STATENS SERUM INSTITUT

Growth rates for the omicron variants BA.1 and BA.2

The expert group for mathematical modeling of covid-19 on 27 January 2022

The expert group for mathematical modeling has estimated growth rates and weekly percentage growth for the sub-variant BA.2 of the omicron variant, which took over from the original omicron variant BA.1 in mid-January 2022. The growth rates are estimated from sequenced samples taken from the 8th to the January 21, 2022 and is divided into age groups, previous infection and time since effect vaccination. The conclusions are:

- There are only small regional differences in the proportion of the omicron variant BA.2, which is expected to account for up to 100% of infections in mid-February.
- The growth rate for BA.2 is significantly higher than for BA.1 in all five age groups in the period from 8 to 21 January. In 3 of the age groups, a minimum doubling of the number of cases in less than a week is expected.
- The difference in growth rate between the two subvariants corresponds to BA.2 being around 30% more contagious than BA.1.
- In the youngest age groups, there has been a recent decline in growth rates for subvariant BA.2. It is also expected that the growth rates have fallen in all age groups since the calculations were made, as otherwise higher infection rates would have been observed in week 4.
- The growth rate for BA.2 is highest among the 5-17-year-olds and lowest among the + 60-year-olds.
- A higher growth rate for BA.2 compared to BA.1 can be expected to give a steeper epidemic curve with a higher peak for the spread of infection, just as it may delay the time when the expected decrease in infection sets in, as a larger proportion of the population must infected to obtain temporary population immunity.

Estimation of growth rates for BA.2 is subject to uncertainties, as there has only been a short period of time with sufficient data to estimate the growth rates in. With further data, BA.2's characteristics can be determined more accurately. Due to the high daily infection rate in the community, there is no capacity to completely sequence all positive samples, and the results must therefore be taken with the proviso that only a small proportion of the samples are sequenced. Thus, in weeks 1 and 2, about 8% of the positive samples were sequenced[1] .

In the community track, where the majority of the sequences come from, the samples are representatively selected for sequencing. There is also a delay on data for

[1] Danish Covid-19 Genome Consortium (covid19genomics.dk)

virus variants, as it takes about 6 days from a sample is taken until data is available to the expert group. The estimates will be adjusted on an ongoing basis as more sequencing results are obtained.

Omicron variant BA.2

The omicron variant took over most of the infection with SARS-CoV-2 in Denmark during December 2021. At the same time, the omicron variant has developed, so that there are now several different subvariants. The subvariant BA.1 became the dominant variant during December, at the same time as there was a large decrease in the occurrence of the delta variant. The subvariant BA.2 was introduced in Denmark at the beginning of December and has since accounted for an increasing proportion of cases of infection. In week 2, BA.1 and BA.2 thus amounted to 34% and 65% of the sequenced samples in Denmark[2]. BA.2 thus appears to have a significantly higher dispersal potential than BA.1. Preliminary analyzes of household infection indicate that BA.2 is primarily more contagious than BA.1, and only to a lesser extent escapes immunity from vaccination. This note examines growth rates in five age groups (0-4 years, 5-11 years, 12-17 years, 18-59 years and 60+ years), where time since vaccination is taken into account (2nd plug or 3rd plug) , and previous infection. Corrections are also made for test behavior, regional differences in infection, day of the week, population size and the proportion of positive samples that are sequenced. BA.2 has grown rapidly across all age groups, and it is relevant to be able to follow the growth in different age groups in order to be able to observe a possible generational leap for the older part of the population, which has largely received revaccination, as well as declining growth rates in other age groups may indicate that the peak of infection has been reached.

Results

Figure 1 shows the development in the share of BA.2 in the five regions up to 21 January, as well as a projection of future developments. It can be seen that there are only small regional differences in the prevalence of BA.2, and that BA.2 is expected to account for up to 100% of cases in mid-February.

[2] Danish Covid-19 Genome Consortium (covid19genomics.dk)

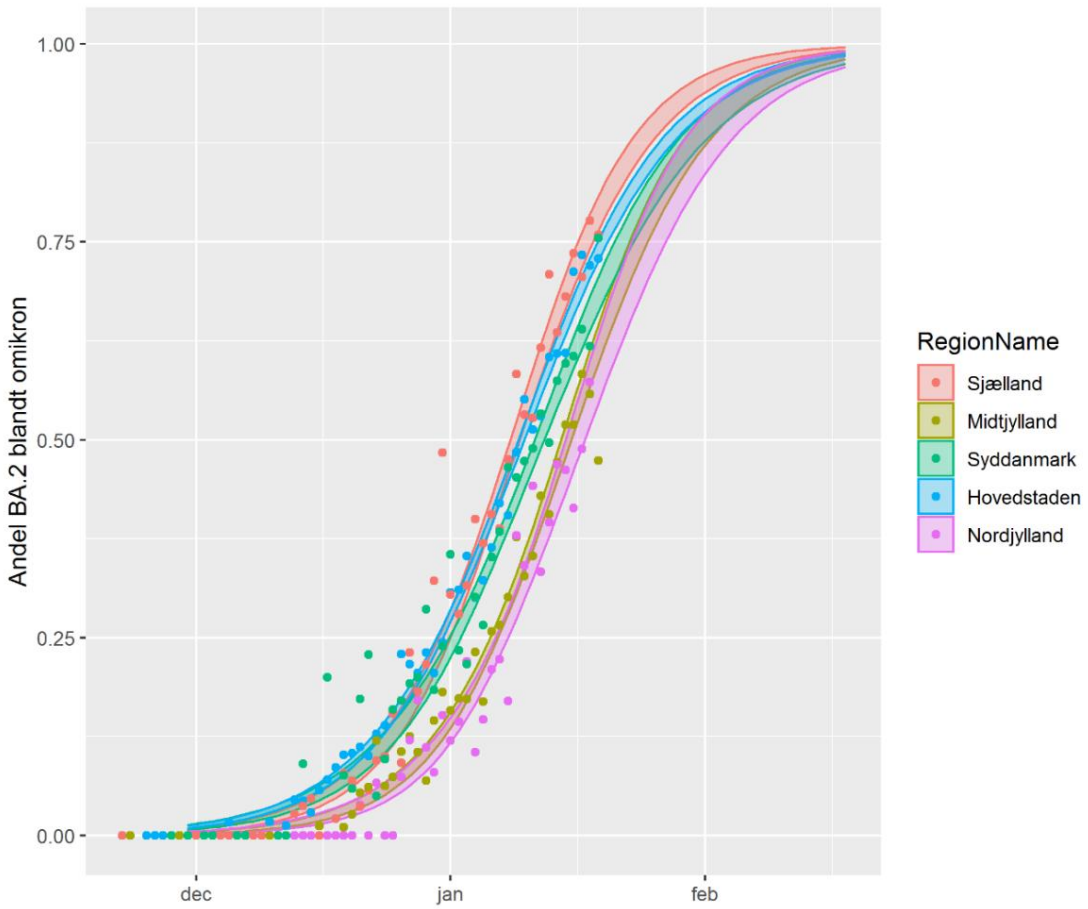

Figure 1: Projection of the proportion of BA.2 cases in the five regions. The colored dots shows the observed share of BA.2 in the regions up to 21 January.

Based on the sequenced samples, the Expert Group has estimated the growth rates (see the method section) for the subvariants BA.1 and BA.2. These estimated growth rates are shown in Appendix Table B1, and are converted in the note to weekly percentage growth (Table 1).

Table 1 thus shows the weekly percentage growth of BA.1 and BA.2 divided into the age groups 0-4 years, 5-11 years, 12-17 years, 18-59 years and 60+ years, time since protection of 2. or 3. vaccine stings, as well as whether one has previously been infected with SARS-CoV-2.
Note that people who have received the first but not the second vaccine sting are excluded from the analysis, as the group is very small and dynamic. Time since protection of 2nd or 3rd vaccine sting is found by taking the time since 2nd vaccine sting + 14 days or 3rd vaccine sting + 7 days for those who have obtained protection from 3rd vaccine sting. In other words, the weekly growth is calculated on the time since the protection of the latest vaccine sting has been achieved.
Gone infection can be with all the previous virus variants for which the natural immunity may be declining. However, it is a smaller proportion of the total number of infected,

who have been infected with the original variant and the alpha variant. Please note that estimates are for a 14-day period from 8 to 21 January.

The table shows that the subvariant BA.2 is in significant growth in all the groups studied. Thus, BA.2 has a weekly growth of at least 100% in most age groups except among the + 60-year-olds and 0-4-year-olds. Among the 5-17-year-olds, BA.2 has increased by almost 140% weekly. Different for subvariant BA.1, a moderate growth is seen in many groups. Thus, the infection with BA.2 grows 109% weekly in the age group 18-59 years, while BA.1 is constant in the age group.

Divided by vaccination status, it can be seen from the table that BA.2 has the lowest weekly growth among unvaccinated with a point estimate of 90%. Among persons who have received their 2nd or 3rd plug within the previous 59 days, the point estimate is about one-third higher, namely 120% weekly growth. It is not yet known what causes this difference. One possibility is that it is behavioral. SSI will revisit these estimates when additional data is available.

Table 1 also shows that the weekly growth is about 20% higher among individuals who have not had a known history of infection for both subvariants.

Table 1: Estimated weekly growth with 95% confidence intervals in five age groups, time since 2nd or 3rd vaccine sting, and known infection status for the period 8 January to 21 January.

Group	Weekly growth BA.2 (%)			Weekly growth BA.1 (%)		
	Estimate	Lower	Upper	**Estimate**	Lower	Upper
Age group						
0-4-year-olds	**84**	59	113	**16**	-2	36
5-11-year-olds	**132**	104	164	**36**	18	58
12-17-year-olds	**142**	119	168	**33**	19	49
18-59-year-olds	**109**	96	124	**0**	-7	7
+ 60-year-olds	**76**	55	99	**9**	-5	26
Time since vaccination						
0-59 days	**120**	101	141	**25**	14	38
60-119 days	**118**	96	142	**24**	12	38
+120 days	**102**	85	120	**15**	5	26
Unvaccinated	**90**	76	105	**8**	0	17
Gone is the infection						
No	**118**	108	129	**24**	18	32
Yes	**96**	74	121	**12**	-1	26

Figure 2 shows growth rate estimates calculated from rolling 14-day intervals. The graph shows the estimates of the growth rate as a function of the last date in each of the intervals, divided by subvariant and age group. The figure shows growth rates directly and is thus not presented as weekly increments. The estimates from the last day are presented as growth rates in Table B1 and as weekly increments in Table 1. When the growth rate is above 0, the subvariant is in growth, and vice versa, when the growth rate is below 0, the subvariant decreases. The figure shows that subvariant BA.2 is consistently estimated to be growing (on some dates, this estimate is not significant in some age groups). For subvariant BA.1, previous estimates have indicated that the variant is declining in most age groups, but in the recent period, the trend has reversed in some age groups where the subvariant is thus growing. In the recent period, the growth rates are for BA.2 decreased in the youngest age groups so that the subvariant grows more slowly than before.

For all age groups, BA.2 has higher growth rates than BA.1. The difference in growth rate between the two subvariants corresponds to BA.2 being about 30% more contagious than BA.1.

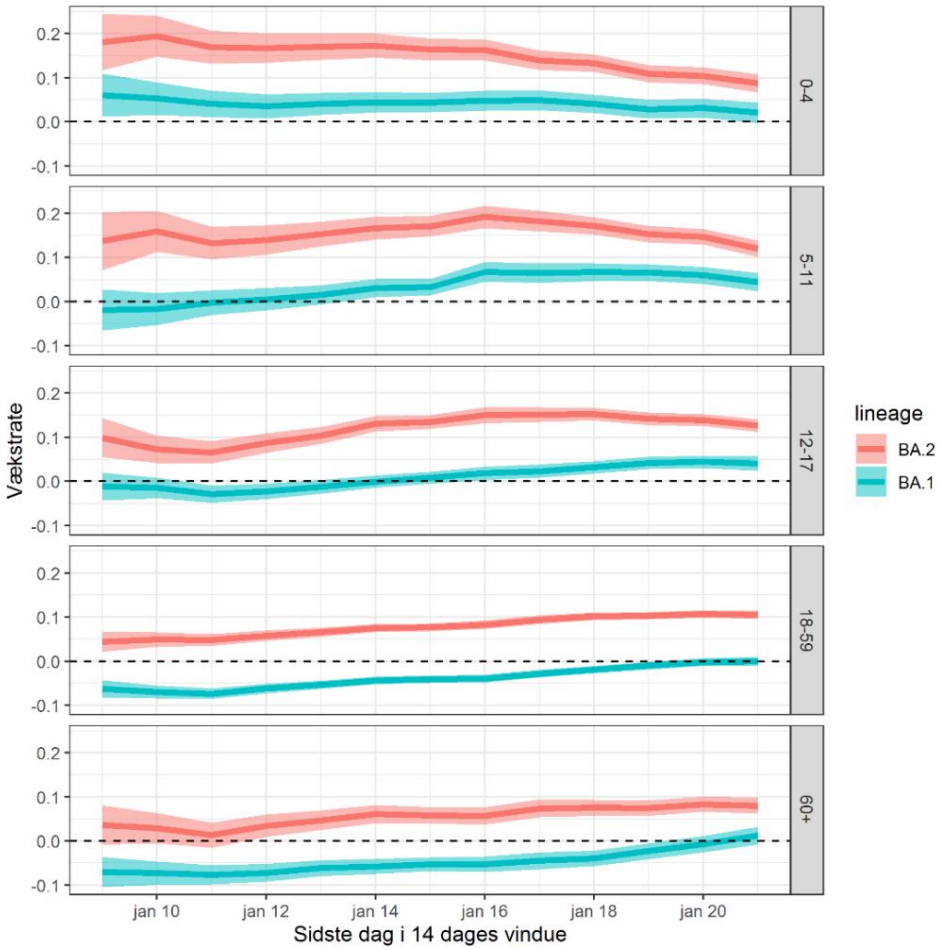

Figure 2: The development in the growth rate for the subvariants BA.1 (blue) and BA.2 (red). The growth rate is estimated from a 14-day interval, and is shown in the figure for the last day of the interval. Growth rates greater than 0 indicate that the subvariant is growing, while growth rates below 0 indicate that the subvariant is declining.

Method

Estimation of the growth rates of the two omicron subvariants BA.1 and BA.2 is made with a quasipoisson regression to allow overdispersion. However, it is found that the overdispersion factor is close to 1. The regression model compares the number of cases with each subvariant over time with correction for the population size and test intensity in the respective subgroups. Subvariant, age group, vaccine status, day of the week and region are used as explanatory variables. The model selection is started by including up to third order interactions between test date, subvariant, age group and vaccination status, while further taking into account regional differences in the level of infection with the two subvariants as well as differences in test behavior.

The correction for the varying test intensity is performed by estimating beta correction as described in *"Expert report of 23 October 2020 - Incidence and projection of COVID-19 cases" 3 .* Here, however, there is an extra element, as it is only a proportion of those
positive samples, which are sequenced and this proportion,, change significantly from day to day. The model therefore checks for this proportion in each of the groupings examined, just as the groupings of different sizes are taken into account in the same way.
(). These are introduced as offsets in the model, thus estimating the development in the number of sequenced omicron cases per citizen.

Of the explanatory variables, there are a number of interactions that are not significant (5% level), which are therefore removed from the model to reduce the model complexity. The model estimates growth rates which are assumed to vary across the combinations of subvariant and time since vaccination. In addition, a further separate variation in the growth rates is assumed which depends on the age group and whether there is a known previous infection.

Written in the programming language R, the model is written as follows: glm.nb (P ~ Time * lineage * AgeGr + Time: Vac + Time: reinf + AgeGr * Vac + AgeGr * reinf + Vac * reinf + lineage * Vac + lineage * Region + weekday + log (nTest) + offset (log (St) + log (N)), data = ...)

Where P is the number of cases broken down by date ("" Time "), subvariants (" lineage "), time since 2nd or 3 vaccine stings (" Vac "), known infection status (" reinf "), age group (" AgeGr ") , and region ("Region"). The number of tests ("nTest") is included as an explanatory variable and since the log function occurs as a link in the negative binomial distribution is thus corrected for the test intensity. The proportion of sequenced samples ("St") and the population size in the group ("N") are included as an offset so that the estimated growth rate can be interpreted in units of sequenced samples per citizen per day. The model has been reduced based on data from the period 2022- 01-06 to 2022-01-19. Based on data available 2022-01-25.

[3] https://covid19.ssi.dk/-/media/ssi-files/ekspertrapport-af-den-23-oktober-2020-incidens-og fremskrivning-af-covid19-tilflde.pdf? la = da

Annex 1

Table B1: Estimated growth rates with 95% confidence intervals in five age groups, time since vaccination, and known infection status for the period 8 January to 21 January.

Group	Growth rate BA.2 (1 / day)			Growth rate BA.1 (1 / day)		
	Estimate	Lower	Upper	**Estimate**	Lower	Upper
Age group						
0-4-year-olds	**0.09**	0.07	0.11	**0.02**	-0.003	0.04
5-11-year-olds	**0.12**	0.10	0.14	**0.04**	0.02	0.07
12-17-year-olds	**0.13**	0.11	0.14	**0.04**	0.02	0.06
18-59-year-olds	**0.11**	0.10	0.11	**0.00008**	-0.010	0.010
+ 60-year-olds	**0.08**	0.06	0.10	**0.012**	-0.008	0.03
Time since vaccination						
0-59 days	**0.11**	0.10	0.13	**0.03**	0.019	0.05
60-119 days	**0.11**	0.10	0.13	**0.03**	0.016	0.05
+120 days	**0.10**	0.09	0.11	**0.02**	0.007	0.03
Unvaccinated	**0.09**	0.08	0.10	**0.011**	-0,0003	0.02
Gone is the infection						
No	**0.11**	0.10	0.12	**0.03**	0.02	0.04
Yes	**0.10**	0.08	0.11	**0.016**	-0.0013	0.03