Research Square

Preprints are preliminary reports that have not undergone peer review.
They should not be considered conclusive, used to inform clinical practice,
or referenced by the media as validated information.

Biomarker-based patterns related to respiratory diseases and the risk of multimorbidity: A real-world study based on a regional information sharing platform from Northwest China

Xuanchen Yan
School of Basic Medical Sciences, Lanzhou University
Zijun Wang
The First Hospital of Lanzhou University
Fei Yang
Gansu Provincial Health Commission
Yuefeng Li
Gansu Provincial Health Statistics and Information Center
Yaolong Chen
chevidence@lzu.edu.cn

School of Basic Medical Sciences, Lanzhou University
Jie Lu
Gansu Provincial Health Statistics and Information Center

Research Article

Keywords: Multimorbidity, Respiratory diseases, Real-world data, Health information exchange, Biomarkers

Posted Date: November 25th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-11302467/v1

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
Read Full License

Additional Declarations: No competing interests reported.

Abstract

Objective

To identify respiratory disease-related biomarker co-occurrence patterns using real-world data from a regional health information-sharing platform in Gansu Province, China, and assess their potential value for population-level multimorbidity surveillance.

Methods

We analyzed data from the Gansu Provincial Examination and Laboratory Results Sharing Platform between January 2024 and December 2025. Thirty-one respiratory disease-related indicators were included. Abnormality rates were summarized descriptively, and co-occurrence associations between indicators measured within the same clinical encounter were quantified using lift and Jaccard coefficients derived from association rule mining.

Results

The platform recorded 59.61 million shared examination and laboratory encounters during the study period. Five major patterns were identified: (1) respiratory dysfunction–inflammation, characterized by high abnormality rates for PO_2 (71.3%), PCO_2 (52.2%), hs-CRP (43.9%), and CRP (35.4%); (2) viral infection spectrum, with influenza A having the highest testing volume and rhinovirus the highest positivity rate; (3) cardiopulmonary injury, with abnormal PO_2 and elevated cardiac troponin T showing positive co-occurrence (lift = 1.80); (4) antimicrobial resistance-associated inflammation, characterized by co-occurrence of bacterial culture abnormalities and elevated inflammatory markers; and (5) respiratory–immune–metabolic networks involving respiratory, cardiovascular, and metabolic conditions.

Conclusions

Regional health information-sharing platforms may provide valuable real-world data for population-level multimorbidity surveillance. The identified patterns suggest interconnected respiratory dysfunction, inflammation, infection, cardiopulmonary injury, and metabolic abnormalities, supporting more integrated approaches to respiratory multimorbidity surveillance and management.

Introduction

Respiratory diseases represent a major global public health challenge and are frequently accompanied by multimorbidity which substantially increases disease burden, healthcare utilization, and management complexity.[1–3] Multimorbidity (the co-occurrence of at least two chronic conditions in the same individual)[4] is particularly common among older adults, with approximately two-thirds of individuals aged 65 years or older in high-income countries having at least two chronic conditions.[5] In China, the

prevalence of multimorbidity has also increased rapidly in recent years, with substantial coexistence of particularly diabetes, hypertension, dyslipidaemia, and respiratory disorders being observed.[6]

Gansu Province, located in Northwest China, is characterized by unique geographic and environmental features, including high-altitude areas, arid climate conditions, and seasonal dust exposure, together with an ageing population.[1,7,8] These factors may contribute to distinctive respiratory disease profiles and multimorbidity patterns. However, most existing multimorbidity studies are based on hospital records, questionnaire surveys, or disease registries, which often lack continuous cross-institutional data and objective biomarker information at the population level.

In recent years, Gansu Province has established a regional examination and laboratory results sharing platform covering laboratory testing, radiological imaging, and ultrasound examinations across multiple healthcare institutions. This study aimed to use data from the Gansu Provincial Examination and Laboratory Results Sharing Platform to: (1) describe the operational characteristics of the regional examination and laboratory results sharing system; (2) identify and quantify major respiratory disease-related biomarker co-occurrence patterns as population-level signals of possible multimorbidity; and (3) compare the real-world findings with existing literature to assess the complementary value of regional health information exchange data and to provide evidence for improving the surveillance, early warning, and management of respiratory multimorbidity.

Methods

Data source

This study used data from the Gansu Provincial Examination and Laboratory Results Sharing Platform between January 2024 and December 2025. The platform is a province-wide initiative led by the provincial health authority, covering laboratory testing, radiological imaging, and ultrasound examinations across multiple institutions. At the time of this study, the platform covered all secondary and tertiary hospitals, as well as hospitals directly administered by the provincial health authority and a proportion of private healthcare providers, across all 14 prefecture-level cities and prefectures of Gansu Province. In total, the platform was connected to 2,330 healthcare institutions of different levels. Primary Care Cloud HIS, the official health information system used by primary healthcare institutions throughout Gansu Province, is fully integrated with the provincial examination and laboratory results sharing platform, enabling complete data exchange from participating primary care facilities. Healthcare institutions are required by mandatory provincial policy to recognize and reuse existing laboratory and examination test results from the provincial catalogue of items whenever appropriate, rather than routinely repeating examinations.

The platform currently supports approximately 300 interoperable examination and laboratory items and provides large-scale structured real-world healthcare data. As of July 2026, the platform had supported

the mutual recognition and reuse of examination and laboratory results for 1,933,328 individuals, with an average of approximately 966,664 individuals benefiting from the program each year.

Selection of respiratory disease-related indicators

We selected 31 from the approximately 300 interoprable examination and laboratory items collected by the platform, comprising radiological imaging items, ultrasound examinations, and laboratory testing indicators (Supplement File 1). The included laboratory indicators covered blood gas parameters, inflammatory biomarkers, cardiac injury biomarkers, microbiological examinations, and respiratory pathogen nucleic acid testing. Specifically, blood gas analysis included partial pressure of oxygen (PO_2), partial pressure of carbon dioxide (PCO_2), and pH values. Inflammatory biomarkers included C-reactive protein (CRP) and high-sensitivity C-reactive protein (hs-CRP). Cardiac injury biomarkers included cardiac troponin T (cTnT) and cardiac troponin I (cTnI). Additional indicators included bacterial culture, antimicrobial susceptibility testing, and nucleic acid detection for multiple respiratory pathogens (Supplement File 1).

Statistical analysis

Descriptive statistics were used to summarize testing frequencies, result distributions, and temporal trends. Abnormality rates were calculated as the proportion of abnormal results among all tests performed, and the corresponding 95% confidence intervals (95% CIs) were estimated using the Wilson score method.

Association rule mining, a data-mining and machine-learning technique, was used to explore co-occurrence associations between abnormal laboratory findings. For pairs of indicators measured within the same clinical encounter, four measures were calculated: support, defined as the frequency with which two abnormalities co-occurred; confidence, defined as the conditional probability of one abnormality occurring given the presence of the other; lift, defined as the ratio of the observed frequency of co-occurrence to that expected if the two abnormalities occurred independently; and the Jaccard coefficient, defined as the proportion of the intersection of two abnormalities relative to their union. A lift value > 1 was considered indicative of a positive co-occurrence association, with larger values representing stronger associations, whereas the Jaccard coefficient was used to characterize the extent of overlap between two abnormalities.

Biomarker co-occurrence patterns were identified using an exploratory, data-driven process rather than a predefined classification or clustering algorithm. First, abnormality rates were calculated for all 31 respiratory disease-related indicators to characterize the overall distribution of abnormal findings. Second, pairwise co-occurrence associations were examined among indicators measured within the same clinical encounter. Indicator pairs with a lift value > 1 were considered to show positive co-occurrence, while their Jaccard coefficients were used to characterize the extent of shared abnormal occurrences. Third, the overall structure of these pairwise associations was examined together with the

abnormality rates of individual indicators. Indicators showing recurrent positive co-occurrence with other indicators and relatively frequent abnormalities were grouped into candidate patterns. No additional fixed cut-off values for the Jaccard coefficient or abnormality rate were specified for pattern formation, because the analysis was intended to explore the structure of co-occurring abnormalities rather than to assign indicators to statistically predefined clusters. Finally, candidate patterns were interpreted and refined according to their clinical relevance and pathophysiological plausibility.

No biomarker co-occurrence patterns or pattern labels were specified before the analysis. Pattern labels were assigned only after completion of the quantitative co-occurrence analysis and subsequent clinical interpretation. Accordingly, the resulting patterns should be interpreted as exploratory population-level patterns of co-occurring biomarker abnormalities rather than clinically diagnosed multimorbidity entities.

Ethical considerations

This study was based on retrospective analysis of de-identified administrative and laboratory data obtained from the Gansu Provincial Examination and Laboratory Results Sharing Platform. No personally identifiable information, including names, identification numbers, or contact information, was accessible to the investigators.

Results

Operational characteristics of the regional sharing platform

Between January 2024 and December 2025, the regional platform recorded a total of 59.61 million shared examination and laboratory encounters, corresponding to an average of approximately 81,500 encounters per day. Laboratory testing accounted for the vast majority of encounters (58.74 million, 98.6%), followed by ultrasound examinations (0.45 million, 0.8%) and radiological imaging examinations (0.41 million, 0.7%). The monthly volume of shared examinations increased steadily during the study period, rising from 0.70 million encounters in January 2024 to 4.34 million encounters in December 2025. This trend suggested increasing utilization and integration of the regional information-sharing system across healthcare institutions.

Radiological imaging activities related to respiratory diseases demonstrated notable temporal variation. Chest computed tomography and chest digital radiography were the most frequently shared imaging examinations. Imaging volumes generally increased during late autumn and winter periods, although this pattern was not observed at the end of 2025. According to verification with the platform management team, the decline in radiological imaging volume during the second half of 2025 was mainly attributable to adjustments in the scope of data aggregation and the platform's data submission mechanisms, rather than a true decline in respiratory disease activity.

Laboratory testing activity also showed progressive growth over time, with higher testing volumes observed during the second half of 2025 (Fig. 1).

Characteristics of respiratory disease-related laboratory indicators

Blood gas analysis indicators

A total of 20,236 PO_2 tests were performed, among which 10,401 were below and 4,020 above the reference range, yielding an overall abnormality rate of 71.3%. For PCO_2, 19,154 tests were performed, including 8,716 below-range and 1,279 above-range results, corresponding to an abnormality rate of 52.2%. A total of 29,881 pH measurements were available, with an abnormality rate of 23.2%. Overall, abnormal blood gas, particularly reduced PO_2 levels, were common. (Table 1)

Inflammatory biomarkers

A total of 76,287 hs-CRP tests were performed, among which 33,524 showed elevated levels, corresponding to an abnormality rate of 43.9%. For CRP, 192,830 tests were available, with 68,309 elevated results and an abnormality rate of 35.4%. (Table 1)

Cardiac injury biomarkers and microbiological examinations

For cTnT, 1,445 tests were available, among which 437 had elevated values, yielding an abnormality rate of 30.4%. For cTnI, 32,812 tests were performed, with 4,429 elevated results and an abnormality rate of 13.5%. Microbiological examinations demonstrated a bacterial culture abnormality rate of 12.6%, while antimicrobial susceptibility testing showed an abnormality rate of 6.8%. (Table 1)

Respiratory pathogen nucleic acid testing

Respiratory pathogen testing included rhinovirus, influenza A virus, Mycobacterium tuberculosis DNA, respiratory syncytial virus (RSV), adenovirus, Mycoplasma pneumoniae, and influenza B virus. Respiratory pathogen nucleic acid testing showed that influenza A virus had the highest testing volume (15,907 tests), with an abnormality rate of 4.0%, demonstrating a marked seasonal circulation pattern. Rhinovirus was tested in 12,007 cases and showed the highest abnormality rate (4.1%), consistent with its role as a common pathogen causing upper respiratory tract infections. Respiratory syncytial virus (RSV) was tested in 12,992 cases, with an abnormality rate of 2.7%, and is commonly associated with respiratory infections in vulnerable populations, particularly young children and older adults. In contrast, influenza B virus (14,835 tests) and Mycoplasma pneumoniae (11,785 tests) showed relatively low abnormality rates (both < 0.01%), suggesting comparatively limited circulation in the tested population during the study period (Table 1).

Table 1
Frequency and abnormality rates of respiratory disease-related laboratory indicators

Indicator	Total tests (n)	Below reference range (n)	Above reference range (n)	Abnormality rate, % (95%CI)
Partial pressure of oxygen (PO_2)	20,236	10,401	4,020	71.26 (70.64–71.88)
Partial pressure of carbon dioxide (PCO_2)	19,154	8,716	1,279	52.18 (51.47–52.89)
High-sensitivity C-reactive protein (hs-CRP)	76,287	1	33,524	43.95 (43.59–44.30)
C-reactive protein (CRP)	192,830	5	68,309	35.43 (35.21–35.64)
Cardiac troponin T (cTnT)	1,445	2	437	30.38 (28.06–32.80)
pH	29,881	1,152	5,771	23.17 (22.69–23.65)
Cardiac troponin I (cTnI)	32,812	58	4,429	13.67 (13.31–14.05)
Bacterial culture and identification	69,725	6,073	2,716	12.61 (12.36–12.85)
Antimicrobial susceptibility testing	3,239	32	189	6.82 (6.00–7.74)
Rhinovirus nucleic acid test	12,007	0	487	4.06 (3.72–4.42)
Influenza A virus nucleic acid test	15,907	0	634	3.99 (3.69–4.30)
Mycobacterium tuberculosis DNA (TBDNA)	1,406	0	42	2.99 (2.22–4.01)
Respiratory syncytial virus nucleic acid test	12,992	40	308	2.68 (2.41–2.97)
Adenovirus nucleic acid test	11,306	0	68	0.60 (0.47–0.76)
Mycoplasma pneumoniae nucleic acid test	11,785	0	10	0.08 (0.05–0.16)

Note: the confidence interval (CI) was calculated using the Wilson score method. Due to the large sample size, the obtained CI is relatively narrow and only reflects random sampling variation, rather than systematic bias.

Indicator	Total tests (n)	Below reference range (n)	Above reference range (n)	Abnormality rate, % (95%CI)
Influenza B virus nucleic acid test	14,835	0	4	0.03 (0.01–0.07)

Note: the confidence interval (CI) was calculated using the Wilson score method. Due to the large sample size, the obtained CI is relatively narrow and only reflects random sampling variation, rather than systematic bias.

Respiratory multimorbidity patterns based on the shared examination and laboratory data

Respiratory dysfunction–inflammation pattern

The respiratory dysfunction–inflammation pattern was the most prominent pattern identified among the indicators included in the analysis, characterized by high abnormality rates and strong co-occurrence associations. Among the 16 indicators included in the statistical analysis, PO_2 and PCO_2 had the highest abnormality rates, at 71.26% and 52.18%, respectively, followed by hs-CRP at 43.95%. Abnormal PO_2 and PCO_2 also showed one of the strongest co-occurrence patterns among all indicator pairs, with a Jaccard coefficient of 0.6109 and a lift value of 1.30. Abnormal PCO_2 and pH showed the highest lift value among all indicator pairs (2.20). Abnormalities in these respiratory function indicators also co-occurred with elevated inflammatory biomarkers, including CRP and hs-CRP. Overall, this pattern was characterized by the co-occurrence of respiratory dysfunction, acid–base imbalance, and systemic inflammatory abnormalities in respiratory disease-related clinical settings.

Viral infection spectrum pattern

Distinct respiratory pathogens demonstrated different testing frequencies and positivity profiles. Based on the findings, two potential co-occurrence scenarios were observed: seasonal clustering of influenza-related and RSV-related respiratory infections; and possible coexistence between viral upper respiratory infections and bacterial respiratory infections.

Cardiopulmonary injury pattern

The cardiopulmonary injury pattern was characterized by the coexistence of respiratory dysfunction and elevated cardiac injury biomarkers. Abnormal PO_2 results and elevated cTnT levels demonstrated a lift value of 1.80, indicating positive co-occurrence associations between hypoxia-related abnormalities and cardiac injury markers. In addition, elevated hs-CRP levels and abnormal cTnT results demonstrated moderate co-occurrence associations, suggesting potential overlap between systemic inflammation and cardiopulmonary injury processes. These findings highlight the potential importance of integrated cardiopulmonary assessment in patients with respiratory disease-related abnormalities.

Antimicrobial resistance-associated chronic inflammatory pattern

Another identified pattern was characterized by the coexistence of abnormal bacterial culture findings and elevated inflammatory biomarkers. Microbiological testing showed a bacterial culture abnormality rate of 12.6% and an antimicrobial susceptibility testing abnormality rate of 6.8%, suggesting that bacterial colonization and antimicrobial resistance may represent important concerns in patients undergoing respiratory infection-related investigations. Co-occurrence analysis further demonstrated positive associations between bacterial culture abnormalities and elevated inflammatory biomarkers, with lift values of 2.00 for CRP and 1.80 for hs-CRP, indicating a strong co-occurrence between bacterial infection-related findings and inflammatory responses. Notably, the number of antimicrobial susceptibility tests performed (3,239) was substantially lower than the number of bacterial culture tests (69,725), suggesting potential gaps in antimicrobial resistance surveillance. Optimizing testing strategies may therefore improve the coverage of antimicrobial resistance monitoring in routine clinical practice.

Discussion

Co-occurrence of respiratory dysfunction and inflammation

This study identified high abnormality rates in blood gas analysis indicators among the tested individuals in Gansu Province, with 71.3% of PO_2 and 52.2% of PCO_2 values being outside of the reference range. These findings are generally consistent with previous studies reporting a high burden of chronic respiratory diseases and COPD-related risk factors in Northwest China.[9,16] Earlier epidemiological studies in Gansu Province have shown high proportions of adults aged ≥ 40 years to be at elevated risk of COPD.[16] In addition, COPD–asthma overlap syndromes have been associated with accelerated pulmonary function decline and increased exacerbation risk.[10]

Inflammatory biomarker analysis further demonstrated relatively high abnormality rates for hs-CRP (43.9%) and CRP (35.4%). Previous studies have suggested that systemic inflammatory responses play an important role in COPD progression and respiratory disease exacerbations.[13] The present study, with its large real-world biomarker data describing the distribution of inflammatory abnormalities in routine clinical practice, gives further support for this claim. Taken together, the coexistence of abnormal blood gas parameters and elevated inflammatory biomarkers may reflect combined respiratory dysfunction and inflammatory responses in patients undergoing respiratory disease-related examinations.

Clinical implications of cardiopulmonary multimorbidity

Elevated cardiac injury biomarkers were frequently observed, with abnormality rates of 30.4% for cTnT and 13.5% for cTnI. The difference in abnormality rates between the two biomarkers may reflect differences in clinical testing practices and diagnostic applications.

It should be noted however that abnormal biomarker results do not directly correspond to confirmed clinical disease prevalence. Elevated cardiac troponin levels may result from multiple clinical conditions, including infection, physiological stress, and renal dysfunction. Therefore, the observed abnormality rates should be interpreted cautiously.

Co-occurrence analysis demonstrated a positive association between abnormal PO_2 and elevated cTnT levels (lift = 1.80). Elevated hs-CRP and abnormal cTnT also showed positive co-occurrence associations. These findings suggest potential overlap between respiratory dysfunction, systemic inflammation, and cardiac injury-related abnormalities.

Previous studies have reported substantial cardiovascular comorbidity burden among patients with COPD, which was also observed by our study.[11] Cardiovascular abnormalities, including pulmonary hypertension and cardiac dysfunction, are increasingly recognized as important contributors to adverse outcomes in chronic respiratory diseases.[11,12] The present study extends these observations by demonstrating cardiopulmonary co-occurrence patterns using regional real-world laboratory data.

Infection- and inflammation-related patterns

Respiratory pathogen nucleic acid testing demonstrated substantial variation in positivity rates across pathogens. Influenza A virus showed the highest testing volume, whereas rhinovirus demonstrated the highest positivity rate. RSV also accounted for a considerable proportion of positive respiratory pathogen findings.

Based on these pathogen distribution patterns, two potential biomarker co-occurrence patterns were inferred. The first was an influenza–RSV pattern, in which the seasonal circulation of influenza A and the broad age distribution of RSV may contribute to periods of concurrent respiratory viral activity, particularly during the winter season, potentially increasing the burden of respiratory diseases such as COPD and asthma. The second was a rhinovirus–bacterial infection pattern. Rhinovirus demonstrated the highest abnormality rate among all tested respiratory viruses but is generally associated with relatively mild upper respiratory tract infections. Together with the large number of bacterial culture tests performed (69,725 tests) and a bacterial culture abnormality rate of 12.6%, these findings suggest that bacterial respiratory infections may coexist with, or occur following, viral upper respiratory tract infections. It should be emphasized that these patterns were inferred from the co-occurrence of laboratory findings and do not establish causal relationships.

Previous regional studies have reported increasing respiratory disease burden and seasonal variation in respiratory healthcare utilization in Gansu Province.[14] In addition, environmental and climatic factors have been suggested to influence respiratory disease exacerbations and respiratory infection-related healthcare demands.[14,17]

Microbiological testing demonstrated bacterial culture abnormality rates of 12.6%, while antimicrobial susceptibility testing showed an abnormality rate of 6.8%. Co-occurrence analysis indicated positive

associations between bacterial culture abnormalities and elevated inflammatory biomarkers, including CRP and hs-CRP.

The comparatively low volume of antimicrobial susceptibility testing relative to bacterial culture testing may suggest potential limitations in routine antimicrobial resistance surveillance.

Strengths and limitations

This study has several strengths. First, it used large-scale real-world data derived from a regional health information-sharing platform covering multiple healthcare institutions across Gansu Province. Second, the study incorporated structured laboratory and examination indicators, enabling multimorbidity pattern analysis based on objective biomarker-related data rather than self-reported information alone.

Several limitations should also be acknowledged. First, the pathogen spectrum captured by the platform was incomplete, and fungal pathogen-related information was not available. Second, the volume of antimicrobial susceptibility testing was substantially lower than that of bacterial culture testing, potentially limiting analyses of antimicrobial resistance-related patterns. Third, psychological and psychiatric comorbidity-related information was unavailable in the current dataset, although previous studies have suggested potential interactions between chronic respiratory diseases and depression-related conditions.[8] Fourth, changes in platform operations may have affected the observed temporal trends in examination volumes. In particular, according to verification with the platform management team, the decline in shared radiological imaging volume during the second half of 2025 was mainly attributable to adjustments in the scope of data aggregation and data submission mechanisms. Therefore, temporal and seasonal trends in imaging volumes should be interpreted with caution, as changes in platform activity may not necessarily reflect corresponding changes in respiratory disease activity. Fifth, the study was based on cross-sectional co-occurrence analyses, which identify statistical associations rather than causal relationships. Future studies using longitudinal follow-up data may help clarify temporal relationships and dynamic multimorbidity trajectories.

Implications for future surveillance and management

The findings of this study suggest several potential directions for respiratory multimorbidity surveillance and integrated management in Gansu Province. First, respiratory diseases may coexist with broader immune, metabolic, and cardiovascular abnormalities, forming interconnected multimorbidity networks rather than isolated disease entities (Fig. 2) [18–22]. Therefore, it is important to integrated cardiopulmonary assessment into respiratory disease-related clinical management, particularly in regions characterized by high-altitude and hypoxic environmental conditions and for patients with abnormal respiratory function indicators. Second, optimization of microbiological testing and antimicrobial susceptibility testing strategies may improve regional antimicrobial resistance surveillance capacity. Third, future studies integrating environmental, climatic, and longitudinal healthcare data may further improve understanding of respiratory multimorbidity patterns in Northwest China.

Conclusions

Using real-world data from the Gansu Provincial Examination and Laboratory Results Sharing Platform, this study identified several major respiratory disease-related multimorbidity patterns based on laboratory and examination indicators. Respiratory dysfunction and inflammatory abnormalities represented the most prominent co-occurrence pattern. Cardiopulmonary injury-related abnormalities and infection-related inflammatory patterns were also commonly observed. In addition, respiratory diseases appeared to coexist with broader metabolic and cardiovascular conditions, forming interconnected multimorbidity networks.

These findings show that regional health information-sharing platforms may provide valuable data resources for population-level multimorbidity surveillance and integrated respiratory disease management. Further longitudinal and patient-level studies are needed to better understand the temporal evolution and clinical implications of respiratory multimorbidity patterns.

Declarations

Acknowledgements

We thank Janne Estill for careful revision and language editing of the manuscript.

Ethical considerations

This study was reviewed and approved by the Ethics Committee of the Institute of Health Data Science, Lanzhou University (approval number: HDS-202610-01). This retrospective study was conducted using de-identified administrative and laboratory data extracted from the Gansu Provincial Examination and Laboratory Results Sharing Platform. No personally identifiable information, including names, identification numbers, or contact details, was accessible to the research team. The requirement for written informed consent was therefore waived by the ethics committee.

Consent to participate

Not applicable.

Consent for publication

Not applicable.

Declaration of conflicting interest

The author(s) declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

Funding statement

National Key Science and Technology Program 2026 Project for Prevention and Control of Emerging, Re-emerging and Major Infectious Diseases — Research on Construction of Scientific Database and Sharing Platform for Infectious Disease Prevention and Control Theme (Project No.: 2026ZD01911504)

Data Availability

The data used in this study were obtained from the Gansu Provincial Examination and Laboratory Results Sharing Platform. In accordance with national health data security regulations and the platform's data access agreement, the raw individual-level data are not publicly available to protect personal health privacy. Researchers may apply for authorized data access via the platform's official application channel. The analytical code used in this study is available from the corresponding author upon reasonable request.

Author Contribution

X.Y. and Z.W. contributed equally to the study design, conception, methodology and interpretation of the results. F.Y. and Y.L. contributed to data curation, data validation, and statistical analysis. Y.C. and J.L. supervised the study and coordinated the project. X.Y. drafted the manuscript. All authors reviewed and approved the manuscript.

References

1. López-Campos LJ, Soler-Cataluña JJ, Miravitlles M. Global Strategy for the Diagnosis, Management, and Prevention of Chronic Obstructive Lung Disease 2019 Report: Future Challenges. Arch Bronconeumol. 2020;56(2):65–67.
2. Ansiaux L, Bonhomme O, Heinen V, et al. The GOLD (Global Initiative for Chronic Obstructive Lung Disease) 2023: a substantial revision. Rev Med Liege. 2024;79(4):235–240.
3. Cheng Z, Zhang R, Xu H, et al. Systematic Cluster Analysis of Comorbidity Patterns in Patients with Chronic Obstructive Pulmonary Disease and the Impact on Hospitalization Costs. Chinese General Practice. 2025;28(17):2127–2133.
4. World Health Organization. Technical Series on Safer Primary Care: Multimorbidity. Geneva, Switzerland: World Health Organization; 2016. Available from: https://www.who.int/publications/i/item/9789241511650
5. Schoenbeck K, Clements J, Demairo K, et al. The humanistic burden of patients with chronic myeloid leukemia treated with first-line tyrosine kinase inhibitors. Blood. 2025;146(Suppl 1):6388–6388. doi:10.1182/BLOOD-2025-6388.
6. Guan F, He Y, Su C, et al. Distribution and epidemic trends of chronic multimorbidity among adult residents in 10 provinces(autonomous regions)of China in 2009-2023. Journal of Hygiene Research. 2024;53(6):887–892.

7. Yang T, An X, Hong Z, et al. The prevalence of comorbidity of diabetes, hypertension and hyperlipidemia among Chinese residents: a Meta-analysis. Journal of Mathematical Medicine. 2025;38(8):611–619.
8. Sun L, Qin X, Liu X. Research progress on bidirectional regulatory mechanism and Chinese and Western medicine treatment of depression in pulmonary diseases. Chinese Traditional and Herbal Drugs. 2025;56(24):9172–9184.
9. Li W, Yang T, Wang C. Current status and progress of prevention and treatment of chronic obstructive pulmonary disease in China. Chinese Research Hospitals. 2020;7(5):1–5.
10. Celli BR, Fabbri LM, Aaron SD, et al. An updated definition and severity classification of COPD exacerbations: the Rome proposal. Am J Respir Crit Care Med. 2021;204(11).
11. Beshiri D, Muji J, Kacari N, et al. Cardiovascular comorbidity in patients with chronic obstructive pulmonary disease: echocardiography changes and their relation to the level of airflow limitation. Open Access Maced J Med Sci. 2019;7(21):3568–3573.
12. Suri AR. Comorbid cognitive impairment in chronic obstructive pulmonary disease (COPD): current understanding, risk factors, implications for clinical practice, and suggested interventions. Medicina (Kaunas). 2023;59(4).
13. Fang Y, Hu D, Li Q, et al. Influence mechanism of serum free immunoglobulin light chain on pulmonary inflammatory response and serum inflammatory factor levels in patients with chronic obstructive pulmonary disease. J Med Biochem. 2024;43(6):908–914.
14. Wang Y, Yan X, Lu J, Chen Y. Epidemiological characteristics of asthma in Gansu, 2018 - 2024. Disease Surveillance. 2025; 40(10): 1297-1302.
15. Gao Y, Zheng JP, Liang JL, et al. Overview of standardized training programs for clinical application and quality control of pulmonary function testing in China. Chinese Journal of Practical Internal Medicine. 2019;39(8):746–750.
16. Huang LX, Chen LJ, He HP, et al. High-risk factors and distribution characteristics of high-risk populations for chronic obstructive pulmonary disease among individuals aged ≥40 years in Gansu Province. Chinese Journal of Chronic Disease Prevention and Control. 2023.
17. Liu Y, Liao L. Predictive study of exercise-induced hypoxemia during the six-minute walk test in patients with chronic respiratory diseases. Journal of Clinical Pulmonary Medicine. 2025;30(8):1218–1222.
18. Kononova N, Einvik G, Holmedahl NH, Hagve TA, Omland T, Søyseth V. It is unlikely that oxygen supplementation in COPD patients with chronic respiratory failure reduce cardiac troponin level. BMC Pulm Med. 2022;22(1):392.
19. Ragnoli B, Chiazza F, Tarsi G, Malerba M. Biological pathways and mechanisms linking COPD and cardiovascular disease. Ther Adv Chronic Dis. 2025;16:20406223251314286.
20. Majumder D, Manjunath M, Jayprakash S, et al. A Study of Cardiac Troponin T Levels in Acute Exacerbation of COPD and its Correlation with Severity. Journal of the Association of Physicians of India 70(4):11-12

21. Hilderink BN, Crane RF, van den Bogaard B, Pillay J, Juffermans NP. Hyperoxemia and hypoxemia impair cellular oxygenation: a study in healthy volunteers. Intensive Care Med Exp. 2024;12(1):37.
22. Ricco GMG, Radovanovic D, Pecchiari M, et al. Prevalence, Clinical and Functional Determinants of Chronic Hypoxemia and Respiratory Failure in Patients with Stable COPD. J Clin Med. 2026;15(12):4605.

Figures

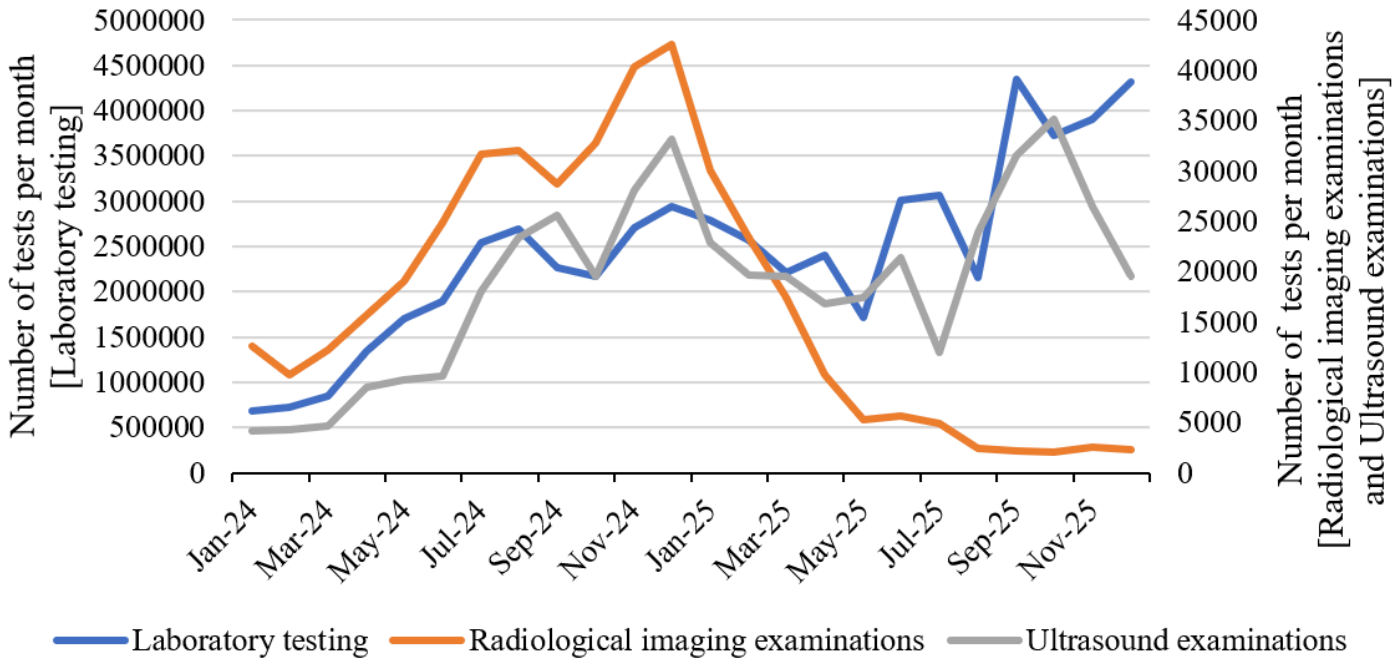

Figure 1

Operational characteristics of the regional sharing platform

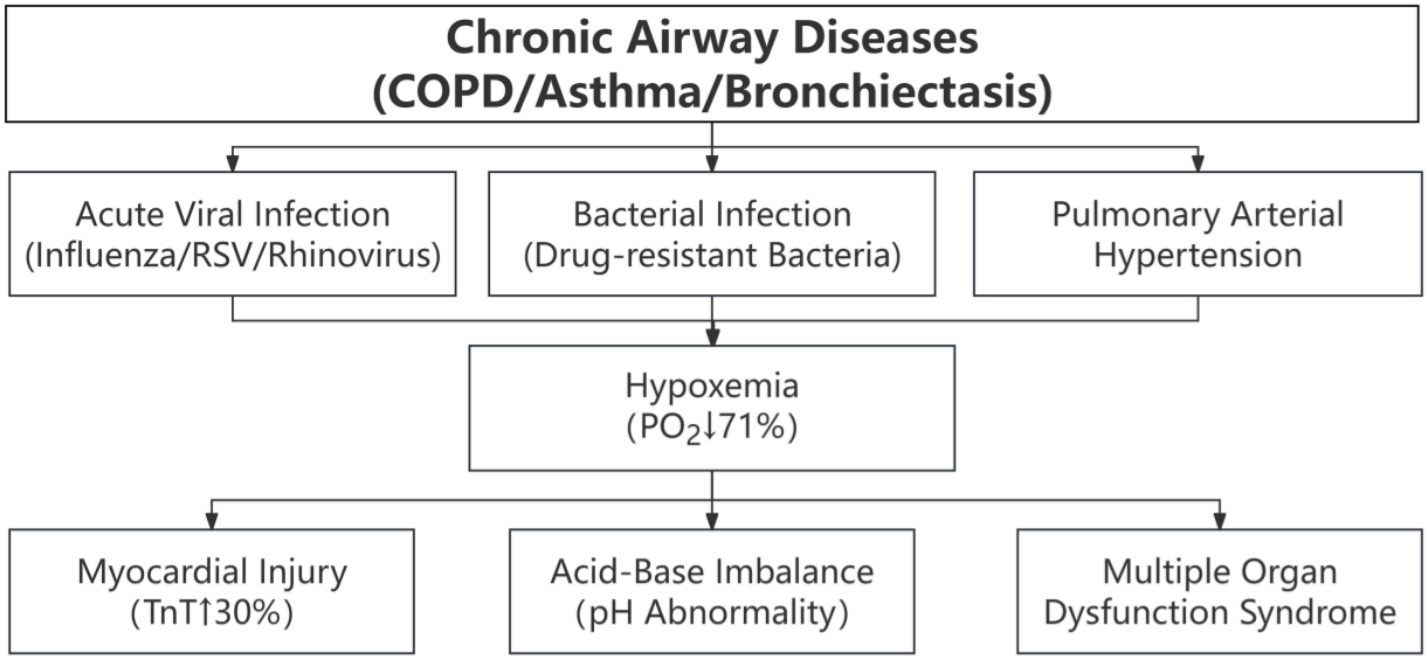

Figure 2

Respiratory multimorbidity network inferred from regional health information-sharing data in Gansu Province

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- SupplementFile1.xlsx