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BRIEF REPORT

Upsurge of *Chlamydia pneumoniae* respiratory tract infections in 2024/2025 in Southern Germany

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Abstract

We report a never seen before upsurge of *Chlamydia pneumoniae* (*Cp*) respiratory tract infections in 2024/25 in southern Germany. Regarding 43,558 *Cp* PCR tests analyzed, the positivity rate increased from 0.3% in 2015–2020 to 2.6% in 2024, and 2.4% in 2025 until August 2025, peaking at ≥6.0% with >100 monthly cases in October and November 2024. Children aged 6–14 years were predominantly affected, and co-infections with other pathogens were frequently detected. We aim at raising awareness concerning *Cp* infections.

The bacterium *Chlamydia pneumoniae* (*Cp*) is a known cause of respiratory disease ranging from mild upper respiratory tract infection (RTI) to bronchitis and severe community-acquired pneumonia (CAP) [1, 2]. It mainly affects children but can occur in all age groups [2, 3]. In contrast to a high seroprevalence [3, 4] detection rates of *Cp* by molecular methods were low until the end of 2023 among patients with acute RTI and CAP in several studies [1, 5–7] including data from German surveillance networks [8, 9]. The role of *Cp* as a cause of CAP has therefore even been questioned by some authors [10].

In our laboratory we observed a surprising increase in *Cp* detection rates in September 2024 followed by a previously unseen infection wave wide into 2025. We here present detailed surveillance data on *Cp* infections in order to raise awareness for this pathogen and enable preparedness for the upcoming winter seasons.

In our analysis, all *Cp* PCR tests (Cp singleplex real-time PCR (AmpliGnost *C. pneumoniae*, PIIM, Karlsruhe, Germany) and respiratory multiplex real-time PCR assays, starting from February 2022 [for bacteria: AllPlex PneumoBacter Assay, Seegene, Seoul, South Korea; UC-TIB-Respi-BAC-1 (S.pneu/B.pert./B.para/H.inf), UC-TIB-Respi-BAC-2 (L.pneu/C.pneu/M.pneu), TIB MOLBIOL, Berlin, Germany; for viruses: AllPlex RV Master Assay, Seegene Inc., Seoul, South Korea; cobas Respiratory flex, Roche Diagnostics, Mannheim, Germany]) performed on nasopharyngeal swab or lower respiratory tract samples between 01.01.2015 to 31.08.2025 (n=43,558) were included. Our laboratory receives samples from hospitalized and ambulatory patients from all over southern Germany. The observed increase of *Cp* infections started slowly in autumn 2023 and, therefore, samples investigated during 2023 to 31.08.2025 (n=35,152) were further analyzed in detail.

The number of *Cp* positive samples increased from 0 to 4 per year in pre-pandemic years (0.3% of all samples) to 37 out of 7,705 samples in 2023 (0.5%), to 404 out of 15,320 samples in 2024 (2.6%), and 290 out of 12,125 samples (2.4%) until August 2025. The positivity rate of the *Cp* PCR assays rose in September 2023 to 0.9%, and surged in September 2024 reaching values of 6.1% and 6.0% in October and November 2024, respectively, which represented>100 cases per months (Fig. 1). Recent data for September to November 2025 were added retrospectively in Fig. 1 but were not included in the main dataset for statistical analysis.

When looking at the autumn/winter seasons (September to April) of the past ten years, there is a significant increase between the pre-pandemic seasons and 2023/2024 and 2024/2025, respectively (p<0.01; Fig. 2).

The *Cp* PCR positive samples during the *Cp* outbreak years 2023 to 2025 (n=731 from 35,152 samples investigated) included nasopharyngeal swabs in 88% and lower respiratory tract specimens in 12%. They were obtained in 93.4% from outpatients, i.e. ambulatory patients from private practices, and in 52.5%/47.5% from males/females. *Cp*

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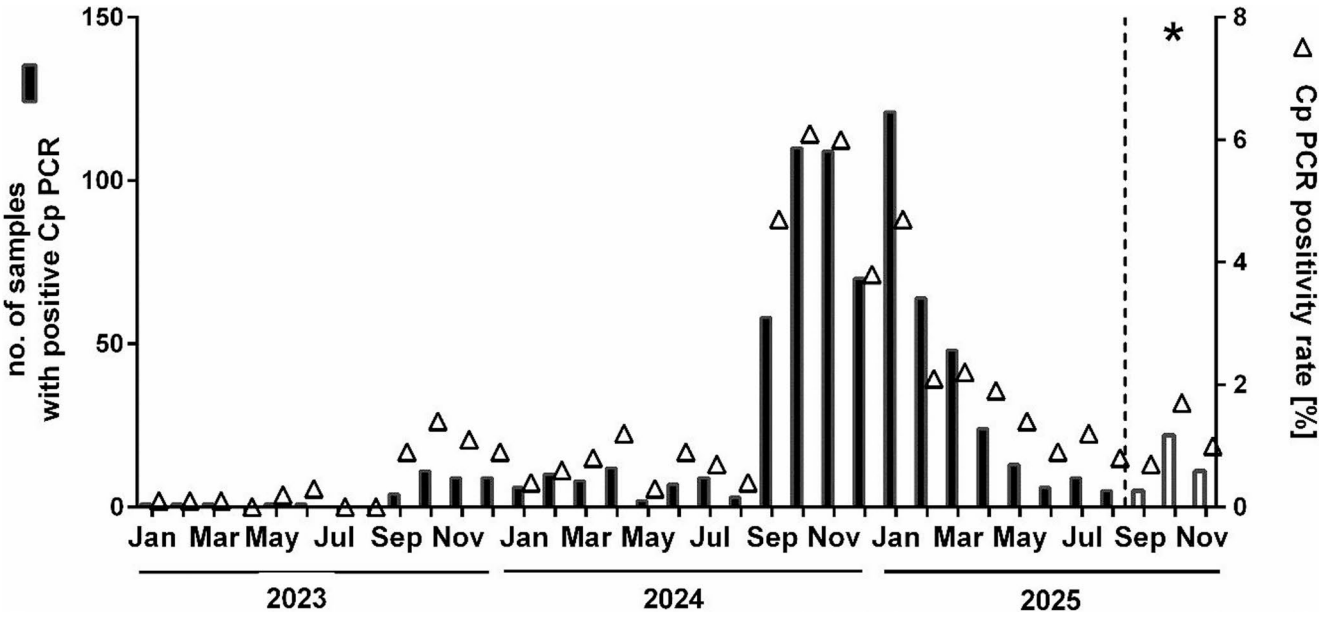

Fig. 1 Monthly numbers of samples with positive Cp PCR and Cp PCR positivity rate from 2023 to 2025 (*recent data added retrospectively but were not included in the main data set for statistical analysis)

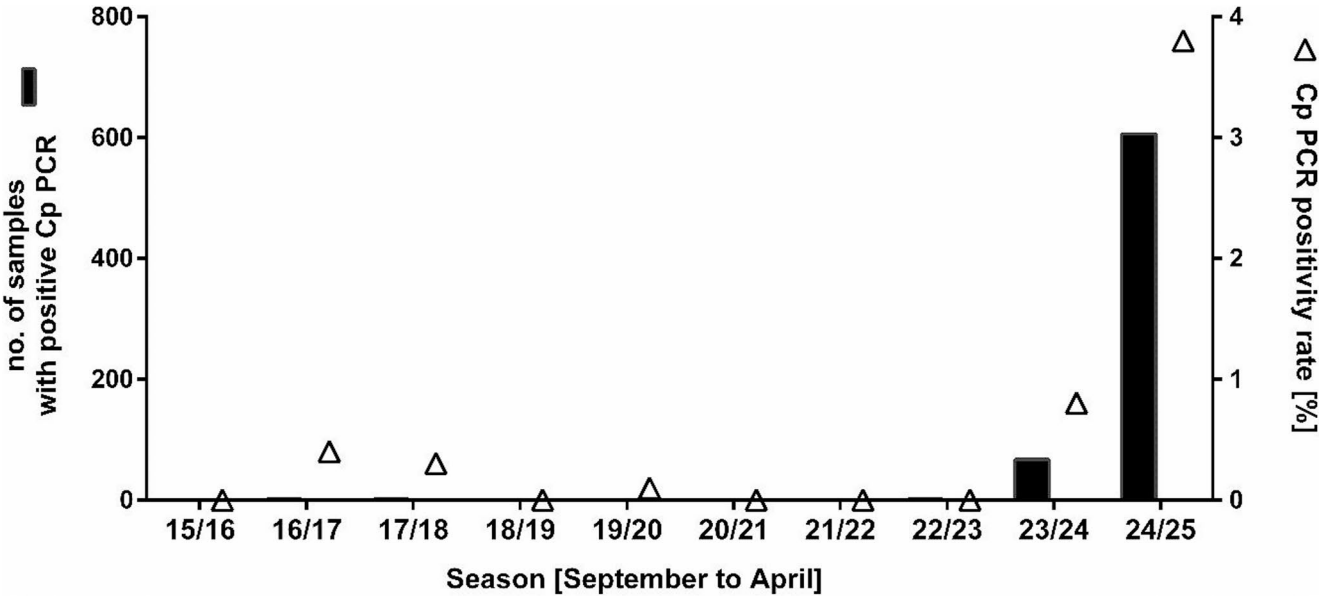

Fig. 2 Number of samples with positive Cp PCR and Cp PCR positivity rate in autumn/winter seasons (September to April) from 2015/16 to 2024/25

was detected more frequently in children, reaching highest *Cp* PCR positivity rate of 10.4% in 11-year-olds. (Fig. 3).

Based on the age distribution four age groups of patients were considered separately: Group A: 0–2 years, B: 3–17 years, C: 18–55 years, and D 56–100 years old patients. *Cp* infection rate in small infants (age group A) was surprisingly low despite high number of patients tested (5/1,894 (0.26%) samples positive). *Cp* PCR positivity rate was significantly higher in patients of group B (6.33%) compared to each of all other age groups ($p < 0.001$; Fisher's exact test with Holm-adjusted p-values [11]). Concerning age group C, *Cp* PCR positivity rate (1.84%) was significantly higher than in age groups A (0.26%, $p < 0.001$) and D (0.34%, $p < 0.001$) but lower than in age group B (6.33%, $p < 0.001$).

In order to identify possible co-factors of the surprising increase of *Cp* infections we investigated bacterial and viral co-infections in all samples investigated by multiplex respiratory PCR from 2023 to 2025 ($n = 31,541$ of the $n = 35,152$ samples). In 73.2% of *Cp* PCR positive samples co-infection with at least one other bacterial or viral species was

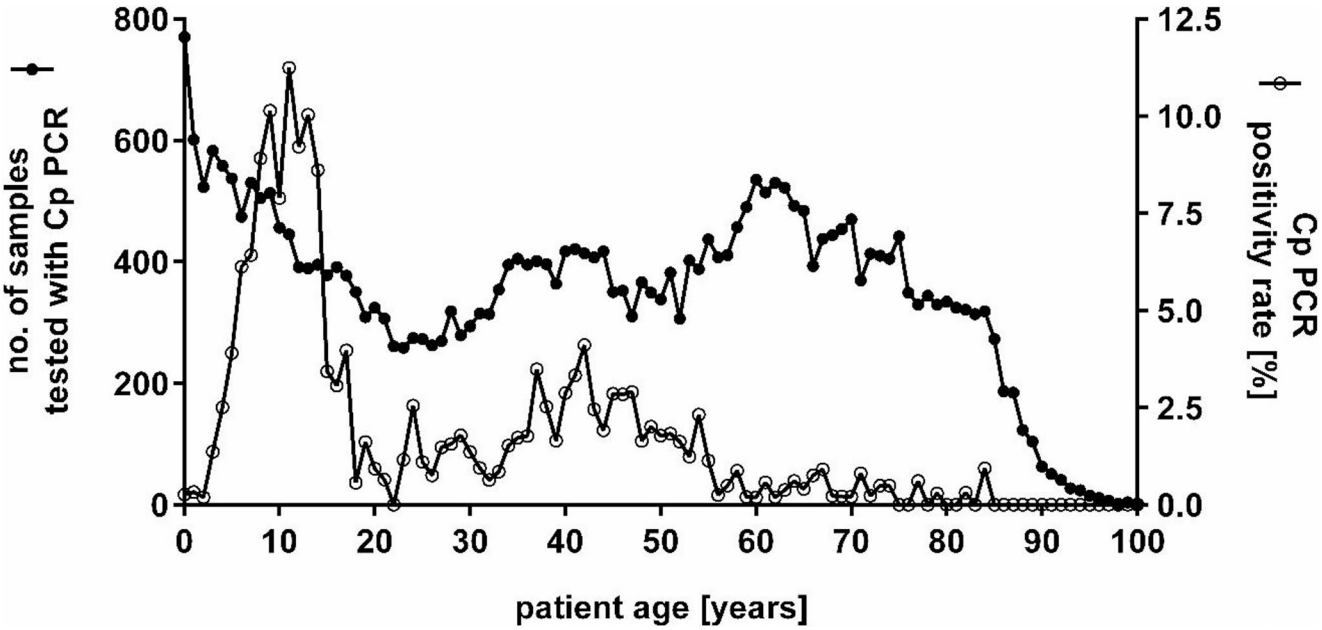

Fig. 3 Age distribution of *Cp* PCR positive patients and Cp PCR positivity rate

detected. Co-infections occurred in 34.3% of cases with one, in 27.1% with two, in 10.2% with three, and in 1.4% with four additional species.

Since the *Cp* positivity rate was influenced by age we analyzed the occurrence of coinfections in the four age groups separately. Samples with a positive PCR result for *Cp* were significantly more frequently also positive for *a*denovirus in all patients > 2 years of age (Table 1). In contrast, among patients with the highest rate of *Cp* infections (age group B) *Mycoplasma pneumoniae (Mp)* was detected significantly less frequently in *Cp* positive patients compared to *Cp* negative patients although the *Mp* infection rate was highest in this age group compared to all other age groups. In addition, PCR for influenzavirus A and B, parainfluenzavirus, and rhinovirus were significantly less frequently positive in *Cp* positive samples of patients from age group B and C compared to *Cp* PCR negative samples. Co-infections with SARS-coronavirus-2 were significantly less common exclusively in adults of age group C (Table 1).

After coronavirus pandemic a significant rise of *Cp* infections was also noted in Switzerland in autumn 2023, in Marseille, France, in 2024, and in Germany in 2024 [5, 9, 12]. However, the number of *Cp* PCR positive samples as well as the *Cp* PCR positivity rate were much higher in our study population compared to the data from Switzerland and France (405 versus 37 positive samples and 2.6% versus 0.64% positivity rate in 2024, respectively). The marked increase of *Cp* infections in 2024 observed in our laboratory confirm the data of the German Clinical Virology Network published by Boutin et al. [9]. Interestingly, the *Cp* PCR positivity rate in our region was even higher than that published by Boutin et al. indicating a pronounced circulation of *Cp* in the community in southern Germany in 2024. Interestingly, large variations between pre- and post-pandemic *Cp* detection rates (years 2018 to 2023) in European countries have been published, and even significant lower detection rates after pandemic were reported in some countries [6]. The primarily affected age group in our population corresponds to that reported from Marseille and from the German Clinical Virology Network in 2024 [9, 12]. The *Cp* infection rate increased with age in children from the age of 3 years onwards, while Edouard et al. found very low infection rates up to the age of 5 years [12].

After pandemic also re-emergence of *Mp* respiratory infections has been noted in Germany and other European countries [8, 13]. *Mp* epidemic after SARS-CoV-2 pandemic occurred with delay compared to other respiratory pathogens [8, 13].

Interestingly, the increase of *Cp* infections in our population occurred even later than the upsurge of *Mp* infections. Remarkably, although *Mp* infections were detected most frequently in children (age group B) in our study, they occurred significantly less often in *Cp* PCR positive patients compared to *Cp* negative patients. Edouard et al. also analyzed co-infections in *Cp* PCR positive patients and found co-infections in only 38% of *Cp* PCR positive patients in 2024 with highest positivity rate for rhinovirus (9/37; 24.3%) [12]. However, the study included only a small number of patients investigated by different multiplex PCR assays compared to our study. While SARS-CoV-2 was significantly less frequently detected in *Cp* PCR positive samples of age group C in our study, *Cp* infection was

Table 1 Co-infections in *Chlamydia pneumoniae* (*Cp*) PCR positive and *Cp* PCR negative samples investigated by multiplex PCR (total $n=31,541$) separated by age groups

Pathogens detected by multiplex PCR	Age group*	Samples with positive *Cp* PCR ($n=568$) *n* %		Samples with negative *Cp* PCR ($n=30,973$) *n* %		Significance of difference**
	A	2		1,722		
	B	290		5,427		
	C	234		12,361		
	D	42		11,463		
Bordetella pertussis	A	0	0	161	9.35	n.s.
	B	7	2.41	314	**5.79**	$p<0.05$
	C	2	0.85	230	1.86	n.s.
	D	1	2.38	94	0.82	n.s.
Bordetella parapertussis	A	0	0	9	0.52	n.s.
	B	0	0	12	0.22	n.s.
	C	0	0	5	0.04	n.s.
	D	0	0	1	0.01	n.s.
Legionella pneumophila	A	0	0	0	0	n.s.
	B	0	0	1	0.02	n.s.
	C	0	0	4	0.03	n.s.
	D	0	0	11	0.10	n.s.
Haemophilus influenzae	A	1	50.00	906	52.61	n.s.
	B	191	65.86	3,275	60.35	n.s.
	C	77	32.91	4,417	35.73	n.s.
	D	13	30.95	2,447	21.35	n.s.
Mycoplasma pneumoniae	A	0	0	141	8.19	n.s.
	B	37	12.76	1,224	**22.55**	$p<0.001$
	C	11	4.70	887	7.18	n.s.
	D	0	0	279	2.43	n.s.
Streptococcus pneumoniae	A	2	100	1,126	65.39	n.s.
	B	170	58.62	2,924	53.88	n.s.
	C	77	32.91	3,451	27.92	n.s.
	D	12	28.57	2,436	21.25	n.s.
Adenovirus	A	1	50.00	180	10.45	n.s.
	B	31	**10.69**	319	5.88	$p<0.01$
	C	12	**5.13**	233	1.88	$p<0.01$
	D	2	**4.76**	65	0.57	$p<0.05$
Human metapneumovirus	A	0	0	124	7.20	n.s.
	B	3	1.03	227	4.18	$P<0.01$
	C	2	0.85	338	2.73	n.s.
	D	1	2.38	370	3.23	n.s.
Influenzavirus A	A	0	0	91	5.28	n.s.
	B	3	1.03	318	**5.86**	$p<0.001$
	C	3	1.28	879	**7.11**	$p<0.001$
	D	1	2.38	690	6.02	n.s.
Influenzavirus B	A	0	0	47	2.73	n.s.
	B	16	5.52	527	**9.71**	$p<0.05$
	C	4	1.71	748	**6.05**	$p<0.01$
	D	1	2.38	55	0.48	n.s.
Parainfluenzavirus	A	0	0	126	7.32	n.s.
	B	3	1.03	190	**3.50**	$p<0.05$
	C	0	0	218	**1.76**	$p<0.05$
	D	0	0	304	2.65	n.s.
Respiratory syncytial virus	A	0	0	182	10.57	n.s.
	B	7	2.41	184	3.39	n.s.
	C	1	0.43	217	1.76	n.s.
	D	0	0	319	2.78	n.s.

Table 1 (continued)

Pathogens detected by multiplex PCR	Age group*	Samples with positive *Cp* PCR (n=568) n %		Samples with negative *Cp* PCR (n=30,973) n %		Significance of difference**
Rhinovirus	A	0	0	357	20.73	n.s.
	B	12	4.14	658	**12.12**	$p<0.001$
	C	6	2.56	1,036	**8.38**	$p<0.001$
	D	0	0	770	6.72	n.s.
SARS-Coronavirus-2	A	1	50.0	58	3.37	n.s.
	B	1	0.34	77	1.42	n.s.
	C	1	0.43	620	**5.02**	$p<0.001$
	D	1	2.38	702	6.12	n.s.

Age group A: 0–2 years, B: 3–17 years, C: 18–55 years, D: 56–100 years old; Significance of differences in relative frequencies between Cp PCR positive and negative samples was evaluated using Fisher's exact test (n.s. = not significant for p>=0.05)

reported in SARS-CoV-2-infected patients with varying frequency in a recent review [14].

The reasons for the unexpected increase of *Cp* infections are still unknown. Waning adaptive immunity to *Cp* due to non-pharmaceutical interventions against COVID-19 may be an important reason. However, considering the almost complete absence of detection of *Cp* before the pandemic, the significant wave of infections after the pandemic is particularly remarkable. Local outbreaks with increased circulation of *Cp* in kindergartens, schools, and families could be another explanation [15, 16]. We observed infection clusters in some families affecting two or three household members (data not shown) but further studies are necessary to investigate clonality of isolates as well as dynamics of *Cp* transmission. Co-infections with other bacteria and/or viruses may also play a role by enhancing or reducing the susceptibility for *Cp* infection in exposed patients. Higher detection rate of adenovirus but lower of several other respiratory viruses as well as *Mp* in *Cp* positive patients is remarkable and warrants further investigation. Furthermore, it should be clarified whether circulating *Cp* isolates exhibit genetic characteristics which may, for example, be responsible for a higher transmission rate and/or increased pathogenicity. Next-generation sequencing (NGS) of (nearly) full-length genomes of four *Cp* isolates from French patients out of the 2024 outbreak revealed serotype ST16 in all four patients [12]. Although data about genetic characterization of circulation *Cp* strains are scarce ST16 has also previously been found [12]. Genetic studies including NGS of whole genomes of *Cp* isolates from our region are currently underway.

Another wave of *Cp* infections in winter 2025/2026 cannot be ruled out since we observed a recent increase of cases in October/November this year. In contrast, the positivity rate of *Mp* PCR did not change yet (data not shown). Increased vigilance along with appropriate diagnostics in patients with respiratory tract infections is warranted. Targeted detection of *Cp* infections allows adequate antimicrobial therapy with substances effective against intracellular bacteria, like macrolides. Increased surveillance of *Cp* infections may also contribute to our understanding of epidemiology and transmission dynamics of this actually emerging pathogen.

Author contributions N.W. designed and supervised the data analysis and wrote the main manuscript text; S.D., L.W.,and M.V. analyzed the data and prepared figures and tables; R.F. were responsible for PCR analysis and data validation; D.P. analyzed the data and performed statistical tests. All authors reviewed the manuscript.

Data availability No datasets were generated or analysed during the current study.

Declarations

Competing interests The authors declare no competing interests.

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