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Multi-omics integration to understand pathogen impacts in farmed and aquaculture animals

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INTRODUCTION & AIM

Infectious diseases represent a major challenge for **farming** and **aquaculture** industries, causing substantial economic losses worldwide. Recent advances in **high-throughput sequencing** have enabled detailed multi-level molecular analyses of **pathogen** impacts on host organisms (Natnan *et al., 2021)*. Multi-omics **integration** provides a holistic view of biomolecular interactions, essential for precision livestock and aquaculture development (Yu *et al., 2025)*. This study reviews **integrative** multi-omics applications in economically relevant species (cattle, pigs, goats, sheep, and aquatic organisms) affected by **diverse pathogens** (viruses, bacteria, fungi), focusing on integration methods, species-specific omics tools, and underlying host response mechanisms.

METHOD

A systematic **bibliometric analysis** was performed using the **Web of Science Core Collection**, accessed on 2 March 2026. Publication trends (**TS = Topic Search**) related to **multi-omics integration** in animal production systems were quantified using the following search strategy:

TS=("integromics" OR "multi-omics integration") AND TS=(“livestock” OR “cattle” OR “pig” OR “sheep” OR “goat” OR “fisheries” OR “aquaculture” OR “fish”)

Network analysis was subsequently conducted with **VOSviewer** v1.6.20. To specifically examine research associated with animal health, pathogens, and **host–pathogen interactions**, a refined search query was applied:

TS=("integromics" OR "multi-omics integration") AND TS=(“livestock” OR “cattle” OR “pig” OR “sheep” OR “goat” OR “aquaculture” OR “fisheries” OR “fish”) AND TS=(“pathogen” OR “disease” OR “infection” OR “virus” OR “bacteria” OR “immunity”)

Term **co-occurrence maps** were generated from the retrieved bibliographic data by extracting terms from titles and abstracts using the **full counting method**. A minimum threshold of **five occurrences** per term was applied. For network construction, **association strength** was used as the normalization method. Clustering **resolution** was performed with at 1.0, and **small clusters were merged** following VOSviewer default.

RESULTS & DISCUSSION

The **bibliometric analysis** generated a total of **53** publications (Fig 1), revealing a **marked increase** in integrative multi-omics research in recent years. Most studies (**66%**) were published in **2025**, followed by 2024 (11%), while the period 2020–2023 showed limited but sustained activity. Only isolated publications appeared in 2010 and 2015. This trend reflects the **rapid expansion of multi-omics** approaches driven by accessible **high-throughput** and **computational** methodologies, while earlier years reflect methodological immaturity, fragmented workflows, and **lack of established integration** frameworks (Yu et al., 2025). The strong dominance of recent publications indicates **growing interest in applying multi-omics to animal health**, disease resistance, and precision livestock production.

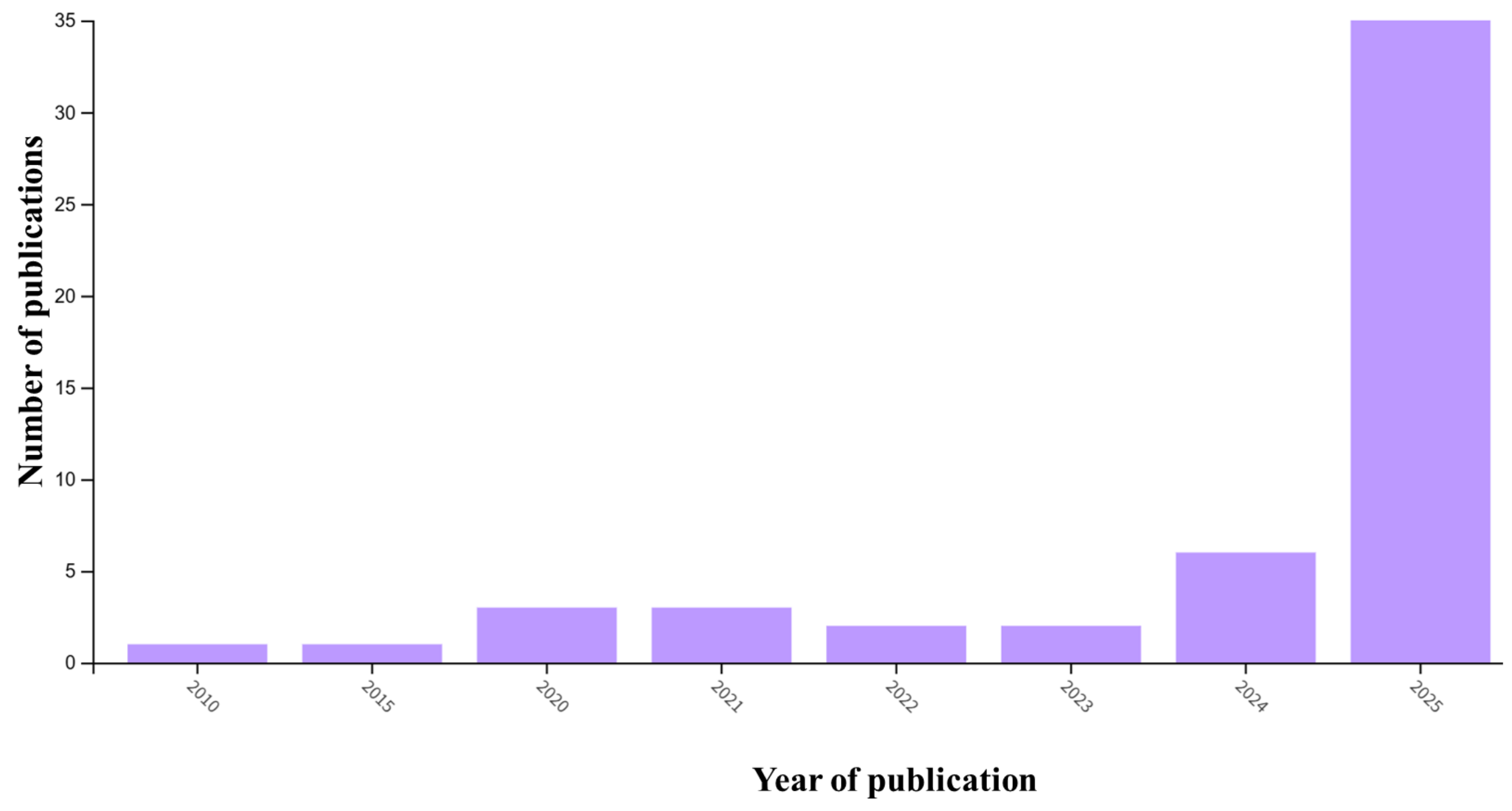

Fig. 1. Number of publications in Web of Science (WOS) database from the last 15 years

The **co-occurrence** network formed **six clear clusters** (Fig. 2). The largest grouped general integrative **omics terms** (genomics, transcriptomics, proteomics, metabolomics, spatial omics, bioinformatics) together with **welfare** and **productivity** concepts, reflecting strong links between **methodological** development and **applied livestock** goals. Other clusters focused on porcine muscle growth (DEGs, CNVs, lipid metabolism), metabolomics and stress responses, **immune-related mechanisms** (microbiota, apoptosis, vaccination), bovine health around parturition and mastitis, and protein biomarkers linked to meat tenderness.

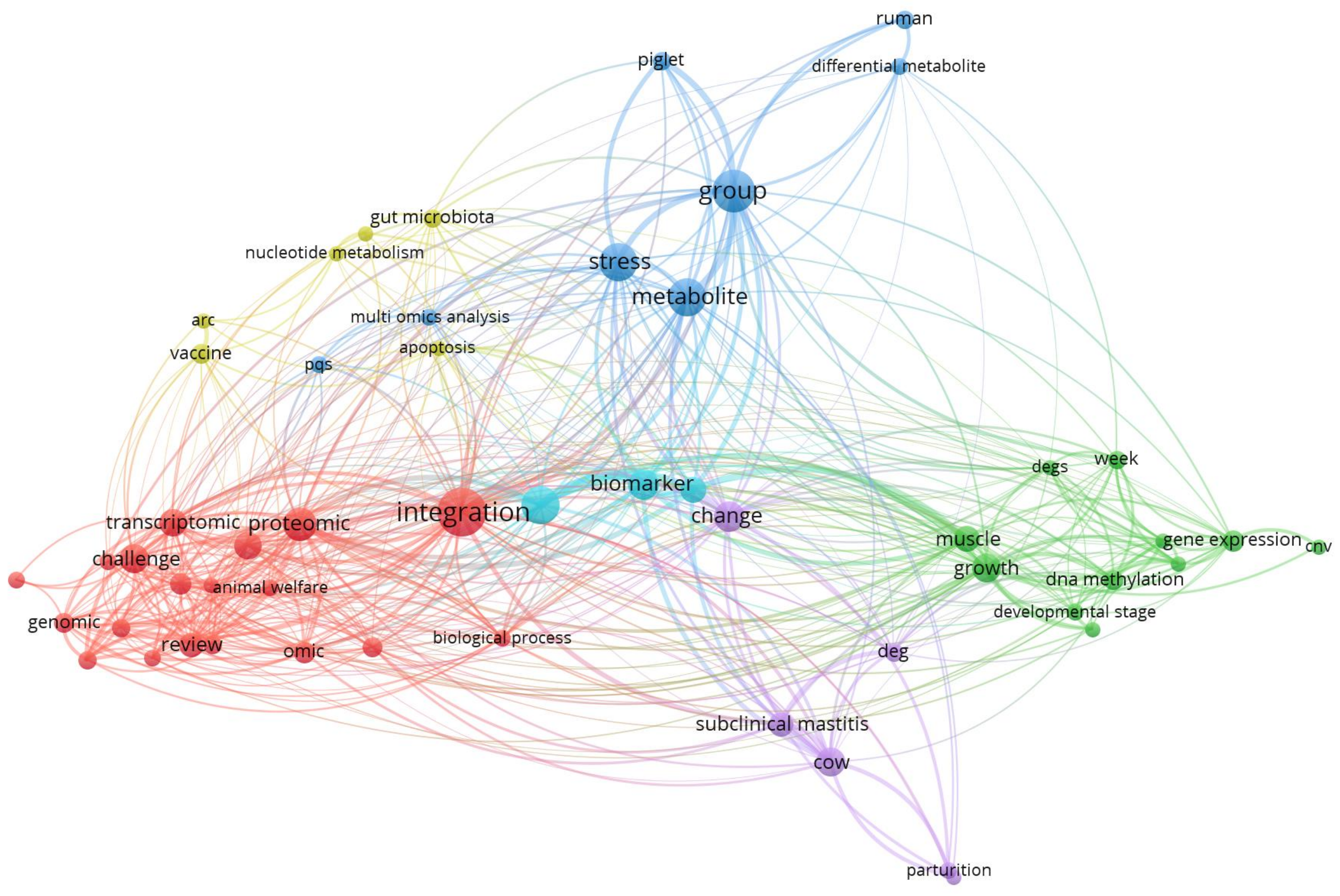

Fig. 2. Co-occurrence network of integromics, livestock-aquatic species and pathogen-related terms.

Overall, the network was dominated by **porcine** and **bovine** terminology, with **little aquaculture representation**, suggesting **fewer integrative studies** or inconsistent terminology in fish (Zhang et al., 2025). The results highlight how **disease-related** processes are closely connected to production traits, while emerging terms like spatial multi-omics point to increasing methodological sophistication. The **limited presence of pathogen-specific terms** underscores the need for stronger host–pathogen integration and greater methodological standardization (Natnan *et al., 2021)*.

CONCLUSION

- **Bibliometric** analysis confirms a sharp **rise in integromics research** (66% of records in 2025) in livestock/aquaculture.
- Six clusters **integrate omics** approaches with **welfare**, **health** and **productivity** traits, with a strong porcine-bovine focus.
- Improved standardization and deeper **host-pathogen integration** offer key opportunities for advancing precision **livestock** and **aquaculture**.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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