

# Within-flock Transmission of Highly Pathogenic Avian Influenza (HPAI) Virus subtype H5N8 during the 2014 Outbreaks in Chicken Farms in the Netherlands

Tagrid A. Dinar<sup>1</sup> | Francisca C. Velkers<sup>1</sup> | Egil A.J. Fischer<sup>1</sup> | J. Arjan Stegeman<sup>1</sup> | Jan van den Broek<sup>1</sup>

<sup>1</sup> Department of Farm Animal Health, Faculty of veterinary medicine, Utrecht University, The Netherlands

## 1. Introduction

- **Avian Influenza (AI)** viruses are associated with worldwide morbidity and mortality in birds and mammals (including humans).
- In November and December 2014 outbreaks of **HPAI virus subtype H5N8** occurred in **four chicken farms and one duck farm** in the Netherlands.
- Quantifying the transmission of the virus within the infected flocks is crucial for evaluating **intervention policies and control measures**.

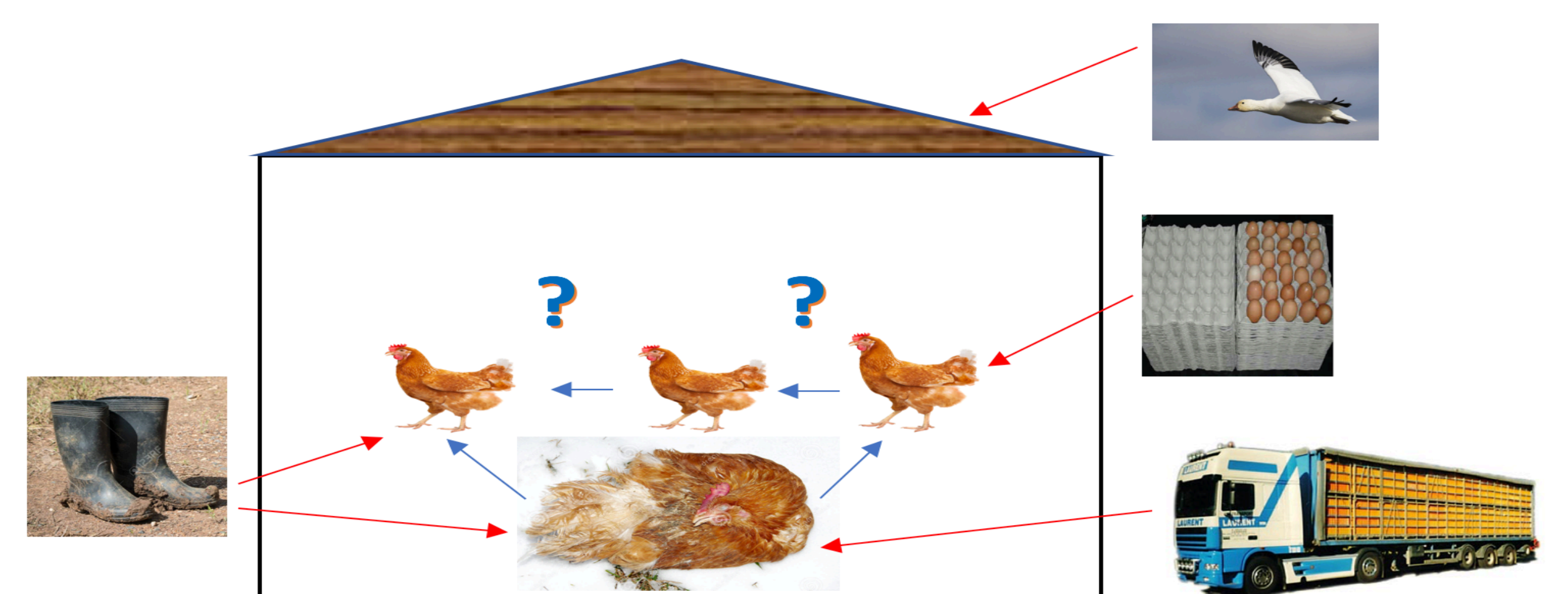
## 2. Aim

To quantify the **transmission of HPAI subtype H5N8 virus within chicken flocks** during the 2014 outbreaks in the Netherlands.

## 3. Study population

Four infected chicken flocks → 3 layer flocks + 1 broiler breeder flock

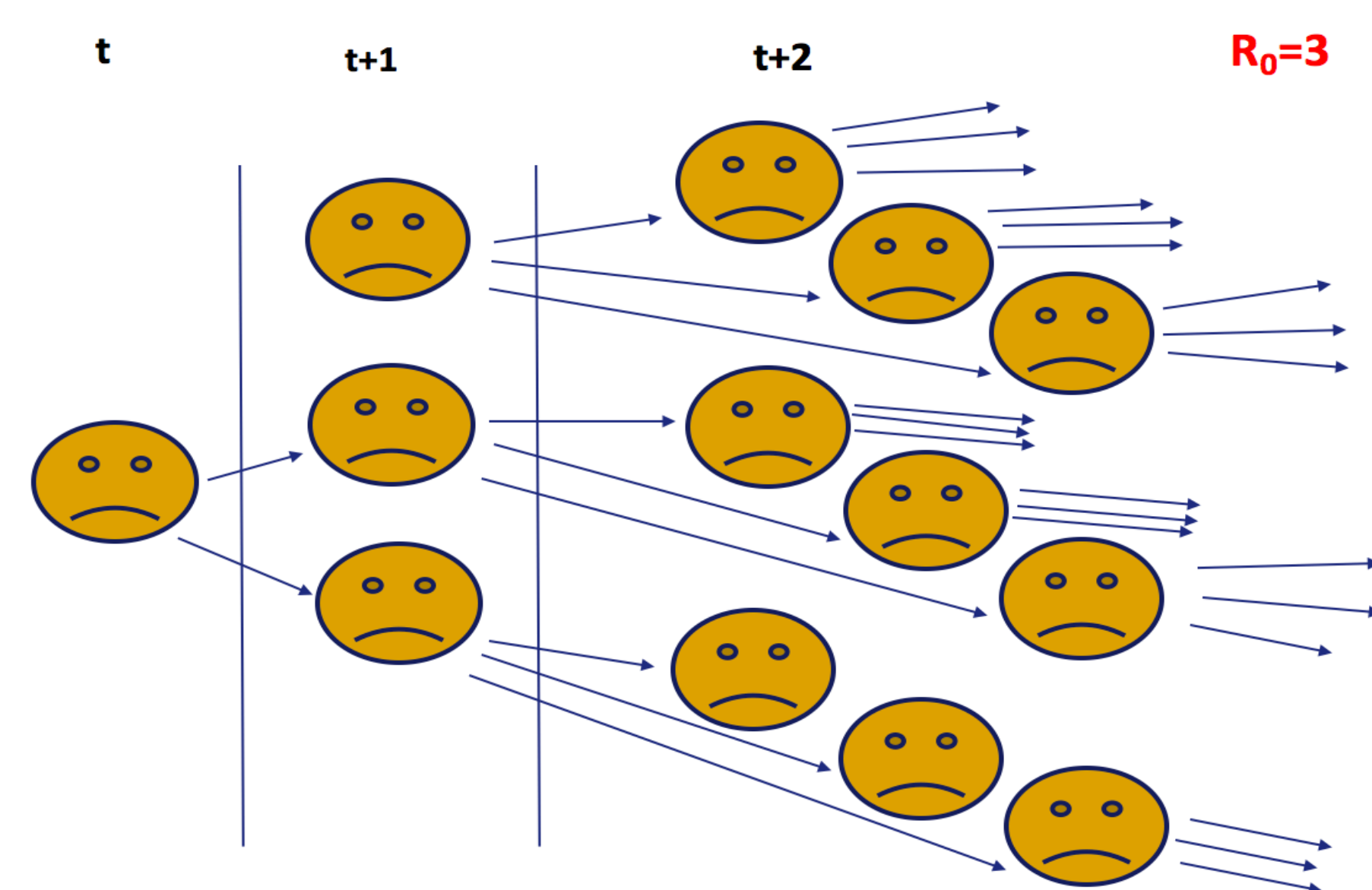
## 4. Transmission routes of Avian Influenza viruses



**Figure 1:** Some of the transmission routes of AI viruses in poultry farms. The **red arrows** indicate how the infection can be introduced to the flocks. The **blue arrows** indicate **within-flock transmission**.

## 5-a. Methods

- The main outcome of the study is the **basic reproduction number ( $R_0$ )**;
- $R_0$  is the average number of secondary infections produced by one primary infection in a fully susceptible population;
- If  $R_0 < 1$ : the outbreak will **fade out**;
- If  $R_0 > 1$ : the outbreak will **grow**.



**Figure 2:** Cartoon illustration of  $R_0 = 3$

## 5-b. Methods

- $R_0$  was calculated From the Exponential growth phase of the outbreak.
- Parameters used to calculate  $R_0$ :
  - Infectious period ( $T$ ) → Estimated from experiments on H5N8
  - Generation time ( $T_G$ ) → Estimated from experiments on H5N8
  - Latent period ( $T_E$ ) → Estimated from experiments on H5N8
  - Exponential growth rate ( $r$ ) → Estimated from the outbreak data

### • Two equations were used to calculate $R_0$ :

**Equation 1:** Calculating  $R_0$  assuming an exponential distribution of the generation time

$$R_0^{exp} = 1 + rT_G^{exp} + r^2T_E(T_G^{exp} - T_E)$$

**Equation 2:** Calculating  $R_0$  assuming fixed distribution of the generation time

$$R_0^{fix} = \frac{r(T_G^{fix} - T_E)}{\sinh r(T_G^{fix} - T_E)} e^{rT_G^{fix}}$$

## 6. Results

**Table 1:** The values of the growth rate ( $r$ ), the latent period ( $L_E$ ), the infectious period ( $T$ ), the generation time ( $T_G^{exp}$ ) and ( $T_G^{fix}$ ) assuming exponential and fixed lengths of  $L_E$  and  $T$  and 95% confidence intervals between brackets. The corresponding values of  $R_0$  are shown as ( $R_0^{exp}$ ) and ( $R_0^{fix}$ ) respectively.

	$r$ (day <sup>-1</sup> )	$L_E$ (day)	$T$ (day)	$T_G^{exp}$ (day)	$R_0^{exp}$	$T_G^{fix}$ (day)	$R_0^{fix}$
<b>Farm 1</b>	0.70 (0.69-0.71)	1	4	5	6.45 (6.35-6.57)	3	7.52 (7.33-7.75)
<b>Farm 2</b>	0.97 (0.96-0.99)	1	4	5	9.66 (9.45-9.87)	3	15.93 (15.35-16.64)
<b>Farm 3</b>	1.69 (1.62-1.75)	1	4	5	20.81 (19.60-22)	3	101.91 (86.10-119.51)
<b>Farm 4</b>	0.75 (0.67-0.82)	1	4	5	6.96 (6.15-7.79)	3	8.57 (6.93-10.49)

## 7. Conclusion

- All  $R_0$  values were substantially **larger than 1**.
- This indicates that the virus **would have spread efficiently within the chicken flocks** if no control measures were applied.

## Acknowledgements:

- Dr. Francisca Velkers, Dr. Egil Fischer and Prof. Dr. Arjan Stegeman for their patient guidance and support during this research project for the Master Epidemiology.
- **Dutch society for veterinary epidemiology and economics (VEEC) for sponsorship of attendance of the SVEPM conference.**

## References

- Stegeman, A., Elbers, A.R., Bouma, A., De Smit, H., De Jong, M.C. (1999). Transmission of classical swine fever virus within herds during the 1997-1998 epidemic in the Netherlands. *Prev. Vet. Med.* 42, 201-218.
- Vynnycky, E., White, R.G. (2010). An introduction to infectious disease modelling. New York: Oxford University Press.
- Bos, M.E., Van Boven, M., Nielen, M., Bouma, A., Elbers, A.R., Nodelijk, G., Koch, G., Stegeman, A., De Jong, M.C. (2007). Estimating the day of highly pathogenic avian influenza (H7N7) virus introduction into a poultry flock based on mortality data. *Vet Res.* 38:493-504.
- Diekmann, O., Heesterbeek, H., Britton, T. (2013). *Mathematical Tools for Understanding Infectious Disease Dynamics*. Princeton University Press.