Prognosis and Biology of Postpartum Breast Cancer: A Protocol for Meta-Analysis of Survival and Systematic Review of the Tumour Microenvironment

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Running Title: Postpartum Breast Cancer Meta-Analysis Protocol

Abstract

Postpartum breast cancer (PPBC) is associated with poorer survival, higher metastatic rates, and distinct tumor biology versus breast cancer in nulliparous women or those with a longer delivery interval. Lactation, weaning, and postpartum mammary involution may create a pro-metastatic microenvironment, but evidence linking these exposures to prognosis and tumor-immune-stromal features has not been synthesized. The review will follow PRISMA. PubMed/MEDLINE, Embase, Scopus, and Web of Science will be searched from inception using terms for breast cancer, postpartum status, lactation, involution, prognosis, and tumor microenvironment. Eligible studies will be observational (cohort, case–control, cross-sectional) studies of women with breast cancer defining a postpartum subgroup (by time since last childbirth, parity, lactation, or weaning), including a comparator (nulliparous women or longer birth interval), and reporting at least one prognostic outcome (overall, distant metastasis-free, or disease-free survival, or recurrence), an aggressive clinicopathological feature, molecular/immune profile, or a treatment response. We will exclude experimental studies without human endpoints, risk-factor/incidence studies, reviews, and case reports. Two reviewers will independently screen, extract data, and assess risk of bias using the Newcastle–Ottawa Scale. If at least five studies report comparable hazard ratios for the same exposure–outcome pairing, we will perform a random-effects meta-analysis using restricted maximum likelihood; if 3–4 studies are available, a fixed-effect meta-analysis will be considered as a sensitivity analysis. If fewer than three studies are available, findings will be synthesized narratively. Heterogeneity will be assessed with I^2 and Cochran's Q, with I^2 informing interpretation rather than model choice.

Keywords: Breast Neoplasms, Survival Analysis, Postpartum Period, Lactation, Parity

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Background

The relationship between pregnancy and breast cancer is complex. While early first birth and prolonged breastfeeding confer long-term protection against certain subtypes, a diagnosis within five years of a completed pregnancy, commonly termed postpartum breast cancer (PPBC), is associated with a significantly worse prognosis. This elevated risk appears highest in the first two years after childbirth and may persist for up to 10–15 years in estrogen-receptor-positive disease. Cohort studies have shown that women diagnosed at ≤45 years and within five years postpartum have poorer overall survival (OS), higher rates of distant metastasis, and greater lymph node involvement than nulliparous women or those diagnosed ≥10 years after delivery, independent of stage, grade, and hormone-receptor status [1-4]. The risk appears highest within the first two years after childbirth, especially among women who were breastfeeding at diagnosis, and may persist for up to 15 years in estrogen-receptor-positive disease [5, 6].

The biological basis for this poor prognosis is increasingly linked to the postpartum microenvironment. After lactation ceases, the mammary gland undergoes involution, a remodeling process characterized by immune cell influx, extracellular matrix reorganization, and lymph angiogenesis. In rodent models, the involuting gland promotes tumour growth, invasion, and metastasis [7, 8].

Human data corroborate these findings, demonstrating that Postpartum breast cancer (PPBC) tumours harbor altered immune infiltrates (increased plasma B cells, $CD8^+$ T cells with dysfunction markers), differential protein expression (such as SEMA7A, COX-2, PR, PTEN), and distinct gene signatures involving cell cycle, T-cell activation, and reduced estrogen receptor signaling [9-11].

Despite these consistent signals, the literature remains fragmented. Studies define "postpartum" variably (<2, <5, or <10 years), seldom account for lactation or weaning status, and report outcomes on different scales. While individual studies have described molecular features of postpartum breast cancer, including differentially expressed microRNAs [11], no systematic review has specifically examined postpartum status, defined by time since last childbirth, parity, and lactation characteristics, as a determinant of prognosis, aggressive clinicopathological features, and tumour microenvironment remodeling using a rigorous epidemiological framework.

This protocol describes a systematic review designed to fill that gap.

Objectives

1. To determine the association between (i) postpartum status (time since last childbirth), (ii) parity, and (iii) breastfeeding/weaning status, and breast cancer prognosis, captured through all available survival endpoints (overall survival, distant metastasis-free survival, disease-free survival, recurrence, and others).
2. To evaluate whether postpartum status is associated with aggressive clinicopathological features at diagnosis, such as higher stage, lymph node involvement, lymphovascular invasion, and high-grade tumours.
3. To describe molecular and micro-environmental alterations (differential protein/gene expression, miRNA profiles, immune cell infiltration, markers of immune exhaustion, and others) in PPBC compared to nulliparous women, those with a longer birth interval, women with fewer prior births (lower parity), and those who underwent gradual (vs. abrupt) weaning.
4. To identify whether treatment responses are influenced by postpartum status, based on available clinical evidence.

Methods

This protocol is reported according to the Preferred Reporting Items for Systematic Review and Meta-Analysis Protocols (PRISMA-P) 2015 statement [12].

The review will be registered in PROSPERO and will follow PRISMA.

Eligibility criteria

Eligibility is defined using the PICOS (Population, Intervention/Exposure, Comparator, Outcome, Study design) framework (Table 1).

Case series will be excluded, even if they contain an internal comparison group. Only cohort, case–control, and cross-sectional studies with a defined comparator will be eligible.

Only studies published in English will be included. No restrictions on publication date or geographic setting will be applied.

Information sources

The following electronic databases will be searched from inception: PubMed/MEDLINE, Embase (via embase.com), Scopus, and Web of Science Core Collection.

Published studies will be identified through electronic databases (PubMed/MEDLINE, Embase, Scopus, Web of Science Core Collection) and reference/forward citation searching.

Grey literature, conference proceedings, and dissertation/thesis databases will not be systematically searched. Study authors will be contacted only where essential data are missing from otherwise eligible reports.

Table 1. PICOS criteria for study inclusion and exclusion

PICOS element	Inclusion criteria	Exclusion criteria
Population	Women (female sex) of any age with a diagnosis of invasive or in situ breast cancer. Studies must define a postpartum subgroup using time since last childbirth, parity, lactation status, or weaning characteristics. Populations from clinical cohorts, cancer registries, or population-based studies are eligible.	Studies that do not include a defined postpartum breast cancer subgroup (such as all parous women grouped without time-since-birth stratification). Studies exclusively in men, animal models, or in vitro systems. Studies focusing solely on breast cancer risk/incidence in women without a cancer diagnosis.
Exposure	Exposures: (1) Postpartum status, defined by time since last childbirth (categorized as <5 years vs. nulliparous or ≥10 years; sensitivity analyses will use <2 years and 5–10 years as alternative postpartum definitions). (2) Parity (nulliparous versus parous, or number of births). (3) Lactation/breastfeeding characteristics (duration, exclusive breastfeeding, breastfeeding at diagnosis, weaning type: gradual vs. abrupt/forced). Studies that additionally examine related molecular or micro-environmental features in the context of PPBC are eligible, provided they compare postpartum tumours to those of nulliparous women or women with longer birth intervals.	Studies evaluating exposures unrelated to pregnancy, postpartum biology, or lactation (such as purely genetic risk scores without reproductive data, environmental exposures with no link to postpartum status). Experimental in vivo or in vitro studies without any human prognostic or clinic-pathological endpoint.
Comparator	Nulliparous women (no prior live birth). Women with a longer interval since last childbirth (such as ≥10 years postpartum). For studies examining breastfeeding or weaning effects: non-lactating postpartum women, those who breastfed for a shorter duration, or those who underwent gradual (vs. abrupt) weaning.	Studies lacking a defined comparator group (such as single-arm case series without internal or external comparison).
Outcomes	Primary: OS, DMFS, DFS, recurrence (local, regional, distant). Both all-cause and breast cancer-specific mortality are eligible. Secondary: aggressive clinicopathological features (tumour stage, histological grade, lymph node involvement, lymphovascular invasion); molecular and tumour microenvironment alterations (differential protein/gene expression, miRNA profiles, immune cell infiltration, markers of immune exhaustion, extracellular matrix remodeling); Treatment response data, principally pathological complete response to neoadjuvant chemotherapy, where reported in relation to postpartum status. Data on endocrine therapy and CDK4/6 inhibitors will be summarized narratively if available.	Studies not reporting any of the specified prognostic, clinic-pathological, or molecular outcomes.
Study design	Observational epidemiological studies: Observational epidemiological studies: cohort (prospective and retrospective), case–control (including nested case–control), and cross-sectional studies with molecular phenotyping and a comparator group. Case series, including those with an ad-hoc internal comparison, will be excluded.	Single-arm case reports or case series without a comparator. Reviews, editorials, commentaries, conference abstracts without full data. Experimental animal or in vitro studies (unless they also contain a human component meeting inclusion criterion, in which case only the human data will be extracted).

Search strategy

The search strategy was developed with input from a medical information specialist and combines controlled vocabulary (MeSH, Emtree) with free-text keywords for three conceptual groups: (1) breast cancer, (2) postpartum status/lactation/weaning/parity, and (3) prognosis / clinic-pathological features/tumour microenvironment (Table 2). The truncation lactat* was intentionally replaced with the specific terms lactation, lactating to eliminate large numbers of irrelevant records on lactate metabolism while retaining all lactation-related concepts. The full PubMed/MEDLINE strategy is presented below; adaptations for Embase, Scopus, and Web of Science are provided in the uploaded search strategy document. The strategy was validated by confirming that all 11 references cited in the Introduction were retrieved by the PubMed search.

Table 2. Overall search concept table

Concept	MeSH terms (PubMed)	Free-text terms (all databases)
Population: Breast cancer	"Breast Neoplasms"[Mesh]	breast cancer*, breast carcinoma*, breast tumor*, breast neoplasm*, breast tumour*
Exposure: Postpartum status, lactation, weaning, parity	"Postpartum Period"[Mesh], "Parity"[Mesh]	postpartum, post-partum, after childbirth, after delivery, time since last birth, TSLB, postweaning, weaning, involution, lactation, lactating, breast milk, breastmilk, human milk, mother's milk, breastfeed*, breast feed*, breast-feed*, nursing, parity, nulliparous, gradual weaning, abrupt weaning, forced weaning
Outcome: Prognosis, clinic-pathological features, tumor microenvironment	"Prognosis"[Mesh], "Lymphatic Metastasis"[Mesh], "Tumor Microenvironment"[Mesh], "Biomarkers, Tumor"[Mesh]	prognos*, survival, overall survival, disease-free survival, relapse-free survival, recurrence, metastasis, metastatic, lymph node, lymphovascular invasion, tumor microenvironment, immune infiltrat*, immune exhaustion, gene expression, protein expression, microRNA, miRNA

Note. * = truncation (captures variant endings). Free-text terms are searched in title, abstract, and keyword fields (ti, ab for PubMed; ti, ab,kw for Embase; TITLE-ABS-KEY for Scopus; TS for Web of Science).

PubMed/MEDLINE search strategy

((("Breast Neoplasms"[Mesh] OR breast cancer*[tiab] OR breast carcinoma*[tiab] OR breast tumor*[tiab] OR breast neoplasm*[tiab] OR breast tumour*[tiab]) AND ("Postpartum Period"[Mesh] OR postpartum[tiab] OR post-partum[tiab] OR "after childbirth"[tiab] OR "after delivery"[tiab] OR "time since last birth"[tiab] OR TSLB[tiab] OR postweaning[tiab] OR weaning[tiab] OR involution[tiab] OR lactation[tiab] OR lactating[tiab] OR "breast milk"[tiab] OR breastmilk[tiab] OR "human milk"[tiab] OR "mother's milk"[tiab] OR breastfeed*[tiab] OR breast feed*[tiab] OR breast-feed*[tiab] OR nursing[tiab] OR "Parity"[Mesh] OR parity[tiab] OR nulliparous[tiab] OR "gradual weaning"[tiab] OR "abrupt weaning"[tiab] OR "forced weaning"[tiab])) AND ("Prognosis"[Mesh] OR prognos*[tiab] OR survival[tiab] OR "overall survival"[tiab] OR "disease-free survival"[tiab] OR "relapse-free survival"[tiab] OR recurrence[tiab] OR metastasis[tiab] OR metastatic[tiab] OR "Lymphatic Metastasis"[Mesh] OR "lymph node"[tiab] OR "lymphovascular invasion"[tiab] OR "Tumor Microenvironment"[Mesh] OR "tumor microenvironment"[tiab] OR "immune infiltrat*"[tiab] OR "immune exhaustion"[tiab] OR "gene expression"[tiab] OR "protein expression"[tiab] OR microRNA[tiab] OR miRNA[tiab] OR "Biomarkers, Tumor"[Mesh])) AND (english[lang])

The full strategies for Embase, Scopus, and Web of Science are available in the supplementary search strategy document uploaded to PROSPERO.

Selection process

All records will be imported into EndNote (version X9, Clarivate) for deduplication. Two reviewers will independently screen titles and abstracts against the eligibility criteria using Rayyan. Full texts of potentially eligible studies will be obtained and independently assessed. Disagreements at each stage will be resolved by discussion or by a third reviewer. The selection process will be documented using a PRISMA 2020 flow diagram.

Data collection process

A standardized data extraction form will be piloted on five studies and refined accordingly. Two reviewers will independently extract the following data from each included study: first author, year of publication, country, study design, sample size, population characteristics (age, menopausal status, tumour stage, histological subtype, hormone receptor status), exposure details (definition of postpartum status, time since last birth categories, parity, lactation/weaning characteristics), comparator group definition, outcome data (overall survival (OS); disease-free survival (DFS); distant metastasis-free survival (DMFS), recurrence rates with effect estimates and 95% CIs; clinic-pathological features; molecular/immune data), and adjustment variables. Discrepancies will be resolved by discussion or by a third reviewer. Study authors will be contacted for missing data only where the report is otherwise eligible and the missing data are essential. Reports with unavailable full text will be excluded and documented.

Risk of bias assessment

The Newcastle–Ottawa Scale (NOS) will be used to assess the quality of all included observational studies, including cross-sectional studies. JBI checklists will not be used. To avoid ambiguity, only the numerical NOS score will be used: 7–9 = high quality, 5–6 = moderate quality, and <5 = low quality. The percentage-based cut-off is not used. Two reviewers will independently rate each study. Disagreements will be resolved by consensus or by a third reviewer. For molecular outcomes, additional items related to assay validity, batch correction, and independent validation will be extracted and discussed narratively.

Reporting bias assessment

If ≥10 studies are available for an outcome, publication bias will be assessed using funnel plots and Egger's regression asymmetry test. If <10 studies are available, publication bias will be assessed qualitatively through inspection of forest plots for small-study effects and through evaluation of study size, precision, and direction of effect. If funnel-plot asymmetry or Egger's test suggests publication bias, trim-and-fill analysis will be performed as a sensitivity analysis where appropriate. Selective outcome reporting within studies will be examined by comparing reported results with pre-specified methods when a protocol or trial registry entry is available.

Certainty assessment

Certainty of evidence will not be formally graded using GRADE. Risk of bias, inconsistency, indirectness, imprecision, and publication bias will be described narratively for each key outcome.

Data synthesis

Data will be synthesized using both narrative and quantitative approaches. A narrative synthesis will be conducted for all included studies, structured around the four review objectives and presented in evidence tables. Where at least five studies report comparable effect estimates for the same exposure–outcome pairing, a random-effects meta-analysis will be performed using the restricted maximum likelihood (REML) estimator. Random-effects models were pre-specified because of anticipated clinical and methodological heterogeneity across observational studies. If fewer than five studies are available for a given exposure–outcome pairing, findings will be synthesized narratively. If 3–4 studies report comparable estimates, a fixed-effect meta-analysis will be considered and reported as a sensitivity analysis with explicit acknowledgement of the limitations; it will not replace the primary random-effects analysis. Pooled hazard ratios (and, where sufficient data exist, separate pooled odds ratios for binary outcomes) will be calculated with 95% confidence intervals. Odds ratios will not be combined with hazard ratios in the same meta-analysis. Heterogeneity will be assessed with the I^2 statistic and Cochran's Q test. I^2 will be interpreted using standard thresholds: 0–25% low, >25–

75% moderate, and >75% high. The Cochran's Q p-value will also be reported. Between-study variance will be estimated using the restricted maximum likelihood (REML) estimator in random-effects models.

Zero-event or sparse-data outcomes will not be pooled using hazard ratios. If binary outcomes with zero events are encountered, they will be summarized narratively or using risk differences with continuity corrections only where methodologically appropriate. Primary meta-analyses will remain restricted to time-to-event outcomes with reported hazard ratios.

Subgroup analyses by tumour subtype, menopausal status, and postpartum interval will be performed where sufficient stratified estimates are available. Where they are not, this will be reported explicitly as a limitation. These analyses are exploratory and are not adjusted for multiple comparisons; they will be interpreted as hypothesis-generating. If subtype-stratified estimates are too few for pooling, findings will be described narratively. Sensitivity analyses will exclude studies with high risk of bias. Leave-one-out sensitivity analysis will be performed for each meta-analysis with at least three studies to examine whether the pooled estimate is disproportionately influenced by any single study; results will be reported in supplementary material. If a study reports multiple eligible survival endpoints, the following hierarchy will be applied to select the primary estimate for meta-analysis: (1) OS, (2) DMFS, (3) DFS, (4) recurrence. Other endpoints will be synthesized narratively. When multiple publications derive from the same cohort, the study with the largest sample size and most complete outcome data will be retained; others will be listed in a supplementary table. If meta-analysis is not feasible due to clinical or methodological heterogeneity, findings will be presented narratively. Analyses will be performed using Stata (version 18) or R. Time since last childbirth (TSLB) will be the primary exposure and the basis for pooled analyses. Parity and lactation/weaning will be summarized narratively where data are available but will not be analyzed as separate pooled exposure categories, because of sparse and inconsistently reported data. Clinicopathological features will be summarized by TSLB category; parity- and lactation-specific syntheses will be narrative only. Time-to-event outcomes will be synthesized using log hazard ratios and their standard errors as reported in the primary studies. No indirect estimation from Kaplan–Meier curves were performed in the primary analysis. If future updates require extraction from Kaplan–Meier curves, the Tierney et al. method will be used, with the specific software and algorithm reported, and such estimates will be examined in sensitivity analyses [13]. Odds ratios and risk ratios will not be combined with hazard ratios. Studies reporting only odds ratios will be included in narrative and clinic-pathological syntheses, not in the primary time-to-event meta-analyses. No transformation of odds ratios to hazard ratios will be performed. If sufficient OR-only studies address the same binary outcome, they will be pooled separately in a sensitivity analysis and interpreted cautiously.

Patient and public involvement

No patients or members of the public were involved in the design of this protocol.

Ethics and dissemination

This systematic review does not involve primary data collection; therefore, ethical approval is not required. Results will be submitted for publication in a peer-reviewed journal and presented at relevant scientific conferences.

Discussion

This systematic review will provide the first comprehensive, structured synthesis of epidemiological evidence linking postpartum status, defined by time since last childbirth, parity, and lactation/weaning characteristics, to breast cancer prognosis, aggressive clinicopathological features, and tumour microenvironment remodeling. By focusing specifically on the postpartum window rather than pregnancy per se, we aim to clarify whether PPBC constitutes a distinct prognostic entity warranting tailored clinical management. The inclusion of molecular and immune outcomes will help identify biological pathways that may be amenable to therapeutic intervention. A key anticipated challenge is the heterogeneity of exposure definitions across studies; we will address this through careful subgroup and sensitivity analyses. Formal meta-regression and quality-score meta-regression were not planned because the number of studies per exposure–outcome pairing is expected to be small and covariates such as stage, subtype, menopausal status, and treatment era are reported inconsistently across observational studies; residual heterogeneity may therefore remain. These limitations will be explicitly acknowledged in the final review. The findings of this review are expected to inform clinical risk stratification, patient counselling, and the development of future therapeutic strategies for postpartum breast cancer. The review is restricted to English-language publications, which may exclude relevant studies published in other languages and introduce language bias. A limitation of the included observational studies is the potential for immortal time bias, as postpartum women must survive to their breast cancer diagnosis. We will note whether any included study addresses this (such as by using time-dependent covariates).

Abbreviations

ASCO	American Society of Clinical Oncology
BRCA1/2	Breast cancer gene ½
CDK	Cyclin-dependent kinase
CI	Confidence interval
COX-2	Cyclooxygenase-2
CSS	Cancer-specific survival
DFS	Disease-free survival
DMFS	Distant metastasis-free survival
ECM	Extracellular matrix
EMT	Epithelial–mesenchymal transition
ER	Estrogen receptor
ESMO	European Society for Medical Oncology
GRADE	Grading of Recommendations Assessment, Development and Evaluation

HER2	Human epidermal growth factor receptor 2
HR	Hazard ratio
JBI	Joanna Briggs Institute
LN	Lymph node
LVI	Lymphovascular invasion
MeSH	Medical Subject Headings
miRNA	MicroRNA
MOOSE	Meta-analysis Of Observational Studies in Epidemiology
NOS	Newcastle–Ottawa Scale
OR	Odds ratio
OS	Overall survival
PABC	Pregnancy-associated breast cancer
PICOS	Population, Intervention/Exposure, Comparator, Outcome, Study design
PPBC	Postpartum breast cancer
PR	Progesterone receptor
PRISMA	Preferred Reporting Items for Systematic Reviews and Meta-Analyses
PRISMA-P	Preferred Reporting Items for Systematic Review and Meta-Analysis Protocols
PTEN	Phosphatase and tensin homolog
REML	Restricted maximum likelihood
RFS	Relapse-free survival
RR	Risk ratio
SABCS	San Antonio Breast Cancer Symposium
SEMA7A	Semaphorin 7A
TCGA	The Cancer Genome Atlas
TNBC	Triple-negative breast cancer
TSLB	Time since last birth

Declarations

Conflict of Interest: The authors declare no competing interests.

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Author contributions: SH conceived and designed the review, drafted the protocol and search strategy. SS, MDM, MN, and AD contributed to the design of the eligibility criteria and data extraction plan. All authors reviewed and approved the final protocol.

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