

An Assay in Microtitre Plates for Absolute Abundance of Chicken Interferon Alpha Transcripts

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Abstract

Immunosuppression of commercial chickens is a serious animal health and economic problem in the poultry industry. The major causes of the immunosuppression are viruses that suppress transcription of interferon genes, especially interferon alpha. There is a need for monitoring immunosuppression in commercially bred chickens. For this purpose, the absolute abundance of interferon alpha transcripts can be measured in blood of chickens by a suitable assay. Such an assay was used to estimate abundance of chicken interferon alpha in a sample of splenic cells induced with polyinosinic polycytidylic acid. The abundance measured was 29 ± 2 attomoles/ μg total RNA. This assay can be performed in microtitre plates using samples collected from chickens in poultry houses.

mRNA, absolute abundance, poly I:C

Although various agents can cause immunosuppression in commercial chickens, infectious diseases especially caused by viruses are the most frequent and serious causes. There are three such viruses recognized as being economically important; Marek's disease virus, chicken anaemia virus and infectious bursal disease virus. Most viruses cause some immunosuppression and possibly all viruses do, even attenuated vaccines (Strasser et al. 2003), but health of infected animals and economic impact of immunosuppression by these viruses is usually trivial.

Many bacteria are immunosuppressive in various hosts (Schwab 1975), including the chicken (Hassan and Curtiss 1994; Kishida et al. 2004). It has been known since the early 1970s that mycoplasmas are immunosuppressive in several species (Kaklamanis and Pavlatos 1972), chickens among them (Nonomura 1973; Ganapathy and Bradbury 2003). Mycotoxins are immunosuppressive but their effects can be prevented by quality control of feedstock to avoid feeding contaminated feed (Devegowda and Murthy 2005).

It has been known since at least the early 1990s that viruses have assorted strategies for suppressing interferon (IFN) production by an infected host (Goodbourn et al. 2000) and they continue to be actively investigated (Garcia-Sastre and Biron 2006). We hypothesised that the important immunosuppressive viruses of chickens would suppress IFN gene transcription. If true, failure to induce IFN gene activation with an inducer would identify most immunosuppressed chickens, and induction of increased abundance would strongly imply that a flock was immunologically competent.

As there was no fast, facile and inexpensive method to assess immune status of chickens (Bacon 1992), we developed molecular hybridization assays in microtitre plates to assess the abundance of both chicken interferon alpha (ChIFN- α) and interferon gamma (ChIFN- γ) transcripts in chicken blood before and several hours after challenge with an inducer of IFN (Novak et al. 2001). These tests were used to confirm that Marek's disease virus (Quéré et al. 2005), chicken anaemia virus and infectious bursal disease virus suppress gene transcription of both ChIFN- α and ChIFN- γ (Ragland et al. 2002).

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Virulent Marek's disease virus suppressed induction of IFN gene transcription, while the vaccinal turkey herpesvirus did not. The assay lasted two days and it measured just relative and not absolute abundance. These deficiencies led us to improve the assay. We focused on ChIFN- α because of its importance in an early response to infection and because of stronger suppression by the viruses than in case of ChIFN- γ (Ragland et al. 2002).

Materials and Methods

Probes

Biotin-labelled oligo(dT)₂₀ probe (Roche, Penzberg, Germany) was used for capturing samples or standards to streptavidin-coated microtitre plates. Three digoxigenin-labelled ChIFN- α -specific probes were produced by PCR using Roche's Digoxigenin labelled probe synthesis kit according to the manufacturer's instructions. Plasmid DNA extracted from *Escherichia coli* strain DH5 α transformed with SPORT1 plasmid containing ChIFN- α DNA, kindly provided by Drs. Sekellick and Marcus (Sekellick et al. 1994), was used as a template. Primers used for the amplification of ChIFN- α probe were forward 5'-ATGGCTGTGCCTGCAAGCCCA-3' and reverse 5'-CTAAGTGC GCGTGTTCCTGT-3'. The PCR reaction proceeded for 30 cycles with annealing temperature of 60 °C. Product of PCR was analysed by electrophoresis on agarose mini gel stained with ethidium bromide. A difference in migration of digoxigenin-labelled PCR products and unlabelled PCR products was an indicator of incorporation of digoxigenin in the probe.

Assay design

A standard curve was constructed each time an assay was performed (nine for each probe) by using serial dilutions of a defined amount (8,000 to 0 amol/ml) of the synthetic oligonucleotide containing polyA tail for ChIFN- α (5'-TGTAATCGTTGTCTTGGAGGAAAAAAAA-3) (Invitrogen, Carlsbad, CA) in hybridization buffer (0.75 M sodium chloride; 0.75 sodium citrate; 3 μ l/ml Tween-20, 1% BSA). Serial dilutions of total RNA (40-0 μ g/ml) extracted from splenocytes treated with polyinosinic:polycytidylic acid (poly I:C) were prepared in the same buffer. An uncoated, hybridization plate was washed with washing buffer (0.01 M Tris-HCl, pH 7.5; 0.2 M LiCl; 1mM EDTA, pH 8.0; 200 μ l/well), buffer was removed by aspiration and 150 μ l of each dilution of standard or sample was placed in each of three wells. Digoxigenin-labelled ChIFN- α -specific probe (4 μ l of PCR product as per manufacturer's instructions) was denatured by boiling for 10 min and mixed with biotin-labelled oligo(dT)₂₀ probe (0.1 nmol) per millilitre of hybridization buffer. This probe mix was added (50 μ l/well), the plate sealed with adhesive foil and hybridization proceeded for 60 min at 65 °C. A streptavidin-coated microtitre plate (Sigma-Aldrich Chemie GmbH, Steinheim, Germany) was washed twice with 200 μ l of washing buffer, the buffer removed and 150 μ l of the contents of each well from the hybridization plate was, upon completion of the hybridization period, transferred to wells of the streptavidin-coated plate. The plate was sealed with adhesive foil and incubated at ambient temperature to allow binding of biotin to streptavidin. To remove the unbound hybridization mix, the plate was washed 4 \times with 200 μ l of washing buffer per well. Anti-digoxigenin AP conjugate (Roche) was diluted 1:2,000 in antibody dilution buffer (0.1 M Tris-HCl, pH 7.5; 0.15 M NaCl) and 100 μ l was placed into each well. The plate was incubated for 60 min at ambient temperature, followed by washing 5 \times with washing buffer, and then one wash with alkaline phosphatase buffer (1M diethanolamine, 0.5 mM MgCl₂, pH 9.8). An alkaline phosphatase substrate, p-nitrophenyl phosphate (Sigma), was dissolved in alkaline phosphatase buffer and 100 μ l added to each well. The plate was incubated at ambient temperature in the dark for 30 min and the absorbance was measured immediately at 405 nm with a microtitre plate reader.

Induced sample

To prepare a primary spleen cell culture, one-week-old specific pathogen-free (SPF) chickens were killed by cervical dislocation and their spleens were aseptically removed and placed in physiological PBS. The spleens were forced through a 60-mesh screen of a TissueCell Dissociation Kit (Sigma). The cell suspension was collected and centrifuged for 10 min at 350 \times g and the pellet was suspended in physiological PBS. The suspension was carefully layered on top of 4 ml of Ficoll-Paque (Pharmacia Biotech, Inc., Piscataway, NJ), centrifuged at 400 \times g for 15 min and the cells at the interface were harvested. After washing in PBS, the cells were suspended and maintained in RPMI 1640 medium supplemented with 2% chicken serum, 8% FBS, 100 U/ml penicillin and 100 μ g/ml streptomycin and grown at 40 °C in a water-saturated 5% CO₂ and 95% air atmosphere.

These chicken splenocytes were stimulated with poly I:C (25 μ g/ml) for 24 h and their total RNA was isolated using TRI reagent (Sigma) according to the manufacturer's instructions. Integrity of RNA was determined by electrophoresis on a 1% agarose gel. The concentration of total RNA in the sample was determined spectrophotometrically. Poly I:C is a synthetic double-stranded RNA that binds to TLR 3, stimulating production of IFN- α .

Statistical analysis

Regression analysis of each replicate (in triplicate) for two selected probes (probe 1 and probe 3) was performed with JMP statistical software (SAS Institute Inc., Cary, NC). Tests for normal distribution, equal variance and means comparison were performed with JMP. Slopes and intercepts of combined regression curves

for the two probes were compared by *t*-tests (Zar 1984). Regression equations were used to calculate abundance of ChIFN- α mRNA in the unknown sample. The Wilcoxon ranked-sums test was used to compare estimates of absolute abundance of transcripts estimated in the unknown sample with the two probes. Values of $p \leq 0.05$ were considered significant.

Results

All three probes yielded curvilinear plots over the full range of dilution tested (Fig. 1) with an obvious deflection that began between 25 and 50 attomoles. Probes 1 and 3 were linear to 25 attomoles (Fig. 2) but probe 2 was curvilinear (data not shown). Probe 2 could be linearized by log log transformation but was not considered any further. The R^2 for combined replicates was 0.88 for probe 1 and 0.90 for probe 3. Regression slopes and intercepts were different for the two probes.

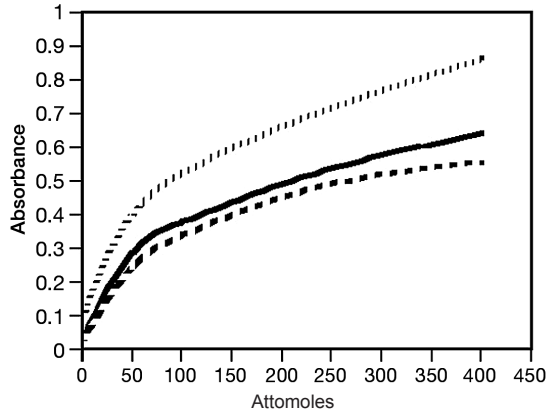


Fig. 1. Correspondence of ChIFN- α oligonucleotide standard hybridized to a capture probe as measured by absorbance signal in microtitre plates (see text for details). Plots are spline best fit, $R^2 = 0.997$ or higher for all 3 probes (solid line = probe 1, hatched line = probe 2, dashed line = probe 3).

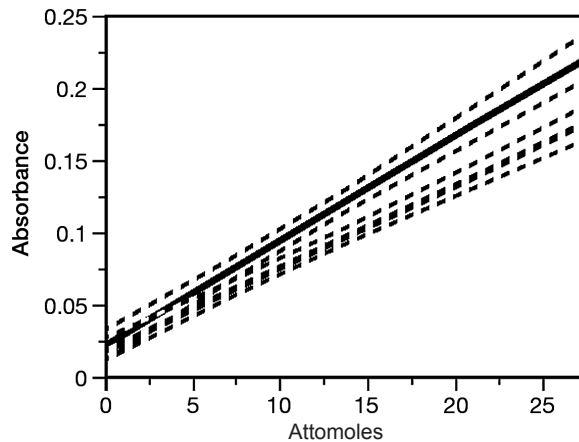


Fig. 2. Linear fit of probe 1 (solid line) and probe 3 (broken line). The accompanying curvilinear plots represent 95% confidence intervals for each probe.

Table 1. Regression coefficients and estimates of ChIFN- α mRNA abundance in an unknown sample using two different probes

Replicate curves		Attomoles mRNA		Attomoles mRNA/ μ g total RNA
Each	R ²	Each replicate	Each probe	Each probe
1.1	0.994	15.5	12.2 \pm 1.6 (13)*	30.5 \pm 4.0 (13)*
1.2	0.996	13.6		
1.3	0.929	12.5		
1.4	0.989	10.3		
1.5	0.975	12.7		
1.6	0.994	12.0		
1.7	0.988	11.0		
1.8	0.978	10.9		
1.9	0.979	11.7		
3.1	0.989	11.5	11.1 \pm 1.0 (9)*	27.8 \pm 2.5 (9)*
3.2	0.987	9.8		
3.3	0.976	10.3		
3.4	0.990	11.3		
3.5	0.990	10.8		
3.6	0.985	10.2		
3.7	0.983	13.0		
3.8	0.990	11.6		
3.9	0.990	11.8		

*Mean \pm SD (% CV) of nine replicates

The R² for individual replicate curves for probes 1 and 3 and estimated abundance in the unknown sample are presented in Table 1. Regression equations for each of the solitary curves (in triplicate) were used to estimate abundance of mRNA in the sample. The data were normally distributed and had equal variance. The CV for probe 1 was 13%, and for probe 3 was 9%. The mean abundances for the two probes were not different ($p = 0.10$), thus they both measured the same abundance in the sample.

Discussion

It is obvious that probes 1 and 3 measured the same absolute abundance in the unknown sample. Precision was better for solitary than for combined assays. Precision still was acceptable for combined assays (CV of 13% and 9%), especially considering that the replicates were performed on different days.

Non-induced cells were not assayed because the abundance of ChIFN- α transcripts is extremely low. Xing and Schat (2000) were unable to detect IFN- α transcripts in spleens of naïve SPF chickens. Abdul-Careem et al. (2008) detected IFN- α transcripts in bursae of Fabricius of one-day-old, naïve SPF chickens but at very low level.

A kit to measure abundance of murine IFN- γ transcripts was developed by R&D Systems (Minneapolis, Minnesota). According to their data, splenocyte cell cultures stimulated with phytohaemagglutinin for 24 h contained 26 attomoles of interferon per μ g total RNA. In our study, we obtained similar abundance of 29 attomoles of ChIFN- α per μ g total RNA.

During an epornitic of infectious chicken anaemia in commercially bred broilers in Croatia and Slovenia, we tested the immune status of affected broilers in Croatia using our original assay (Ragland et al. 2002). We noticed that abundance of IFN- α and IFN- γ in the birds before challenge with an IFN inducer was less than usually observed in healthy chickens. This prompted us to wonder if immunosuppression caused by immunosuppressive viruses could be identified based on absolute abundance and thus avoid the second sample after

challenge with an inducer. Comparison with historical controls is imprecise, and moreover, comparison of relative abundance among flocks assayed at different times would be questionable, hence, there is a need to measure absolute abundance to circumvent these problems.

Measurement of absolute abundance of interferon transcripts has not been done frequently until now. Previous measurements were based on biological assays of interferon produced by cells injected with total RNA, and thus abundance was reported as biological units of interferon produced (Stewart 1981). Quantitative RT-PCR has been used as a research tool to measure absolute abundance of ChIFN- α transcripts, as well as other chicken cytokine transcripts (Hong et al. 2006a,b; Eldaghayes et al. 2006; Li et al. 2007; Patel et al. 2008). We have focused on a less expensive method to assess abundance of ChIFN- α transcripts in commercial chickens.

This assay can be used also for other agents that suppress interferon gene transcription. Bacteria *Mycobacterium tuberculosis*, *M. ulcerans* and *M. avium* are immunosuppressive and cause systemic suppression of IFN- γ gene expression (Lafuse et al. 2006; Yeboah-Manu et al. 2006). Their effect on IFN- α has not been studied but in instances where viral effects on both interferons have been examined, both usually were suppressed. The question is if the same occurs in bacterial infections. Concerning mycoplasma, we have preliminary evidence that mycoplasma suppresses interferon gene expression in chickens (unpublished observations). The fumonisin mycotoxins have been also reported to suppress ChIFN- α transcription (Cheng et al. 2006).

The described assay is adequate for assessment of immune status of commercially bred chickens by laboratories that cannot use the qRT-PCR and are equipped with standard ELISA readers. It will be useful for identifying and monitoring immunosuppressed flocks.

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