

Improving sensitivity of oral fluid testing in IgG prevalence studies: application of mixture models to a rubella antibody survey

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SUMMARY

A method for the analysis of age-stratified antibody prevalence surveys is applied to a previously reported survey of antibody to rubella virus using oral fluid samples in which the sensitivity of the assay used was shown to be compromised. The age-specific distribution of the quantitative results of antibody tests using oral fluids is modelled as a mixture of strong positive, weak positive and negative components. This yields maximum likelihood estimates of the prevalence at each age and demonstrates that, when used in conjunction with mixture modelling techniques, the results of antibody prevalence studies using oral fluids accurately reflect those obtained using sera.

INTRODUCTION

The aim of an age-stratified serological survey is to determine the prevalence of antibody to a specific infection in all age groups [1]. Of particular use in the study of viral transmission and population immunity is the measurement of long lasting IgG antibody in a population. Traditionally serum has been the specimen of choice for such surveys, but blood collection is invasive, hazardous, and relatively expensive, requiring specially trained staff to perform the procedure using sterile equipment. A sample that is simple, safe and cheap to collect is more desirable, especially for population immunity studies where large numbers of specimens need to be easily and economically obtained [2]. Oral fluid is a feasible non-invasive alternative to serum for this purpose as it is very simple, safe and cheap to collect and contains immunoglobulins reflecting those

found in serum. The major drawback is that antibodies are present at considerably lower concentrations in oral fluid and so require particularly sensitive assays. In the context of viral-specific IgG, with the exception of assays for human immunodeficiency virus type 1 (HIV-1) [3], there is some concern that the technology used in current protocols to detect specific antibody in oral fluid are not sensitive enough to enable oral fluid assays to replace serum assays [4–7].

Samples may be tested for the presence of antibody using a variety of laboratory techniques, ELISA being the most commonly used. Many assays also enable results to be expressed numerically, assumed proportional to the quantity of the specific antibody in the sample. When assays are used on an individual basis, perhaps for diagnostic purposes or pre-vaccination screening, samples need to be categorized as positive (containing specific antibody), negative (containing no specific antibody) or equivocal (further tests necessary). Cut-off values are set to define the boundaries of these zones. Setting cut-off values is not straightforward unless there is clear separation of results into

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positive and negative peaks. When using oral fluids it is often difficult to distinguish between negative samples and those with low levels of specific antibody. However, when conducting a serological survey it may be sufficient only to determine accurately the proportion seropositive at each age – individual results are only of interest for the contribution they make to the overall picture (unless, for example, there is interest in identifying predictors of serological status). In this setting, an alternative approach is to derive the prevalence from the age-specific distribution of results, rather than using cut-offs to categorize each sample [8].

Mixture models provide an appropriate method for the analysis of the distribution of results, since the samples are taken from a mixture of individuals who have experienced infection and those who have not [8]. In this study we describe the application of mixture models to a previously reported survey of rubella virus antibody in a rural Ethiopian population using oral fluid samples [7]. Results from paired serum samples were also available. Using a fixed cut-off, the sensitivity of the oral fluid assay relative to the serum results was shown to decrease with increasing age of subject, from more than 90% in those aged less than 10 years to just 65% above age 40 years [7]. We investigated whether analysing the results using an appropriate mixture model would overcome this apparent lack of sensitivity, enabling oral fluid samples to be used successfully to investigate population immunity.

METHODS

Data

The serological data used here are taken from the results of a survey of IgG antibody to rubella virus in a rural Ethiopian population [7] designed to determine the potential of oral fluid to replace serum for the evaluation of population immunity levels. The data comprise 837 optical density (OD) ratios (the OD reading divided by that given by a reference serum sample) obtained using an ‘in house’ amplified IgG antibody capture ELISA (GACELISA) [4] to screen oral fluid samples from persons aged 1–84 years. Individual results were aggregated into six age groups (1–4, 5–9, 10–14, 15–24, 25–44 and 45 years or more) by 20 reactivity categories (equal width bands based on the log(OD ratio)). In the original study [7] these results were categorized as positive or negative using a fixed cut-off [4] (Table 1). Rubella virus-specific IgG results from paired serum samples using a commercial

Table 1. *Age-specific prevalence of rubella virus antibody in paired serum and saliva samples using a fixed cut-off*

Age group	Number of samples	Number (%) positive in serum	Number (%) positive in saliva
1–4	90	27 (30)	30 (33)
5–9	155	101 (65)	99 (64)
10–14	141	108 (77)	94 (67)
15–24	135	123 (91)	109 (81)
25–44	164	163 (99)	112 (68)
45+	152	144 (95)	99 (65)
All ages	837	666 (80)	543 (65)

ELISA (Behring Enzygnost, Dade-Behring, Milton Keynes, UK), classified using the fixed cut-off recommended by the manufacturer, were also available (Table 1).

The age-stratified distribution of results for oral fluid samples was considered in comparison to those from the paired sera. The distribution of reactivity observed in samples for which the paired serum was negative was shown to be independent of age and approximated a Normal distribution (Fig. 1*a*). In samples for which the paired serum was positive the mean reactivity decreased with age (Fig. 1*b*). This information was used to motivate our choice of mixture model below.

Model

In constructing a mixture model, it is assumed that samples in the survey were taken from individuals with one of several different immune statuses. The simplest model has just two statuses, uninfected and previously infected. It is assumed that for each status the antibody results can be described by some distribution. If the parameters of these distributions (e.g. mean and standard deviation for a Normal distribution) and the proportion of samples with each status were known, the overall distribution of antibody results could be determined. Mixture modelling takes the inverse approach and estimates the distribution parameters for each status and the proportion of samples with each status by fitting the overall distribution of results.

For the present analysis, a mixture model was constructed to estimate the prevalence of rubella virus antibody using data from the oral fluid samples on the assumption that each individual had one of three statuses: negative, weak positive and strong positive. The proportion of samples with each status was assumed to be age-dependent. For a given status, the

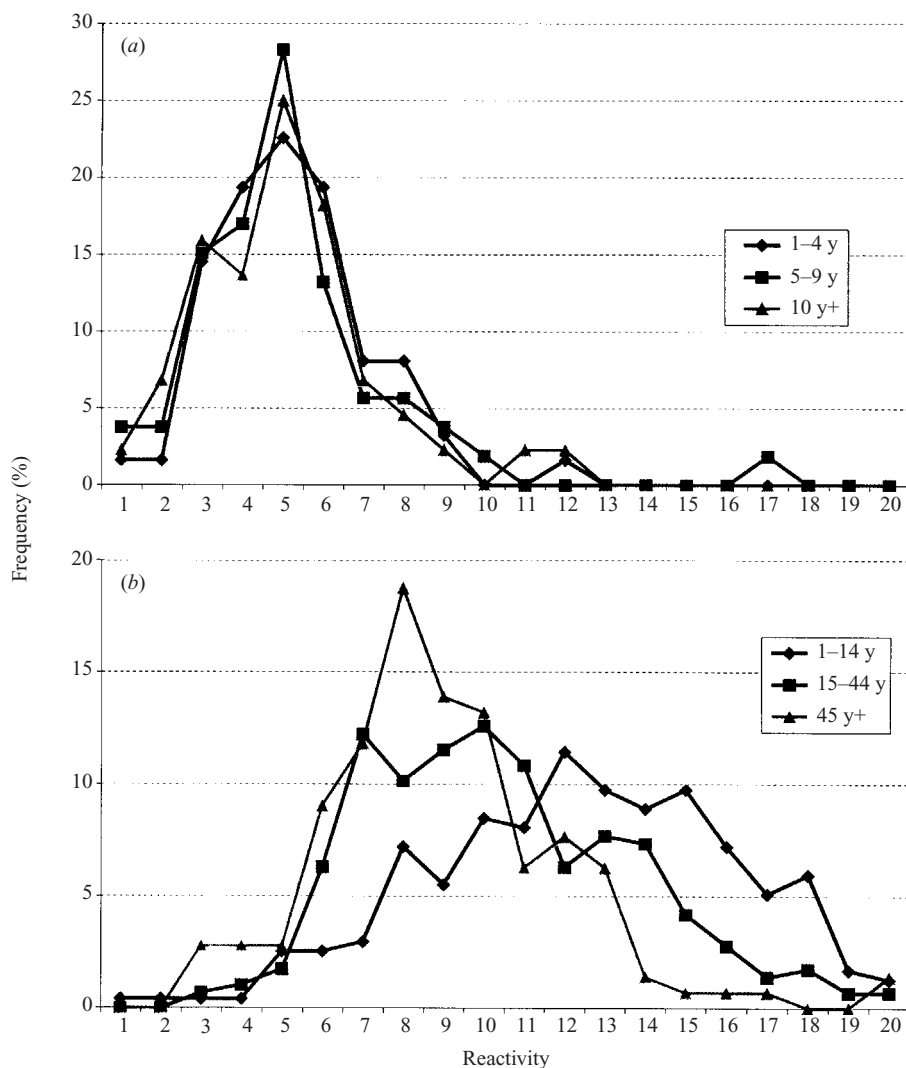


Fig. 1. Distribution of reactivity in the oral fluid assay by age group: (a) samples for which the paired serum sample was negative for rubella antibody; (b) samples for which the paired serum sample was positive for rubella antibody.

distribution of results in the oral fluid assay was assumed to be independent of age, and to follow a Normal distribution. Age-related changes in reactivity of samples from infected persons are reflected in the model by changes in the relative proportions weak and strong positive. In all 18 parameters (12 describing the proportions in each component for each age group and 6 describing the mean and standard deviation of the 3 component distributions) were estimated from 120 data points (the distribution of results in the 6 age groups). Details of the parameter estimation procedure are given in the appendix.

RESULTS

The proportions of samples attributed by the mixture model to the negative, strong positive and weak

positive components are shown in Figure 2. The prevalence of previous infection is calculated as the sum of the strong and weak positive components. The estimated distribution of results within each component is shown in Figure 3.

The model provided a good fit to the data, which is shown in Figure 4 and reflected by the deviance ($D=97.75$ on 102 D.F.). Clearly defined positive and negative distributions can be seen for young children, but these become progressively obscured at older ages. The proportion uninfected estimated by the model (Table 2) is compared to the proportion negative for rubella virus antibody in the original study using both oral fluids and matching sera (Fig. 5). The model estimates are very similar to the serum results, and overcome the lack of sensitivity associated with use of a fixed cut-off in the oral fluid assay.

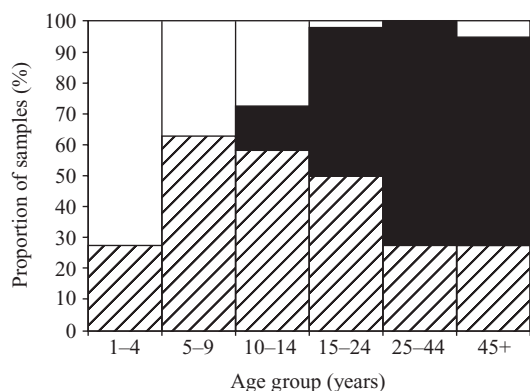


Fig. 2. Estimated proportion of samples negative □, weak positive ■ and strong positive ▨ by age group.

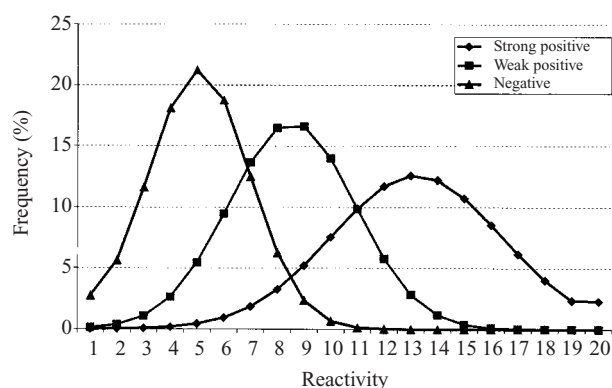


Fig. 3. Estimated distribution of reactivity in the oral fluid assay for negative, weak positive and strong positive samples.

A model using a single Normal component to model the infected population provided a significantly worse fit than the model with two (weak and strong) positive components ($D=212.80$ on 110 D.F., $P<0.00001$). Allowing the parameters of this distribution (mean and standard deviation) to take different values in each age group improved the fit ($D=115.82$ on 100 D.F.), but it was still considerably worse than the fit for the model with weak and strong positive components. Modelling the uninfected population with a Gamma distribution rather than a Normal distribution had little effect on the fit of the model or the estimated prevalence.

DISCUSSION

This study confirms the potential of age-specific mixture models as a tool for the analysis of population-based seroprevalence studies, in particular those that utilize oral fluids rather than serum. In such studies individual test results are only of importance for their contribution to the overall prevalence. Therefore it is not necessary to use a cut-off to categorize individual

samples as positive or negative, but rather use an age-specific mixture model to analyse the distribution of the quantitative results to provide a direct estimate of the age specific prevalence [8]. The prevalence estimates from the age-specific model with three component distributions applied to oral fluid data were in close agreement with results from matching sera using a commercial assay, which may be considered to represent the true prevalence of rubella virus antibody in the population studied.

The principal decisions in conducting a mixture model analysis involve the number of components to use and the choice of distribution for each component. In this analysis, we were able to base our choices on the distribution of reactivity observed in oral fluid samples for which the result on the paired serum was known. As a compromise between simplicity and flexibility, we did not attempt to model the mechanism of decaying antibody levels, only to describe the distribution resulting from this process. We thus modelled the infected population as a mixture of strong positive and weak positive Normal components. The importance of including the 'weak positive' component is demonstrated by the greatly improved fit over a model with just positive and negative components. The increase with age in the proportion of positives in the 'weak positive' component, particularly noticeable after age 15 years, reflects the decay of rubella specific antibody levels in persons infected many years previously as observed in other studies [4-7]. The approach of using strong and weak positive components to introduce flexibility into the infected distribution worked well in this study because the distribution of results for the uninfected population did not change with age (Fig. 1*a*). In a situation where the distribution of results from the uninfected population was also age-dependent (especially if the mean increased with age, perhaps due to acquisition of cross-reacting antibodies) it may be necessary to model the mechanisms producing these effects, rather than employing such an heuristic device.

The availability of serum results in this study directed the construction of the mixture model by enabling us to confirm the validity of our assumptions regarding the distribution of reactivity in infected and uninfected individuals. The serum results, however, were not used in the parameter estimation process. Future studies using the same oral fluid assay in unvaccinated populations may be conducted using oral fluid samples only, without the need for paired serum samples.

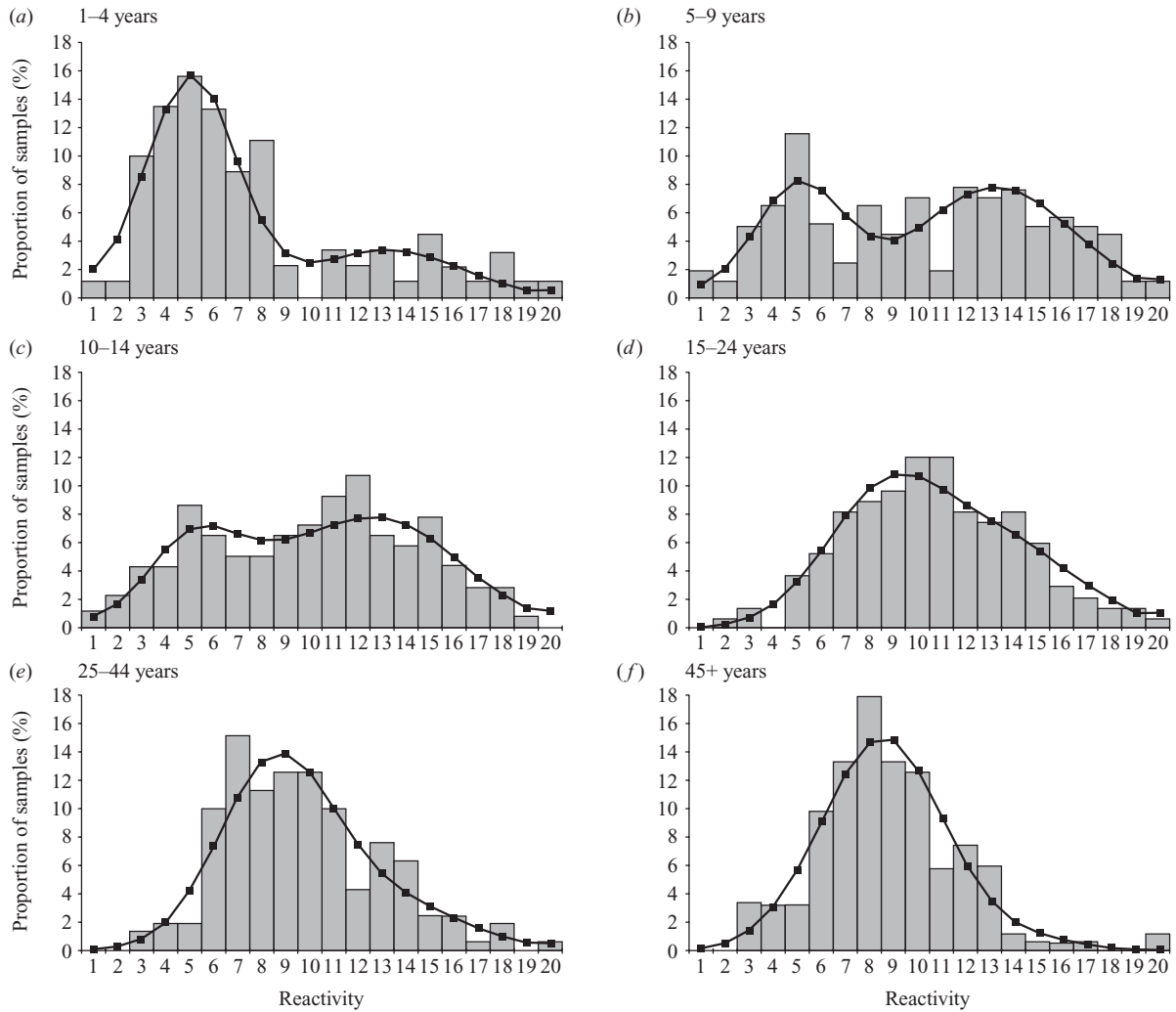


Fig. 4. Distribution of reactivity in the oral fluid assay by age group: observed data (bars) and model fit (line).

Table 2. Maximum likelihood estimates (95% CI) of the age-specific proportion of negative samples

Age group	Proportion negative (%)
1-4	73 (54-83)
5-9	37 (27-47)
10-14	27 (17-39)
15-24	2 (0-11)
25-44	0 (0-10)
45+	5 (0-18)

A variety of IgG assays designed specifically for use with oral fluids are available for a range of other acute self-limiting virus infections [9-14]. Due to decaying IgG over time since exposure, it is likely that these will also experience difficulty in distinguishing weak positive and negative results due to a combination of the low concentration of immunoglobulins found in oral

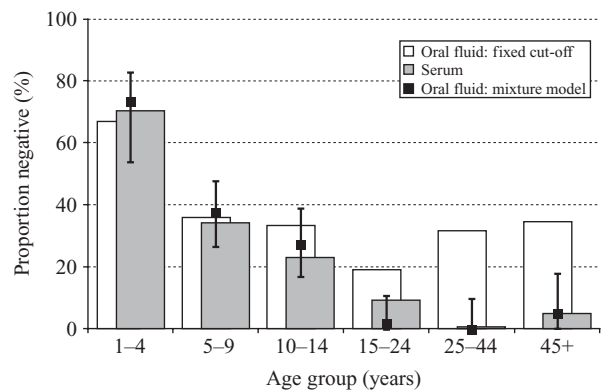


Fig. 5. Proportion of samples negative for rubella antibody by age: comparison of results from serum samples, oral fluid samples with fixed cut-off, and oral fluid samples using mixture model.

fluids and limitations in current immunoassay detection systems. When using a fixed cut-off value, data from prevalence studies utilizing oral fluids are likely to

be compromised and not accurately reflect those using sera, particularly in older age groups. However, this study has demonstrated that an accurate estimate of age-specific antibody prevalence can be achieved if mixture models are applied to results from population immunity studies using oral fluids. This therefore brings a step nearer the realization of using oral fluids to replace serum for prevalence studies, enabling the compliance advantages of oral fluids to be fully exploited for this purpose.

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APPENDIX – DESCRIPTION OF THE MIXTURE MODEL

The reactivity x in the oral fluid assay was defined as the logarithm of the OD ratio. Individual results are aggregated into 120 data points comprising 6 age groups (1–4, 5–9, 10–14, 15–24, 25–44 and 45 years or more) by 20 reactivity categories: n_{jk} denotes the number of results from person in age group j ($j=1, \dots, 6$) falling in the k th reactivity category ($x_{k-1} < x \leq x_k$: $x_0 = -\infty$, $x_{20} = \infty$, $x_k = -0.5 + 0.1k$ for $k=1, \dots, 19$).

Mixture model

Let $f^-(x)$, $f^w(x)$, $f^s(x)$ denote the distributions for the negative, weak positive and strong positive components respectively. Let p_j^-, p_j^w, p_j^s denote the proportion of samples from the negative, weak positive and strong positive components respectively in age group j ($p_j^- + p_j^w + p_j^s = 1$). Then the overall density of results at age j , f_j , is a mixture of the three component densities,

$$f_j(x) = p_j^- f^-(x) + p_j^w f^w(x) + p_j^s f^s(x).$$

Parameter estimation

Let N_j denote the number of individuals of age j , so that $N_j = \sum_k n_{jk}$. Then $(n_{j,1}, \dots, n_{j,20})$ is multinomial with index N_j and probabilities π_{jk} , where

$$\pi_{jk} = \int_{x_{k-1}}^{x_k} f_j(x) dx.$$

Maximum likelihood estimates for the parameters were obtained by minimizing the deviance D

$$D = 2 \sum_{j=1}^6 \sum_{k=1}^{20} n_{jk} \log \left(\frac{n_{jk}}{\pi_{jk} N_j} \right).$$

Likelihood-based 95% confidence intervals for the age specific prevalence were obtained by finding the maximum and minimum values for which the deviance was within 3.84 of the minimum (Table 2).

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