



COVID-19 and X-linked agammaglobulinemia (XLA) – insights from a monogenic antibody deficiency

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Purpose of review

The clinical outcomes from COVID-19 in monogenic causes of predominant antibody deficiency have pivotal implications for our understanding of the antiviral contribution of humoral immunity. This review summarizes the lessons learned from COVID-19 infection in X-linked agammaglobulinemia (XLA) due to genetic defects in Bruton's tyrosine kinase (BTK).

Recent findings

Key molecular pathways underlying the development of severe COVID-19 are emerging, highlighting the possible contribution of BTK to hyperinflammation. SARS-CoV-2 specific T-cell responses and complement activation appear insufficient to achieve viral clearance in some B-cell deficient individuals. Whilst appearing efficacious in this group, use of convalescent plasma has been recently associated with the evolution of viral escape variants. Early data suggests individuals with XLA can mount a viral-specific T-cell vaccine response, however, the clinical significance of this is still emerging.

Summary

In contrast to reports made early in the pandemic, we show XLA patients remain susceptible to severe disease. Persistent infection was common and is likely to carry a significant symptom burden and risk of novel variant evolution. COVID-19 infection in this vulnerable, antibody deficient group due to genetic, therapeutic or disease causes may require prompt and specific intervention for both patient and societal benefit.

Keywords

Bruton's tyrosine kinase, convalescent plasma therapy, immunoglobulin replacement therapy, secondary antibody deficiency, X-linked agammaglobulinemia

INTRODUCTION

Since its emergence in 2019, the novel pandemic coronavirus (SARS-CoV-2) causing COVID-19 has placed enormous pressure on health-care systems worldwide. Individuals with primary immunodeficiency (PID) appear at particularly elevated risk of mortality [1^{*,2*}]. The diagnosis of PID encompasses a heterogeneous patient group, however, with over 430 distinct monogenic disorders recognised to date, accompanied by a spectrum of immunological and clinical phenotypes [3]. Analysis of young individuals hospitalised with COVID-19 has revealed inborn- and acquired- dysregulation of the innate type I interferon signalling pathway is highly enriched within those with risk of severe disease [4^{*,5*}]. However less is known about the impact of monogenic defects affecting other immune compartments.

X-linked agammaglobulinemia (XLA) is a congenital antibody deficiency caused by mutations in

Bruton's Tyrosine Kinase (BTK). Treatment consists of lifelong immunoglobulin replacement therapy (IgRT). It should be noted this treatment does not replace IgA or IgM, nor can current therapies compensate for the other lost roles of BTK outside of

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KEY POINTS

- Despite early reports, this summary of published cases demonstrates that patients with XLA are at risk of severe disease with COVID-19 infection.
- Similar to other viral infections, protracted COVID-19 infection is common in XLA.
- The wider roles of BTK lost in XLA, outside of B cell development, are likely to explain the severity of disease and persistence of infection.
- Evolution of novel variants in XLA patients poses a continued threat to wider herd immunity.
- XLA patients can mount a viral-specific T-cell vaccine response, however, the clinical significance of this is currently unknown.

B-cell development. These limitations in therapy are being increasingly recognised of late, particularly in relation to ongoing risk of recurrent respiratory tract infections and the frequent development of end organ damage such as bronchiectasis.

Initial experience during the pandemic suggested that individuals with congenital forms of agammaglobulinaemia appeared to experience only asymptomatic or milder disease, relative to those with common variable immunodeficiency (CVID), but considered only 2 congenital agammaglobulinemia cases and 7 patients overall [6[¶]]. We and others have recently described the heavy burden associated with persistent and symptomatic respiratory and gastro-intestinal tract infections in individuals with both XLA and CVID [7[¶],8[¶],9,10], suggesting a re-evaluation of this assessment as more reports became available. Here, we conduct a rapid review of the peer-reviewed and preprint literature for the outcomes from COVID-19 in cases of congenital agammaglobulinaemia in relation to disease severity and persistence, and consider biological and epidemiological factors which may contribute to these findings. PubMed, MedRxiv, Medline and EMBASE were interrogated for articles published until June 30th 2021 with the search terms; 'COVID-19', 'SARS-CoV-2', 'XLA', 'Agammaglobulinaemia', 'BTK' and 'Bruton'. Finally, given continued occurrence of new viral variants with enhanced transmissibility, we assess the evidence for T-cell responses to vaccination in this patient group. Together, the findings emphasise the unique balance between pathogen clearance and immunopathology with specific immunological defects, and highlight a need for greater focus on individualised approaches to protect and treat immunocompromised patients.

VIRAL INFECTIONS IN X-LINKED AGAMMAGLOBULINEMIA

Whilst the predisposition to bacterial infection is well recognised in XLA there is in addition both consistent historical evidence of viral susceptibility before and after the advent of IgRT able to maintain stable levels of IgG well into the normal range. This includes enteroviral infection leading to chronic and potentially fatal enteroviral infections (chronic meningoencephalitis in agammaglobulinaemia), from Echovirus type 11 and Coxsackievirus B5 [11,12]. The exact mechanism underlying this susceptibility in XLA is unknown, although it has been suggested the loss of BTK in TLR signalling may play a role [13]. Severe herpesvirus infections are described prior to optimal IgRT and vaccine-associated paralytic poliomyelitis is reported [14]. Live vaccinations are therefore contraindicated in XLA. Respiratory viruses occur more frequently in antibody deficiency and are prolonged with rhinoviral persistence described for 4 months in XLA [10]. Chronic Type 2 norovirus induced gut failure necessitating parenteral nutrition and ultimately HSCT to cure the infection and the antibody deficiency has been recently reported [8[¶]]. Taken together the findings suggest an important role for antibody in viral defence with the caveat regarding the other potential functions of BTK.

A ROLE FOR THERAPEUTIC ANTIBODIES AND BRUTON'S TYROSINE KINASE INHIBITION IN COVID-19 INFECTION?

Antibody responses are active in the early immune response to COVID-19, as demonstrated by detectable SARS-CoV-2 specific antibody responses within the first days to weeks of infection [15]. Neutralising antibodies to viral spike protein are an important correlate of protective immunity following vaccination [16]. Studies of antibody therapy in COVID-19 support the importance of early intervention for convalescent plasma [17[¶]], and whilst initial results from the 5795 patients allocated to convalescent plasma within the RECOVERY trial suggested this to be ineffective, subsequent reanalysis strongly suggests benefit in sero-negative individuals [18]. In addition, 2 monoclonal antibodies targeting the receptor-binding domain of the SARS-CoV-2 spike protein reduce viral load [19], and offer clear benefit in reducing 28-day inpatient mortality amongst hospitalised sero-negative adults with COVID-19 [20[¶]]. Importantly, this benefit was not seen when administered to patients with antibodies to SARS-CoV-2 [20[¶]]. The results support a dose-dependent reduction in viral load with clinical

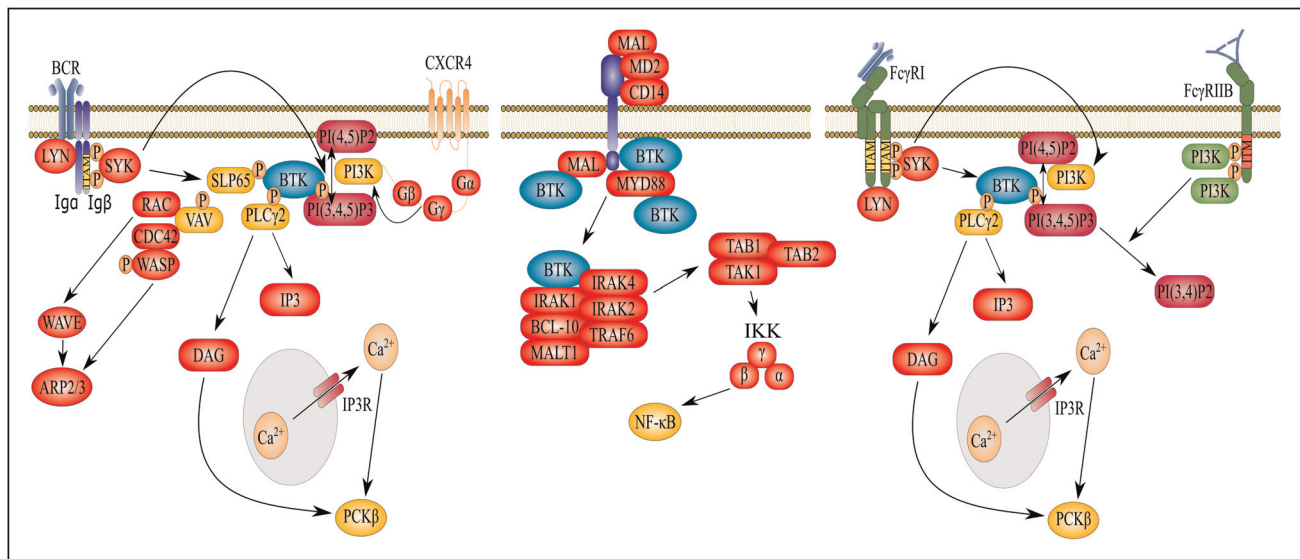


FIGURE 1. The wider roles of BTK in downstream signalling. BTK is widely expressed including in neutrophils, natural killer cells, dendritic cells, macrophages, and monocytes of myeloid origin. The wider functions of BTK are shown with involvement in downstream signalling of not only the B cell receptor (BCR) in B-lymphocytes but also the (i) chemokine receptor (CXCR4) activating PI3K and subsequently BTK, AKT and MAP-K dependent pathways in B cells, (ii) Toll Like receptors (TLRs) recruiting TIR, MYD88, IRAK1, TIRAP/MAL activating NF-κB, in macrophages, basophils and dendritic cells and (iii) the activating Fcγ receptor (FcγRI), activating Src-kinases, SYK, PI3K-γ and BTK in mast cells and basophils. There is increasing evidence for involvement of BTK in roles beyond B cell signalling in phagocytosis, the NLRP3 inflammasome (including thrombo-inflammation in platelets, [23]), microbe recognition via TLRs, nucleic acid recognition, maturation, differentiation signals and chemotaxis [53]. BTK, Bruton's tyrosine kinase; XLA, X-linked agammaglobulinemia.

benefit only when given early and also benefit in seronegative over seropositive individuals [18].

B-cell aplasia and pan-hypogammaglobulinaemia are hallmarks of X-linked and autosomal recessive antibody deficiency [3] which mean that these patients will neither mount an antibody response to COVID-19 and nor are they likely to have anti-interferon antibodies - in contrast to autoimmune polyglandular syndrome type 1 (APS-1), a rare autoimmune disease that results from autosomal recessive mutations of the autoimmune regulatory (AIRE) gene. Instances of severe COVID-19 in individuals with APS-1 coinciding with preexisting neutralising antibodies type I interferons stimulated the search and discovery of similar auto-antibodies in up to 10% of individuals with severe COVID-19 pneumonia [5^{***}].

As noted in Fig. 1, BTK has wide ranging roles beyond B-cell development, and is expressed across haematopoietic lineages apart from T-cells, where it participates in Toll-like receptor (TLR) and NLRP3 inflammasome signalling (including thrombo-inflammation in platelets) (Fig. 1) [21–23]. It has been suggested that BTK deficiency may protect from the cytokine storm seen in severe disease based on the role of BTK in macrophage activation and IL-6 production [6^{*},24–26], although murine and

human studies have shown conflicting results [27]. Recent studies of blood monocytes from general adult patients with severe COVID-19 showed consistent increases in BTK activation and production of interleukin-6 [28^{***}]. Blockade of IL-6 using Tocilizumab has been shown also to improve survival in severe disease [29], and BTK inhibitors (such as ibrutinib and acalabrutinib) are now being studied for the treatment of severe COVID-19 following promise in case series [28^{***},30^{*}]. It is therefore plausible that agammaglobulinaemia or genetic BTK deficiency may confer protection from severe COVID-19.

OUTCOMES FROM COVID-19 IN X-LINKED AGAMMAGLOBULINEMIA PATIENTS

The clinical outcomes 28 XLA patients with SARS-CoV-2 infection identified from peer-reviewed and preprint literature are summarised in Table 1. Age was reported in 23/28 individuals, with a median age at presentation of COVID-19 infection of 30.5 years (range: 5–55 years). Clinical presentations were available in 24 patients, with asymptomatic presentations uncommon (2/24, 8%). Fever was present in 83%, cough in 50%, and shortness of breath in 38%; a background of bronchiectasis

Table 1. A summary of the reported cases of SARS-CoV-2 infection in XLA patients

Paper	Age (years)	Bronchiectasis	Presentation	Peak CRP (mg/L)	Peak Ferritin (ng/mL)	Hospital admission	Oxygen	ICU	Therapies	Length of stay (days)	Virus detection duration (days)
Devassikutty <i>et al.</i> [46]	18	Yes	Fever, myalgia, loss of taste/smell	11.9	NA	Yes ^a	No	No	None	17 ^a	17
Milosevic <i>et al.</i> [47]	19	Yes	Fever, cough	NA	NA	Yes	Yes	Yes	None	22	NA
	34	Yes	Fever	205.8	493	Yes	Yes	No	IVIg, chloroquine, nadroparin, tocilizumab, convalescent plasma, steroids	56	52
Meyts <i>et al.</i> [1▪▪▪]	3–12	No	Fever, cough, shortness of breath, chest pain	NA	NA	Yes	Yes	No	Remdesivir, convalescent plasma, enoxaparin	NA	NA
	19–24	Yes	Fever, cough, shortness of breath	NA	NA	Yes	No	No	Chloroquine, convalescent plasma, enoxaparin	NA	NA
	25–34	No	Cough, fever	NA	NA	Yes	No	No	Steroids, Immunoglobulin, chloroquine	NA	64
	35–44	No	Cough, fever	NA	NA	Yes	No	No	Chloroquine, lopinavir, ritonavir	NA	6–14
	45–54	Yes	Asymptomatic	NA	NA	No	No	No	None	0	NA
	45–54	Yes	Fever	NA	NA	Yes	No	No	None	NA	NA
Shields <i>et al.</i> [2▪▪▪]	Median age 30.5	NA	NA	NA	NA	Yes	NA	NA	NA	NA	NA
		NA	NA	NA	NA	No	No	No	NA	0	NA
		NA	NA	NA	NA	No	No	No	NA	0	NA
		NA	NA	NA	NA	No	No	No	NA	0	NA
Quinti <i>et al.</i> [6▪]	34	NA	Fever	NA	NA	Yes	No	No	Hydroxychloroquine, lopinavir, ritonavir	NA	NA
Marcus <i>et al.</i> [48]	6	No	Fever	NA	NA	No	No	No	None	0	NA
Geutl <i>et al.</i> [49]	5	No	Asymptomatic	NA	NA	No	No	No	None	0	NA
		Yes	Fever, fatigue	NA	NA	Yes	Yes	Yes	Hydroxychloroquine, lopinavir, ritonavir, IVIG, convalescent plasma, tocilizumab	39	49–70 days
Jin <i>et al.</i> [31]	10	No	Fever, cough, chest pain	22.4	642	Yes	Yes	No	Remdesivir, IVIG, Convalescent plasma	29	25
	24	No	Fever, cough, shortness of breath	64	185	Yes	Yes	No	Convalescent plasma	19	NA

Table 1 (Continued)

Paper	Age (years)	Bronchiectasis	Presentation	Peak CRP (mg/L)	Peak Ferritin (ng/mL)	Hospital admission	Oxygen	ICU	Therapies	Length of stay (days)	Virus detection duration (days)
	40	Yes	Fatigue, fever, cough, respiratory distress	16.4	967	Yes	Yes	No	Convalescent plasma	45	NA
Soresina <i>et al.</i> [24]	34	No	Fever, cough	78	269	Yes	No	No	Hydroxychloroquine, lopinavir, ritonavir	22	NA
	26	No	Vomiting, asthenia, fever	3.6	774	Yes	No	No	Hydroxychloroquine		
Mira <i>et al.</i> [50]	39	No	Cough, respiratory distress, fever	NA	NA	Yes	No	No	Hydroxychloroquine, IVIG, Convalescent plasma	30	25
Hovey <i>et al.</i> [51]	26	No	Fever, respiratory distress, diarrhoea	12.86	1324.3	Yes	No	No	IVIG, convalescent plasma	14	NA
Loh <i>et al.</i> [32]	55	Yes	Fever, respiratory distress	258	NA	Yes	Yes	No	Steroids, IVIG	Died	NA
Iaboni <i>et al.</i> [33]	28	No	Respiratory distress	127	> 1500	Yes	Yes	Yes	Remdesivir, convalescent plasma	13	NA
Buckland <i>et al.</i> [34 ^{aa}]	31	Yes	Fever, cough, diarrhoea, vomiting	NA	1063.5	Yes	Yes	No	Hydroxychloroquine, Remdesivir, convalescent plasma	73	64
Almontasheri <i>et al.</i> [52]	19	Yes	Fever, respiratory distress, diarrhoea	47.6	58	Yes	No	No	IVIG	11	NA

NA, Data not available; XLA, Xlinked agammaglobulinemia.

^{aa}Admitted for infection control measures only.

Table 2. Age stratified mortality for individuals with Primary Immunodeficiency, X-linked Agammaglobulinemia, and the general UK population

Age group (years)	Primary Immunodeficiency, all diagnoses (United Kingdom, UK (2))										X-linked agammaglobulinaemic (International)				General Population, (United Kingdom, (36))	
	Patients, n	PCR ⁺ , n	Hospitalised, n (%)	Deaths, n	%	IFR (%)	CFR (%)	Inpatient		XLA, n	Hospitalised, n (%)	Deaths, n	CFR (%)	Inpatient mortality (%)	UK IFR (general population), %	UK inpatient mortality (general population), %
								mortality (%)	mortality (%)							
0-9	2	2	1 (50%)	0	0	0	0	0	0	3	1 (33%)	0	0	0	0.001	0.7
10-19	1	0	0 (0%)	0	0	0	0	NA	NA	4	4 (100%)	0	0	0	0.007	1.9
20-29	12	5	3 (25%)	1	8%	8%	20	33.3	7	7 (100%)	0	0	0	0	0.03	4.3
30-39	12	7	6 (50%)	0	0	0	0	0	9	6 (67%)	0	0	0	0	0.08	4.2
40-49	9	5	4 (44%)	1	8%	11.1	20	25	3	2 (67%)	0	0	0	0	0.16	6.3
50-59	11	7	7 (64%)	4	33%	36.4	57.1	57.1	1	1 (100%)	1	100.0	100.0	100.0	0.6	10.8
60-69	3	2	2 (67%)	1	8.3	33.3	50	50	0	-	-	-	-	-	1.93	20.2
70-79	6	6	5 (83%)	2	16.7	16.7	16.7	40	0	-	-	-	-	-	4.28	34.1
>80	4	4	4 (100%)	3	25	75	75	75	0	-	-	-	-	-	7.8	41.7

Table adapted from Shields *et al.* [2[■]]. IFR, infection fatality rate – proportion of mortality in all suspected or proven infected SARS-CoV-2 infections; CFR, case fatality rate – proportion of deaths from all confirmed infections.

was documented in 11 patients. Twenty-two (79%) were admitted to hospital, including 2 children [1[■],31]. Supplemental oxygen was required in the majority of hospitalised patients (8/11, 73%), with evidence of elevated inflammatory markers. The median length of stay was 22 days (range: 11–73 days) with three patients (11%) admitted to an intensive case setting. A single death was reported, a 55-year-old male [32], equating to an overall mortality rate of 4% (1/28). Therapies were defined in 17/21 hospitalised individuals, and included hydroxychloroquine ($n=10$), remdesivir ($n=4$), and corticosteroids ($n=3$). In contrast to the initial experience of Quinti *et al.* [6[■]], tocilizumab use was reported in 2 individuals with protracted hospital stays (39–56 days). Convalescent plasma therapy (CPT) was the most frequently reported therapeutic agent, employed in 11 patients (52%). Individual groups reported rapid recovery after CPT [31,33,34[■]], including Buckland *et al.* where CPT was successful in achieving viral clearance after two independent courses of remdesivir had failed. Interestingly, remdesivir achieved symptomatic response and suppression of viral load, but its cessation was followed by recrudescence of symptoms and rise in viral load. Genomic sequencing indicated persistent infection rather than re-infection. Detailed longitudinal investigation of this patient confirmed the absence of viral-specific antibodies produced by the patient and within replacement immunoglobulin therapy. Additionally, complement activation similar to critically ill COVID-19 admissions was demonstrated [34[■],35]. Polyfunctional CD8 T-cell responses were also observed, comparable to those seen in healthcare workers, and these increased in magnitude during the course of COVID-19 infection [34[■]]. This case illustrates the power of a personalised experimental approach, and suggests that SARS-CoV-2 specific antibodies provide a nonredundant contribution to reduction in viral load and eventual viral clearance. The patient continued regular IgRT throughout their admission, suggesting that clearance was not due to correction of defects of dendritic cell maturation arising in the absence of IgRT [34[■]].

Overall, the small sample size in the XLA patient group reported to date, possible reporting bias, and high mortality in this age-range leaves us underpowered to address the hypothesis that individuals with XLA have a different inpatient mortality rate to the general population (Table 2). Mortality appears comparable to modelling of inpatient mortality for COVID-19 in the UK population of a similar age-band [36]. Time until viral clearance was reported in 8/23 patients (35%) (Fig. 2). Mean duration was 38.3 days (95% confidence interval: 20.3–56.2 days) and ranged from ‘6 to 14’ days (handled as

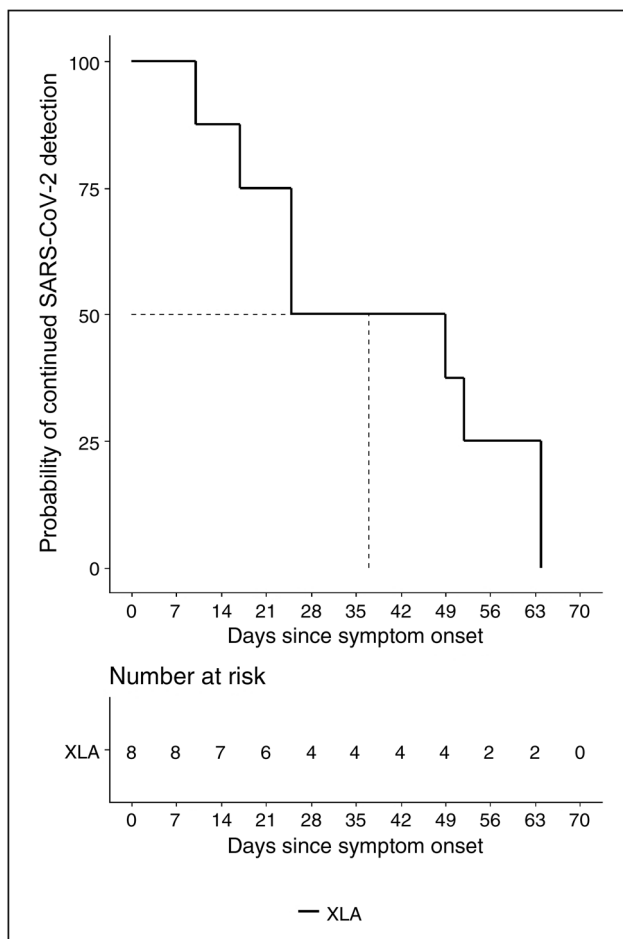


FIGURE 2. SARS-CoV-2 persistence in XLA patients. Kaplan Maier plot showing time until SARS-CoV-2 no longer detectable by respiratory tract RT-PCR sampling in 8 XLA patients. Created using R version 4.0.2 in RStudio (version 1.3.959, R Foundation, Vienna, Austria) using the survival and survminer packages. BTK, Bruton's tyrosine kinase; XLA, X-linked agammaglobulinemia.

10 days) to 64 days. By comparison, a recent meta-analysis estimated the mean duration of SARS-CoV-2 shedding from the upper respiratory tract to be 17.0 days (95% CI: 15.5–18.6 days) and 17.2 days (95% CI: 14.4–20.1 days) from the lower respiratory tract, up to a maximum of 83 days [37]. Similar observations of prolonged SARS-CoV-2 infection in patients who have received Rituximab help triangulate the critical defect in XLA patients to the B-cell compartment [38[■],39]. A case series of 17 B-cell-depleted patients with protracted COVID-19 were treated with CP at a median of 56 days from onset of symptoms. Prior to CPT, SARS-CoV-2 specific IFN- γ producing T-cells were evident in all patients studied, accompanied by profound hypogammaglobulinaemia with absent neutralising antibody responses to SARS-CoV-2 [38[■]]. Similar to the

XLA patient described by Buckland *et al.* [34[■]], symptomatic and inflammatory marker improvement occurred in all but 1 within 48 h, followed by falling viral load and reduction in oxygen requirements [38[■],39]. Together, this provides evidence for viral persistence of SARS-CoV-2 in patients with XLA and iatrogenic B-cell depletion and suggests a role for antibodies in reduction in viral load and contribution to viral clearance. The United States Food and Drug Administration reissued emergency use authorisation for high-titre COVID-19 CPT in hospitalized patients with impaired humoral immunity [39] in March 2021, however, a potential concern in immunosuppressed individuals was raised by Kemp *et al.* [40[■]]. Performing phylogenetic analysis on ultra-deep whole-genome sequential sequencing on samples from a chronically infected immunosuppressed individual with SARS-CoV-2, they showed CPT was accompanied by viral evolution and reduced sensitivity to neutralizing antibodies [40[■]]. Recent analysis of a second immunocompromised adult with hypogammaglobulinaemia and SARS-CoV-2 infection for over 290 days has subsequently demonstrated similar viral escape mutations can also arise independently of CPT [41[■]]. In this instance, following failure of remdesivir, treatment with the combination of casirivimab and imdevimab at day 265 achieved progressive resolution of all symptoms over the next 8 weeks, and clearance by RT-PCR was achieved by day 311 [41[■]].

VACCINE RESPONSES TO SARS-CoV-2 IN X-LINKED AGAMMAGLOBULINEMIA

We identified 2 reports assessing vaccine response following 2 doses of Pfizer-BioNTech in 10 individuals with genetically confirmed XLA [42[■],43[■]]. As expected, these individuals mounted no detectable serological response, however, robust production of IFN γ was evident following stimulation with spike peptide using an *ex vivo* ELISpot approach in 9/10 individuals (and IL-2 production in 5/5). Stimulation with peptides representing SARS-CoV-2 membrane protein induced no cytokine responses, consistent with vaccine-induced cellular immunity over postinfection responses [42[■]]. The relevance of such T-cell assessments, as a reflection of nature and durability of cellular immunity and risk of future severe COVID-19, remain uncertain. The presence of polyfunctional CD8⁺ T-cells during prolonged infection, described by Buckland *et al.* [34[■]], does not exclude protection following vaccination. It is relevant to note both Hagin and Salinas *et al.* identified a higher rate of vaccine-induced T-cell non-responders within genetically undefined COVID

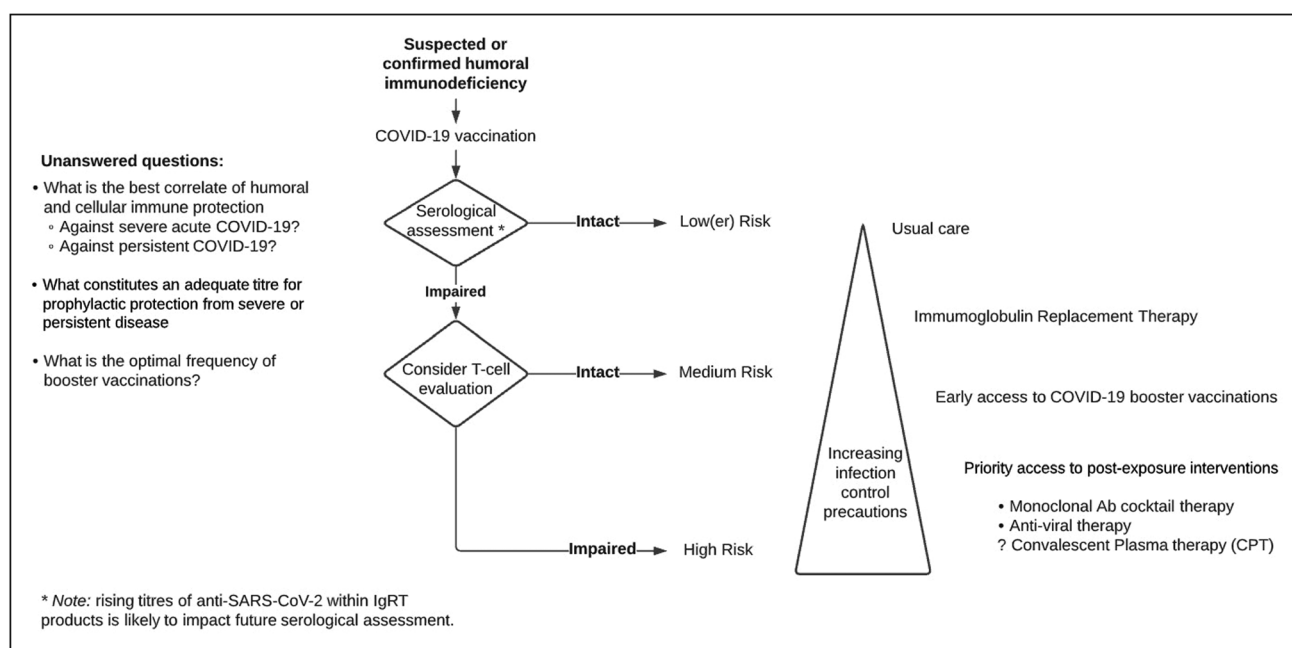


FIGURE 3. Putative role of vaccine response profiling in risk stratification to individualise approaches to SARS-CoV-2 in individuals with suspected humoral immunodeficiency.

patients, compared to XLA [42²²,43²³]. Although patients were not age or gender matched, this difference in T-cell response mirrors differences in reported mortality between XLA and CVID [1²²,6²³], and suggests assessment of T-cell responses maybe relevant to ongoing risk stratification, Fig. 3. The efficacy of alternative vaccination strategies, such as subunit or adenoviral vectors has yet to be examined. However, previous assessment of a trivalent inactivated influenza vaccine in 12 XLA patients showed induction of influenza virus-specific CD4 and CD8 T-cell responses comparable to healthy controls when assessed up to 6 months postvaccination [44].

CONCLUSION

In this review we draw together the international experience of COVID-19 in XLA, representing the largest description of outcomes for this rare patient group to date, highlighting the vulnerability of such individuals to chronic SARS-CoV-2 infection. In contrast to reports made early in the pandemic, we show these patients remain susceptible to severe disease despite any immunomodulation mediated by their underlying selective immunodeficiency. Although low, the crude case fatality rate of 4% associated with acute COVID-19 in XLA should be viewed in the context of the young age of the cohort described, likelihood of reporting bias, and the high level of background lung disease (i.e. bronchiectasis). Protracted SARS-CoV-2 infection appeared

common, with fever and respiratory symptoms in over 80% of cases at presentation, often accompanied by systemic inflammation and respiratory impairment. This is closely analogous to the marked symptom burden and impaired quality of life associated with persistent viral infections of the respiratory tract, gastro-intestinal, and central nervous system reported in this patient group [7²⁴,8²⁵,11,12,14]. The psychosocial impact of protracted COVID-19 infection on these individuals and their families is likely multiplied given requirements to self-isolate accompanied by experiencing progressive debilitation due to declining respiratory function [41²⁶]. We also highlight the far-reaching societal and clinical implications of chronic viral infection within primary and the expanding field of secondary predominant antibody deficiency disorders [45]. Whilst viral reversion of attenuated vaccine strains during chronic infection in XLA can result in vaccine-associated paralytic poliomyelitis for the individual [14], evolution of novel highly transmissible SARS-CoV-2 variants in hypogammaglobulinemic individuals poses a continued threat to vaccine-induced herd immunity [40²⁷,41²⁸]. The significance of increasing titres of anti-SARS-CoV-2 antibody within pooled purified IgRT products over time warrants further investigation, as they may complement T-cell induced vaccine responses. Caution is necessary, however, given immune selection pressure from CPT or future IgRT may accelerate generation of escape variants [40²⁷]. This suggests virological surveillance with immunological risk stratification

should go hand in hand in order to recognise infection in this subset of vulnerable individuals and support a rapid individualised response.

The paradigm that XLA is simply an antibody deficiency is slowly being challenged. In particular, susceptibility to both severe and persistence viral infections is also being recognised. Beyond the lack of ongoing of IgA/IgM in IgRT, the wider roles of BTK that cannot be compensated for in XLA are likely to play a major role in the control of viral infections.

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Conflicts of interest

S.J. has participated in advisory boards, trials, projects, and has been a speaker with Baxalta, CSL Behring, Shire, Thermofisher, Swedish Orphan Biovitrum, Biotest, Binding Site, Grifols, BPL, Octapharma, LFB, GSK, Weatherden, Zarodex, Sanofi, and UCB Pharma. All authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Author contributions: S.J. and A.G. conceived the study. All authors contributed to the literature review. M.J.P. and B.M.J.S. wrote the first draft. Figure 1 was created by B.S.; M.J.P. created Figs. 2 and 3. All authors critically reviewed and approved the final manuscript. Ethical approval: The data used in this work obtained relevant participant consent and ethical approval, therefore no additional approvals were required.

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Papers of particular interest, published within the annual period of review, have been highlighted as:

- of special interest
- of outstanding interest

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