0881	2.92	0.0046
Cn	-0.306	-5.03	< 0.001
Dt	0.202	2.37	0.020
Constant	0.686	-	-

The Suphanburi Province not only forms a hotspot or epicentre for ducks and HPAI, counting 43 percent of total disease outbreaks, the province also has a record high volume of rice production, suggesting a rather typical agro-ecological setting (see Fig. 11).

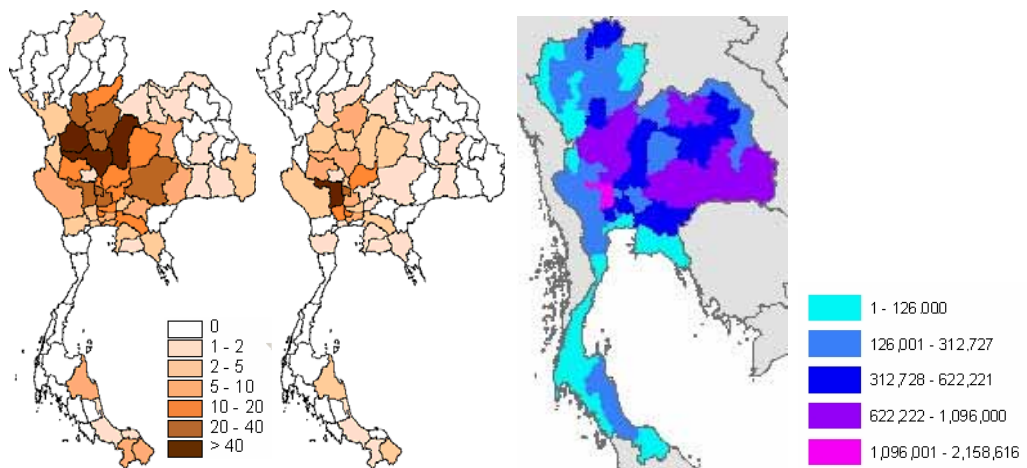


Figure 11 Distribution of HPAI outbreaks by province in chickens (left) and ducks (middle), and rice production (MT).

It is therefore no surprise that the distribution of wetlands (Fig. 12) also shows up as a good predictor of 2nd wave outbreaks in Thailand (see also the outbreaks which occurred in wetland areas in the southern part of the country), and even for 1st wave outbreak data across the Mekong region.

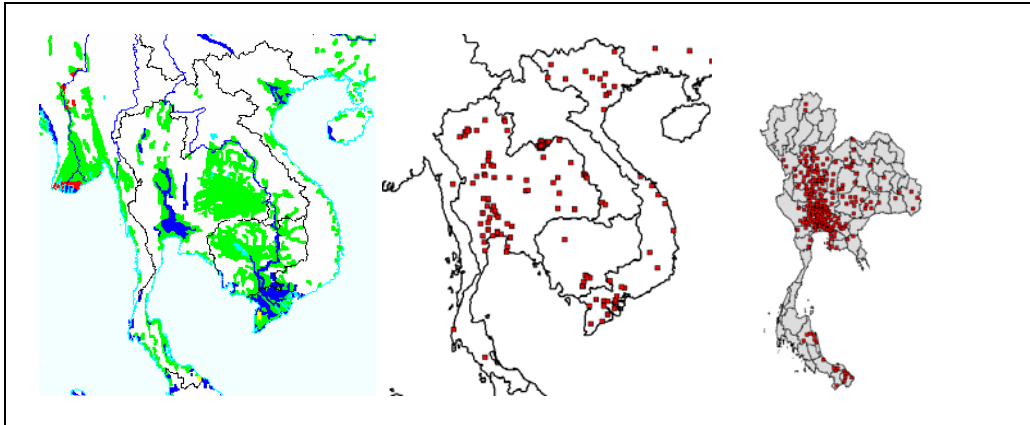


Figure 12 Distribution of wetlands (left), first wave outbreaks in the Mekong countries (middle) and second wave outbreaks in Thailand (right).