The burden of infection with cytomegalovirus in England and Wales: how many women are infected in pregnancy?

A. J. VYSE^{1*}, L. M. HESKETH² AND R. G. PEBODY¹

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SUMMARY

A serological survey was used to investigate the epidemiology of cytomegalovirus (CMV) infection in England and Wales. A total of 5237 sera representing the complete age range were used reflecting the general population. The sera were collected in 1991 and 2002, and screened for CMV-specific IgG by ELISA. Antibody prevalence increased with age from $\sim 15\,\%$ in those aged 1–4 years to $\sim 80\,\%$ in those aged $\geqslant 65$ years with no association with gender or region. Analysing by common birth cohort demonstrated that between 1991 and 2002 incidence was highest in children born 1985–1989 (1·62 % per year, 95 % CI 0·86–2·35), lower in older children and younger adults born 1950–1984 (0·75 % per year, 95 % CI 0·29–1·19) with little evidence of infection in older adults born pre-1950 (0 % per year, 95 % CI 0–0·64). Application to population and live-birth estimates for England and Wales suggested that between 1991 and 2002, 159 996 (95 % CI 67922–278277) CMV infections occurred annually with an annual average of 2133 (95 % CI 816–3435) infections affecting pregnant females.

Key words: Antibody prevalence, burden of infection, CMV, incidence, pregnancy.

INTRODUCTION

There is emerging interest in the epidemiology of cytomegalovirus (CMV) and the burden of disease attributed to it, particularly congenitally acquired CMV infection, reflected by the body of publications recently arising on this topic [1–5]. CMV is a member of the herpes virus family and is able to establish latent infection in the host following primary infection, from which it can periodically reactivate. It is transmitted via close personal contact through infected body

fluids (usually saliva or urine) [1, 6] and can also be transmitted from mother to fetus at any time during pregnancy [5].

The public health impact of CMV results mainly from its often overlooked role as a leading cause of congenital infection, and also as an opportunistic pathogen complicating the care of immunocompromised patients [1, 2, 6]. Whilst CMV is recognized as perhaps the most common intrauterine infection in humans [6], both raising the risk of infant mortality and causing permanent physical sequelae such as sensorineural hearing loss, visual impairment and mental retardation [5, 6], the true burden of congenital infection and its consequences remain unclear since maternal CMV infection is often asymptomatic and

¹ Health Protection Agency, Centre for Infections, Sero-Epidemiology Unit, Immunisation Department, London, UK

² Lancashire Teaching Hospitals NHS Trust, Preston Microbiology Services, Royal Preston Hospital, Fulwood, Preston, Lancashire, UK

^{*} Author for correspondence: Dr A. J. Vyse, Health Protection Agency, Centre for Infections, Sero-epidemiology Unit, Immunisation Department, London NW9 5HT, UK. (Email: andrew.vyse@HPA.org.uk)

there is a lack of data on important outcomes and follow-up of infected children [1, 3]. Estimates of the burden of infection with CMV at the population level, particularly in pregnant women, are therefore important for assessing the extent of CMV infection as a public health issue.

Within the United Kingdom large antibody prevalence studies have been carried out but are restricted to samples from antenatal women [7, 8], and there are no estimates of CMV antibody prevalence and burden of infection across the complete age range representative of the contemporary general population. A large population-based antibody prevalence study in the United States for those aged ≥6 years using sera collected between 1988 and 1994 has recently been published [4] and was subsequently used to estimate incidence in the general population aged 12–49 years [2]. This study estimated the force of infection to be 1.6% in this age group and suggested that ~ 27000 new CMV infections occur annually in seronegative pregnant females, indicating a public health problem of some magnitude in the United States.

In the present study we describe the seroepidemiology of CMV in England and Wales using sera approximating the general population and representing the complete age range collected in 1991 and a decade later in 2002 [9, 10]. This enabled an estimate of the burden of CMV infection to be made, and using samples collected at two time points 11 years apart enabled the effect of time trends to be addressed when calculating an incidence.

MATERIALS AND METHODS

Samples

A total of 5237 serum samples were used in this study with 2477 collected in 1991 (43 % from males and 57 % from females) and 2760 collected in 2002 (44 % from males and 56 % from females), the complete age range (1 to ≥80 years) was represented by samples used from each year of collection. These sera were randomly selected from a convenience collection considered to approximate the general population of England and Wales consisting of anonymized residues of specimens submitted for microbiological or biochemical testing to laboratories that were then part of the Public Health Laboratory Service (PHLS) and contributing to the PHLS Serological Surveillance Programme (now the HPA Seroepidemiology Programme) [9, 10]. A total of 12 laboratories provided the sera used in this study.

Laboratory methods

All samples were tested for evidence of CMV-specific IgG by ELISA (Behring Enzygnost, Dade Behring, Milton Keynes, UK) at Lancashire Teaching Hospitals NHS Trust. Results were expressed quantitatively according to the manufacturer's instructions.

Data

Individual quantitative data from each year of sample collection were aggregated into 35 reactivity categories (equal width bands based on the \log_{10} of the quantitative result) and stratified by 12 age groups (1–4, 5–9, 10–14, 15–19, 20–24, 25–29, 30–34, 35–39, 40–44, 45–54, 55–64 and \geqslant 65 years; number of samples in each age group ranging from 142 to 337) and 11 common birth cohorts (born 1920–1929, 1930–1939, 1940–1949, 1950–1954, 1955–1959, 1960–1964, 1965–1969, 1970–1974, 1975–1979, 1980–1984 and 1985–1989; number of samples in each birth cohort ranging from 72 to 340), enabling frequency distributions to be viewed.

Mixture models

Serological data were modelled as previously described [11, 12], fitting two components to the observed distributions of quantitative results in each age group or birth cohort. For a given component (reactivity level) the distribution of results in the assay is assumed to follow a Normal distribution. Age and birth cohort-related changes in reactivity are reflected in the model by changes in the proportions attributed to each component distribution. A single model was fitted simultaneously to data from each year of sample collection. This was the primary method used to estimate CMV antibody prevalence.

Fixed cut-off

Mixture models enable the proportion of a population with (and without) evidence of specific antibody to be estimated but do not classify results individually according to antibody status, which may be required for statistical modelling with other information available at an individual level. CMV-specific IgG status for individual samples was therefore assigned using a fixed cut-off that yielded an equal number of false-positive and false-negative results, estimated using a least-squares technique

from the degree of overlap between the two component distributions used by the mixture model fitted to the study data to describe those susceptible and those with evidence of previous CMV infection, assuming an overall prevalence of 45% in the population.

Estimating incidence

A model was used to estimate the average proportion of those aged 2–71 years in 1991 susceptible to CMV who acquired this infection over the 11 years between 1991 and 2002. This modelled the prevalence in each birth cohort according to the equation:

$$P02_c = P91_c + (\lambda_{91-02} \times (1 - P91_c)),$$

where λ_{91-02} = the proportion of those susceptible to CMV aged 2–71 years in 1991 who acquire this infection over the 11 years between 1991–2002; P02_c = model prevalence in 2002 in birth cohort 'c'; P91_c = model prevalence in 1991 in birth cohort 'c'.

A binomial maximum-likelihood method was used to fit the model to the observed antibody prevalence data made using the mixture model for each time point, obtaining maximum log-likelihood estimates for the parameters for each time period of the 20th century represented. The model assumed no waning of antibody over time and was constrained to return values for λ_{91-02} that were ≥ 0 , and was not able to consider the potential of CMV to recrudesce.

The complexity of the model was varied by systematically increasing the number of parameters for λ_{91-02} affecting different age groups/birth cohorts to explore the possibility that the risk of CMV infection varied for different age groups/birth cohorts over the time period under investigation. A χ^2 distribution test was used to compare the deviance of each more complex nested model to that of its immediate simpler predecessor, enabling the simplest model that best described the data to be determined [12]. Likelihood-based 95% confidence intervals for estimates of each value for λ_{91-02} included in the final model were obtained by finding the maximum and minimum values for which the deviance was within 3·84 of the minimum [12].

Using mid-1991 population estimates for England and Wales for those aged 2–71 years (www.statistics. gov.uk) and age-specific susceptibility estimates in 1991 made using the mixture model, the average number of CMV infections occurring in those born 1920–1989 susceptible to this infection over the 11

years between 1991 and 2002 were estimated. Thus:

(no. of infections)=(no. of persons) ×(proportion susceptible)×(incidence).

The average annual number of CMV infections occurring during pregnancy in women of childbearing age (15–44 years) was also estimated [13, 14]. This used the numbers of age-specific live births in England and Wales in 2002 (www.statistics.gov.uk), the age-specific proportion susceptible to CMV in 2002 estimated using the mixture model, assuming the duration of a pregnancy to be 9 months and applied the appropriate average annual incidence estimates made over the period 1991–2002 considered to affect females of childbearing age. Thus:

(number of infections in pregnancy)

- =(number of births)
- × (proportion of adults susceptible)
- \times (incidence in adults) \times (duration of pregnancy).

Statistical methods

Samples were classified individually according to age group (as previously described), sex, region, year of sample collection and CMV-specific IgG status. Region was classified as North (50·5%) and South (49·5%) according to the location of the laboratory providing the sample. CMV-specific IgG status for individual samples was assigned using the fixed cut-off identified that gave an equal number of false-positive and false-negative results. A multivariable analysis was then undertaken using logistic regression with CMV-specific IgG status as the dependent variable and age group, region, gender and year of sample collection included as independent variables (Stata 8.2; StataCorp., College Station, TX, USA).

RESULTS

Frequency distributions of age group and birth cohort stratified quantitative serological data are shown in Figure 1(a-d). These show that data aggregates into two distinct distributions. Two normal distributions were therefore used to model these data, which provided a reasonable fit [age group: deviance = 1764 on 812 degrees of freedom (D.F.); birth cohort: deviance = 1435 on 774 D.F.). CMV antibody prevalence estimates resulting from fitting the mixture model to these data are shown by age group (Fig. 2a) and birth cohort (Fig. 2b). Prevalence was very similar for each

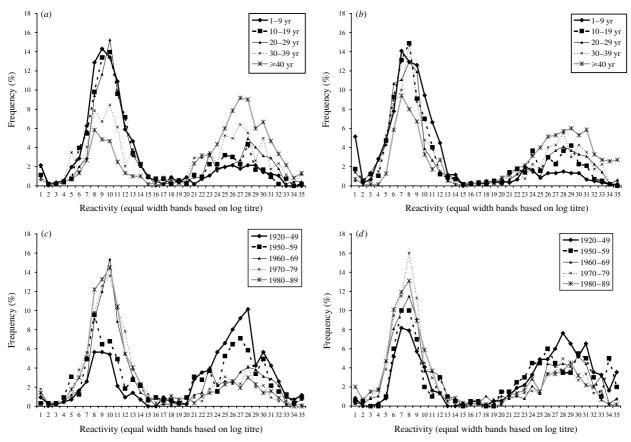


Fig. 1. Frequency distributions of cytomegalovirus serological data stratified by age group. (a) 1991 data, (b) 2002 data and birth cohort, (c) 1991 data, (d) 2002 data.

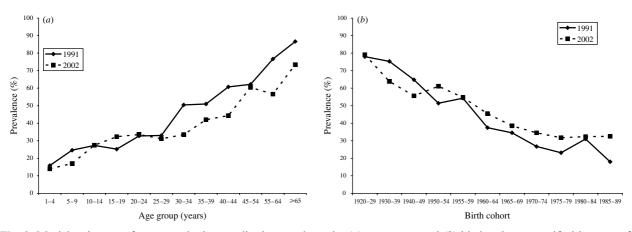


Fig. 2. Model estimates of cytomegalovirus antibody prevalence by (a) age group and (b) birth cohort, stratified by year of sample collection.

of the two time points represented for those aged 1–29 years, but consistently higher in those aged \geq 30 years using samples collected during 1991.

The final model used to estimate the incidence of CMV in those born 1920–1989 over the period 1991–2002 categorized birth cohort according to period of birth (from 1920–1929 to 1985–89 as previously

described) and fitted the data well (deviance = 10.2 on 8 p.f.). There was evidence that incidence varied for different age groups over the period investigated with the simplest model that best described the data requiring separate parameters for λ_{91-02} for those born 1920-1949, 1950-1984 and 1985-1989 (P=0.05) (see Table 1).

Birth cohort (age in 1991)	Incidence 1991–2002 (95 % CI)	Incidence per year (95 % CI)
1920–49 (42–71 yr) 1950–84 (7–41 yr)	0 % (0–7·06) 8·21 % (3·14–13·05)	0 % (0–0·64) 0·746 % (0·29–1·19)
1930–84 (7–41 yl) 1985–89 (2–6 yr)	17.79 % (9.50–25.80)	1.62 (0.86–2.35)

Table 1. Average estimates of cytomegalovirus incidence calculated over the period 1991–2002 in persons born 1920–1989

Applying these estimates to population data for England and Wales obtained in 1991 suggests that between 1991 and 2002 a total of 1759 951 (95% CI 747144–3061046) CMV infections occurred in those born 1920–1989. The annual average estimated incidence of CMV infection stratified by birth cohort using these data is shown in Figure 3. Table 2 shows the average annual number of CMV infections estimated to occur in pregnant females in England and Wales, applying an average annual incidence of 0.75% (95% CI 0.29–1.19) to females aged 15–39 years and 0% (95% CI 0–0.64) to females aged 40–44 years. This equates to ~1 (95% CI 0.38–1.61) CMV infection in every 279 pregnancies annually.

CMV-specific IgG status for individual samples was assigned using a fixed cut-off that gave equal numbers of false-positive and false-negative results, identified as 630 ELISA units (corresponding to the bottom of reactivity category 17). This cut-off was used for the multivariable analysis which showed there was a strong association between CMV antibody prevalence and increasing age (P < 0.001) but no strong evidence to suggest that prevalence increased with age group in those aged 1–29 years in a nonlinear fashion (P = 0.4). There was no strong evidence of an association with gender [odds ratio (OR) 0.93, 95% confidence interval (CI) 0.82-1.06, P = 0.27] or region (OR 1.03, 95% CI 0.91–1.18, P = 0.62), and no evidence of an association with year of sample collection for those aged 1-29 years (OR 1.00, 95% CI 0.85-1.17, P=0.98). However, there was strong evidence that compared to data from 1991, prevalence was lower in samples collected in 2002 for those aged \geqslant 30 years (OR 0.57, 95% CI 0.47–0.69, P < 0.001).

DISCUSSION

The frequency distributions of quantitative data stratified by both age group and birth cohort demonstrates that data aggregate into two very clearly distinguishable distributions reflecting those susceptible

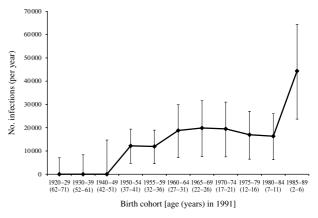


Fig. 3. Model estimates of average annual cytomegalovirus incidence measured over the period 1991–2002.

and those with evidence of past CMV infection. This suggests that the Behring Enzygnost CMV ELISA assay used in the present study performed extremely well and supports the assumption that CMV-specific IgG persists for life and does not wane with time. If there was a tendency for antibody to decline over time, more results falling in between these two major distributions might be expected. Moreover, the proportion in the distribution representing those susceptible consistently decreases with increasing age/birth cohort suggesting that waning of antibody is not a significant factor. Applying the same mixture model to data from each year of collection enabled direct comparisons between prevalence estimates to be made for each time point. However, as only a very small proportion of samples gave a quantitative result that fell into the area where the two distributions overlapped suggests that a fixed cut-off is also a feasible and accurate alternative approach for categorizing these data qualitatively at the population level and will give very similar results to the mixture model.

When stratifying by age group antibody prevalence increased with age from $\sim 15\%$ in those aged 1–4 years to $\sim 80\%$ in those aged $\geqslant 65$ years, reflecting other antibody prevalence studies in developed countries recently carried out [4, 7, 8]. A notable feature is

Age group (yr)	Proportion susceptible	No. of live births (2002)	Number of CMV infections per year (95% CI)
15–19	68%	43 192	164 (63–260)
20-24	66%	110 959	413 (158–656)
25-29	69 %	153 379	591 (226–940)
30-34	67%	180 532	672 (257–1068)
35-39	58 %	90 449	294 (112–467)
40-44	56 %	16 441	0 (0-44)
Total	_	594 952	2133 (816–3435)

Table 2. The average annual incidence of cytomegalovirus (CMV) infection estimated to occur in pregnant females

that whilst antibody prevalence is very similar for each of the two time points represented for those aged 1–29 years, it is consistently higher in those aged ≥ 30 years using samples collected during 1991. This was supported by the multivariable analysis and suggests that the epidemiology of CMV affecting those aged 1-29 years did not change significantly at the end of the 20th century. However, since no information is available to determine precisely when and at what age infection occurred, all that can be inferred from this difference in prevalence observed in older age groups is that at some stage in the more distant past the epidemiology of CMV has altered with the force of infection subsequently decreasing. Low socioeconomic status has been identified as a risk factor for acquiring CMV infection [1], suggesting this observation may reflect improvements in living conditions and hygiene in the latter half of the 20th century.

CMV antibody prevalence was comparatively high in those aged 1-4 years, and was surprisingly high in those aged 1 year (11.5%, data not shown). This phenomenon has also been observed for varicella zoster virus which is also a member of the herpes virus family [11]. Other published large-scale antibody prevalence studies for CMV in similar populations from developed countries do not include samples from those aged 1 year [4, 8]. The high prevalence in this very young age group is unlikely to be due to the persistence of maternal antibody since all persons providing specimens for this study were aged at least 12 months, and the incidence estimated in women of childbearing age indicates that maternal infections during pregnancy will not account for such a high prevalence of antibody at this early age. One explanation is that CMV infection may be acquired particularly rapidly by infants. There is some evidence to support this possibility, a previous study finding that

20% of infants with no evidence of congenital infection were excreting the virus at 12 months [15]. Alternatively, this may reflect a specificity problem with the assay when testing samples from the very young, possibly as a result of some cross-reactivity with antibody to other herpes viruses with a high prevalence in this age group such as HHV-6 and HHV-7. The possibility of maternal recrudescence as a potential explanation for the high prevalence in the very young also needs to be considered, which cannot be addressed by the present study.

When stratifying by common birth cohorts those samples collected from persons in 2002 represent an opportunity to observe the effect of an additional 11 years of time for exposure to CMV infection in comparison to those collected in 1991. Therefore, unless CMV-specific IgG has a tendency to wane significantly, prevalence estimates for common birth cohorts should be higher in 2002 (or at least remain similar if there has been no acquisition of infection), which was observed consistently for those born post-1950. This approach to analysing these antibody prevalence data enabled an incidence of CMV infection to be calculated over the time period investigated (1991–2002).

The model used to estimate CMV incidence between 1991 and 2002 suggested that over this period most infection occurred in children and young adults, with little infection in older adults aged ≥40 years. There was some evidence that the rate of acquisition of CMV infection did not vary in older children and young adults but was higher in the very young. This is consistent with previous findings of high CMV antibody prevalence in young children attending pre-school day-care facilities [6]. This suggests transmission of the virus is propagated by the close personto-person contact common in this environment,

particularly as the likelihood of contact with body fluids such as saliva and urine that are important in the transmission of CMV will be increased in this less hygienically aware population [1, 3, 6]. A previous study found that child-to-parent transmission of infection plays a significant part in the acquisition of CMV infection in adult life, suggesting that adults with young children are most at risk [7]. This is also supported by our finding that between 1991 and 2002 there was no evidence of CMV infection in older adults aged >40 years, but infection was acquired by younger adults more likely to be parents of young children.

The incidence of CMV estimated by this study in older children and young adults was comparable although slightly lower than contemporary force-ofinfection estimates made in a UK population of antenatal women [8] and the general US population aged 12-49 years [2]. This small difference could be attributed to the latter two studies using data from a single point in time where time trends and current incidence could not be addressed, high antibody prevalence in older cohorts possibly causing the models to overestimate the force of infection. The relatively modest incidence estimated by this study in older children and young adults also reflects the low estimates for the basic reproduction number currently available for CMV [2, 8] (~2.5 in a UK population of antenatal women and ~ 1.7 in the general US population aged 12-49 years). This indicates that CMV is not an easily transmitted infection and supports the conclusion that should a suitable vaccine become available, relatively low levels of coverage will be required to control or eradicate the disease [8].

Applying the incidence estimates derived from these data to population estimates and pregnancy data for England and Wales suggests that despite a relatively modest incidence, infection with CMV may represent a significant and overlooked public health concern [1]. Additionally, it is likely that the incidence estimates calculated may be underestimates since a proportion of cases will be due to a reactivation of the latent virus previously acquired earlier in life and not measured by this study, and the estimates in pregnant females do not account for any fetal mortality during pregnancy or abortions as a result of maternal CMV infection. However, whilst it is widely recognized that further work is needed to evaluate more precisely the risk of serious sequelae following a CMV infection, particularly following infection acquired during pregnancy [1-5], some assessment of the scale of the

public health burden in England and Wales due to congenitally acquired CMV can be made using results provided by a recent study that estimated the prevalence of neurological and sensory sequelae and mortality associated with congenital CMV infection [5]. This suggested that 0.5% of children born with congenital CMV will die and 17–20% of those surviving will demonstrate one or more long-term sequelae [5]. Combining these estimates with the incidence estimates provided by the present study implies that in infants born with congenital CMV in England and Wales, an annual total of 11 deaths might be expected with 363–427 children going on to demonstrate long-term sequelae.

Throughout 1992 and 1993 a total of 2938 laboratory reports of CMV infection in England and Wales were received by the Public Health Laboratory Service Communicable Disease Surveillance Centre [16], representing only a small fraction of the total annual number of cases estimated by this study. Approximately 50% of these reports were from immunocompromised patients and only 47 were from pregnant females. This probably reflects the mild or asymptomatic nature of CMV infection in otherwise healthy individuals and indicates that CMV infection is considerably under-recognized outside of immunocompromised groups, particularly in pregnant females who are considered a key risk group.

The present study therefore highlights a need for increased public awareness of CMV infection, particularly in pregnant females, and for interventions to be developed to reduce the substantial burden of this disease. Until a suitable vaccine becomes available better education in key risk groups focusing on improved hygiene to interrupt key transmission routes may be an appropriate strategy that should be considered.

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DECLARATION OF INTEREST

None.

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