Llywodraeth Cymru
Welsh Government

REPORT

Technical Advisory Group: modelling the Impact of Test, Trace and Protect (TTP) on COVID-19 transmissions in Wales

Updated modelling from TAG of changes in self-isolation rules and/or stopping self-isolation for contacts in different scenarios as Wales moves to alert level 0.

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Contents

Summary

- This report updates **previous modelling of the TTP system published on 24 March 2021**. This report focuses on the potential impact of changing the requirements for contacts to self-isolate.
- Data from the Welsh TTP system on the observed delays and efficiency of each component was used to estimate the percentage of transmissions that may have occurred from an index case or their contacts before they were traced and entered isolation. This was then used to estimate an approximate effect on the reproduction number, R.
- Given the observed R value in Wales, the characteristics of TTP at the time can be used to try and infer the value of R in the absence of TTP. During winter high transmission and prevalence (outside of firebreak), we estimated TTP reduced R from approximately 1.7 to 1.3. Using R values in February 2021 and improvements to case ascertainment and test and trace times, the effect may have been a reduction from approximately 1.3 to 0.8.
- Using a recent R value (SPI-M, 15 July 2021), TTP may have reduced R

from around 2.2 to 1.4. If TTP were to continue but with the requirement of fully vaccinated contacts and under 18s to self-isolate removed, then R is estimated to increase from 1.4 to approximately 1.7. Removing both of these requirements therefore is estimated to increase R by around 0.3. We note the magnitude of the impact changes with the absolute R value, and hence changes over the dynamics of the epidemic. At a value of R around 1, the estimated increase is 0.2.

- A major component of the system is rapid isolation of the index case. This is due largely to the current small observed delay between symptoms, and reporting into the TTP system. One consequence of this is that if improvements in index case volume result in longer testing and tracing delays, there can still be an overall improvement in R. In contrast, if changes to contact tracing have a knock-on effect to reduce index ascertainment and isolation, a further significant increase in R could result. The removal of a small percentage of contacts from the process did not have a large impact on R. Nevertheless, contact tracing of major transmission groups remained a significant component in most of our scenarios, especially at high ascertainment of index cases, under the assumed high ascertainment of contacts, and short tracing delays.

Background

The updated **Coronavirus control plan** for Wales was published in July 2021. It set out what Alert level zero would look like for Wales when it enters it on 7 August 2021. Vaccinations have helped to weaken the link between confirmed COVID-19 cases and hospitalisations and/or deaths. However, an increase in COVID-19 cases still remains a concern and efforts should still be taken to reduce chains of transmission. Test, Trace, Protect will need to adapt to respond to the pandemic over the coming months to remain proportionate to the risks from COVID-19 and the wider harms.

The intention is to remove the requirement for people who are fully vaccinated to self-isolate if they are a close contact of someone who has tested positive. Discussions with stakeholders are ongoing regarding the requirements for children and young people who are contacts to self-isolate. Final decisions will

be made as part of the next review, due by 5 August 2021. In the meantime the existing rules apply. However, those with symptoms of coronavirus or those testing positive will need to self-isolate whether fully vaccinated or not.

This paper considers the impact of the self-isolating rules changing as stated above. We consider what would happen if we stop self-isolation for contacts in the following scenarios:

a. Either all contacts

b. Or all under 18s and all fully vaccinated

Analysis

Full methods are outlined in the Appendix. Briefly, this uses a simple branching process model where people who are infected with coronavirus are expected to spread infection onto R people in the next generation and R is attenuated based on case isolation as a result of TTP. The model focuses on the testing and contact tracing elements of TTP; it does not specifically model the support ('protect') element of TTP but this has an impact on individual's likelihood of engaging with TTP which is implicitly included.

Estimating the effect of removing certain isolation requirements in the TTP

Here, we use the modelling framework to estimate the impact of potential changes to TTP. Specifically, we ask what might be the effect if (a) u18s were not required to isolate and (b) vaccinated individuals were not required to isolate? We focus on the parameter q: the probability of a secondary infection (from index case) being traced. Note that we use a branching process model, so only infections are modelled. Changes to the TTP can then be modelled based on an assumption of the proportion of infections that are currently in the u18s or the proportion of infections that are in vaccinated individuals (that can also transmit onward infection). All other parameters were kept at best current

estimates.

We note that these scenarios represent a rapid response guide. The outputs are sensitive to several assumptions, which can be explored framework using a sensitivity analysis.

Baseline Assumptions

- 40% ascertainment of infections (as used in **February 2021 model**)
- 90% tracing and isolation of contacts (as used in February 2021 model)
- Mean delay from symptoms to reporting = 1 day (similar to February 2021 short scenario)
- Mean delay from reporting to end of contact tracing = 2 days (similar to February 2021 short scenario)
- Observed R_{eff} = 1.4 (SPI-M-O estimate 15/07/21)

Assumptions on under 18s and vaccinated individuals

- Currently ~ 60% cases in under 30s, assume cases in u18s ~ 30%. Hence reduce *q* by 30% if these are not traced.
- Assume vaccine efficacy against infection and subsequent transmission ~ 80%. Hence reduce *q* by 20% if these are not traced. Note this is an upper estimate as we do not yet consider vaccine uptake by age in the model.

Results

The impact of TTP on the *R* value in a number of scenarios was considered, broadly reflecting: (1) the performance of TTP in July 2021 under the current TTP requirements (Full) for which all identified contacts are required to isolate; (2) current scenario with the requirement of contacts who are under 18 (No u18) to self-isolate removed; (3) The current scenario but with those contacts who are fully vaccinated (no vaccinated) no longer required to isolate, and (4) The current scenario with both isolation requirements of contacts aged under 18 and

fully vaccinated removed.

Table 1 shows these scenarios where 40% of infections are assumed to be ascertained. Table 2 has a lower ascertainment assumption of 25% of infections. Table 3 considers the scenarios with ascertainment at 40% but reducing to 25% following any significant change to TTP. Table 4 considers the estimate at lower R values.

Table 1: Ascertainment of infections = 40% (baseline)

Contacts traced	R_{eff} realised	Estimated R in absence of TTP (counterfactual)	Impact of TTP on R	Additional R compared to Full
Full (trace 90%)	1.4 (as observed)	2.22	0.82	-
No u18s (trace 63%)	1.55	2.22	0.67	0.15
No vaccinated (trace 72%)	1.51	2.22	0.71	0.11
No u18s or vaccinated (trace 45%)	1.66	2.22	0.56	0.26

In the absence of TTP, *R* is estimated to be 2.22 when ascertainment of infections are assumed to be 40%. A full TTP response is estimated to reduce R to1.4, an absolute reduction of 0.82. Removing the requirement of contacts aged under 18 or fully vaccinated contacts to isolate reduces R from 2.22 to 1.55 and 1.51 respectively. Removing both of these requirements is estimated to reduce R from 2.22 to 1.66. Therefore, removing both of these requirement will lead to an R value 0.26 higher than the current full TTP.

Table 2: Ascertainment of infections = 25%

Contacts traced	R_{eff} realised	Estimated R in absence of TTP (counterfactual)	Impact of TTP on R	Additional R compared to Full
Full (trace 90%)	1.4 (as observed)	1.82	0.42	-
No u18s (trace 63%)	1.48	1.82	0.34	0.08
No vaccinated (trace 72%)	1.45	1.82	0.37	0.05
No u18s or vaccinated (trace 45%)	1.53	1.82	0.29	0.13

With the low ascertainment assumption, in the absence of TTP, *R* is estimated to be 1.82. A full TTP response is estimated to reduce R to1.4 (as observed recently), an absolute reduction of 0.42. Removing the requirement of contacts aged under 18 or fully vaccinated contacts to isolate reduces R from 1.82 to 1.48 and 1.45 respectively. Removing both of these requirements is estimated to reduce R from 1.82 to 1.53. Therefore, removing both of these requirement will lead to an R value 0.13 higher than the current full TTP.

Table 3: Ascertainment of infections = 40% (as expected, and as in table 1) AND change in TTP ascertainment level from 40% to 25%

Contacts traced	R_{eff} realised	Estimated R in absence of TTP (counterfactual)	Impact of TTP on R	Additional R compared to Full and high ascertainment
Full (trace 90%) – no change to ascertainment	1.4 (as observed)	2.22	0.82	-
Full (trace 90%) – AND change to ascertainment	1.7	2.22	0.52	0.3
No u18s (trace 63%) – AND change to ascertainment	1.8	2.22	0.42	0.4
No vaccinated (trace 72%) – AND change to ascertainment	1.77	2.22	0.45	0.37
No u18s or vaccinated (trace 45%) – AND change to ascertainment	1.87	2.22	0.35	0.47

In Table 3, we consider the scenario in which there are changes to contact tracing rules, but also at the same time infection ascertainment is reduced from 40% to 25%. This scenario has the biggest influence on R, and highlights the importance of maintaining the reporting and isolation of index cases under any future changes to TTP. Finally, in table 4 we consider the effects at lower observed R values. In general, the magnitude of the effects are estimated to be reduced, although there could clearly be scenarios were R could be increased from below 1 to above 1.

Table 4. What happens when R reduces? Let observed R = 1

Contacts traced	R_{eff} realised	Estimated R in absence of TTP (counterfactual)	Impact of TTP on R	Additional R compared to Full
Full (trace 90%)	1.0 (as observed)	1.6	0.6	-
No u18s (trace 63%)	1.12	1.6	0.48	0.12
No vaccinated (trace 72%)	1.08	1.6	0.52	0.08
No u18s or vaccinated (trace 45%)	1.19	1.6	0.41	0.19

Conclusions

It is important that a proportionate response is taken with regards to TTP as we move to alert level 1 and restrictions are released. Removing one or both restrictions of contacts aged under 18 and fully vaccinated contacts to isolate may be one way to do this. This analysis suggests it will lead to an increase in the R value but the most vulnerable in society, i.e those who are not vaccinated and adults, will continue to be required to self-isolate. Those with symptoms regardless of age or vaccination status will also be required to self-isolate. Therefore, many chains of transmission will still be caught and prevented/ reduced which will lead to a reduction in the R value even though it may be higher than if the requirement of all contacts to isolate remained. However, there are further harms that need to be consider and a balance needs to be struck so it may be beneficial to remove isolation requirements for the least vulnerable and

most likely to be protected from vaccinations.

Appendix: Detailed Methods

Estimating the effect of TTP on the reproduction number

We considered a simple branching process model, in which individuals expect to spread infection to *R* individuals in the next generation. Individuals are isolated, and hence cannot pass on the infection further, after specific delays that represent the identification of the index case and the tracing of contacts. The model parameters represent the key components of TTP, and the values of these parameters can be manipulated to provide an estimate of the potential reduction in the *R* value. A similar model is considered in [2], and model outputs were cross-checked against a detailed simulation model that included bidirectional contact tracing [3].

We considered the impact of 5 delays in the TTP system:

- Time period 1: Symptoms to Reporting and isolation (for the index case)
- Time period 2: Reporting to Testing (index case)
- Time period 3: Testing to Test Results (index case)
- Time period 4: Test results to Tracing of contacts
- Time period 5: Tracing to Advising of contacts to isolate

The effect of TTP is to reduce the potential for onward transmission from an index case or from its contacts: the earlier in the infectious period that an individual is isolated, the greater the reduction in onward transmissions and the greater the impact on *R*. In order to estimate the % transmissions that occur from an index and contact we assumed:

- The incubation period (time of infection until symptoms appear) is a Weibull distribution with mean 5.8 days and standard deviation 2.6 days [2].
- The serial distribution for an infector is generated by a skewed normal distribution, with mean (xi) 6 days, omega = 2, and k = 0. In this distribution (based on [2]), it is assumed that approximately 50% of transmissions occur

before symptoms appear.

- Setting an infection time for index cases (t=0). We then calculated by sampling from the relevant delay distributions:
  - The time at which symptoms appear in the index case (sample at random from incubation period distribution)
  - The time at which a secondary case would become infected, by sampling at random from the serial distribution
  - The time at which symptoms would appear in the secondary case (sample at random from incubation period distribution)
  - The time at which the primary case is registered in the contact tracing system, by adding 'time period 1' to the incubation time. *The index case enters isolation on this day.*
  - The time at which all contacts are traced, by adding 'time period 2+3+4+5'. Secondary cases enter isolation at the earliest time point: either through contact tracing, or through appearance of their symptoms (plus time period 1, ie by becoming an index case themselves).
  - For both primary and secondary cases we calculated the % of transmissions that were expected to have already occurred before they were isolated. This is calculated from the percentile of the serial distribution, calculated using the value obtained from the difference between the infection day, and the isolation day.

The final step was to link the reduction in transmission potential of traced cases (identified in the above process) to the overall population effect on *R*. For this, we include untraced individuals. These may be fully asymptomatic, or very mild unreported cases, or cases unreported for other reasons. The current assumption is that this represents a significant proportion of overall infections. As a baseline we assumed 25% of infections enter the tracing system in winter 2020 [1], increasing due to improved ascertainment and testing, to 40% by March 2021. The PHW reported number of contacts successfully traced has been consistently high during the pandemic, and is approximately 85% (winter) to 90% (current).

We considered three types of individual, and the proportion of transmissions from the index cases (x) and from the secondary cases (y), due to the effect of TTP, and obtained from the above incubation and serial distribution analysis.

- Type 0: untraced individual. Causes R infections on average
- Type 1: primary individual entering tracing. Causes xR infections
- Type 2: secondary infection of a traced individual. Causes yR infections
- p = probability of an infected entering tracing system (assume ascertainment ~ 25% winter 2020, 40% currently)
- q = probability of secondary infection of someone in tracing being traced (PHW data ~ 90%)
- we allow a missed secondary infection of someone in tracing to be picked up to enter tracing ["second bite of the cherry"]
- Traced secondary infections of type 2 individuals are also type 2.

Given these assumptions, the next generation matrix is as follows, with the effective overall R value, R_{eff}, calculated as the dominant eigenvalue.

Next generation matrix

"To" (secondary infections)	"From" (infecting type) 0	"From" (infecting type) 1	"From" (infecting type) 2
0	$(1-p)R$	$(1-q)(1-p)xR$	$(1-q)(1-p)yR$
1	pR	$p(1-q)xR$	$p(1-q)yR$
2	0	xqR	yqR

The difference between R and R_{eff} represents the impact of TTP. To estimate this difference it is necessary to input the parameters from the TTP (index ascertainment, contact ascertainment, and percentage of transmissions that take place from index/contacts). It is also required to input either R or R_{eff}. In practice we can observe R_{eff} from observed case/hospitalisation incidence (calculated weekly for Wales by PHW and calculated and published weekly by SPI-MO), and hence we take a back-calculation approach to infer the value R, the counterfactual reproduction number in the absence of TTP.

For example, if we assume delays in TTP of 1 day from symptoms to isolation,

and 1 day to trace and isolate contacts, the model estimated that approximately 60% of onward transmissions would have occurred from the index, but only 17% from the contacts. If we then assume that 40% of infections are ascertained, 90% of contacts traced, and we observe that the current R_{eff} is 0.8, the model estimate for impact of TTP is a 0.48 reduction, from an R value of 1.28. This approximates the estimates obtained in Wales in February 2021.

The process can be summarised as:

1. Take observed delays in the TTP system and calculate the expected % transmissions occurring from an index case or a contact from incubation period and serial distributions
2. Take best estimates for the ascertainment of infections, and % contacts traced, combine with current observed R_{eff} value, and estimate the counterfactual current R value in absence of TTP.

References

[1] Colman E, Enright J, Puspitarani GA, Kao RR. (2021). **Estimating the proportion of SARS-CoV-2 infections reported through diagnostic testing**.

[2] J Hellewell et al. (2020). **Feasibility of controlling COVID-19 outbreaks by isolation of cases and controls** (The Lancet).

[3] Bradshaw WJ, Alley EC, Huggins JH, Lloyd AL, Esvelt KM. (2021). Bidirectional contact tracing could dramatically improve COVID-19 control. *Nature Communications* 12, 232.

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