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REVIEW ARTICLE

Quality and performance of validated prognostic models for survival after resection of intrahepatic cholangiocarcinoma: a systematic review and meta-analysis

Stefan Büttner^{1,*}, Boris Galjart^{1,*}, Berend R. Beumer¹, Jeroen L.A. van Vugt¹, Casper H.J. van Eijck¹, Wojciech G. Polak¹, Jeroen de Jonge¹, Marjolein Y.V. Homs², Lydi M.J.W. van Driel³, Timothy M. Pawlik⁴, Ewout W. Steyerberg⁵, Jan N.M. Ijzermans¹ & Bas Groot Koerkamp¹

¹Department of Surgery, ²Department of Medical Oncology, ³Department of Gastroenterology and Hepatology, Erasmus MC Cancer Institute, Rotterdam, Netherlands, ⁴Department of Surgery, Ohio State Medical Center, Columbus, OH, United States of America, and ⁵Department of Biomedical Data Sciences, Leiden University Medical Center, Leiden, Netherlands

Abstract

Background: The objective of this systematic review was to evaluate the performance of prognostic survival models for intrahepatic cholangiocarcinoma (iCCA) when validated in an external dataset. Furthermore, it sought to identify common prognostic factors across models, and assess methodological quality of the studies in which the models were developed.

Methods: The PRISMA guidelines were followed. External validation studies of prognostic models for patients with iCCA were searched in 5 databases. Model performance was assessed by discrimination and calibration.

Results: Thirteen external validation studies were identified, validating 18 different prognostic models. The Wang model was the sole model with good performance (C-index above 0.70) for overall survival. This model incorporated tumor size and number, lymph node metastasis, direct invasion into surrounding tissue, vascular invasion, Carbohydrate antigen (CA) 19-9, and carcinoembryonic antigen (CEA). Methodological quality was poor in 11/12 statistical models. The Wang model had the highest score with 13 out of 17 points.

Conclusion: The Wang model for prognosis after resection of iCCA has good quality and good performance at external validation, while most prognostic models for iCCA have been developed with poor methodological quality and show poor performance at external validation.

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Correspondence

Bas G. Koerkamp, Department of Surgery, Erasmus MC Cancer Institute, 's Gravendijkwal 230, Room H-809, 3015 CE Rotterdam, Netherlands. Tel: +31 10 703 1810. E-mail: b.grootkoerkamp@erasmusmc.nl

Introduction

Intrahepatic cholangiocarcinoma (iCCA) is an adenocarcinoma forming in the peripheral bile ducts. Its incidence in Europe and the United States is approximately 1-2 per 100,000.¹⁻³ iCCA is the second most common malignancy arising from the liver, accounting for 3% of all cases of gastro-intestinal cancer.^{4,5} Only about 10% of patients with iCCA present with resectable

disease.⁶ To obtain negative resection margins, major hepatectomies are required, because tumors are often large and show intraductal and periductal spread.⁴

Many prognostic models have been proposed to predict survival for individual patients after resection of iCCA.^{7–10} More accurate prediction of outcomes may improve shared decision-making and personalized medicine.^{7–10} For example, post-operative models can be used to guide adjuvant therapy and frequency of surveillance for recurrent disease. The performance

^{*} These authors contributed equally to this work.

of a prognostic model is determined by discrimination and calibration.¹¹ Discrimination is the ability of the model to determine which patient is at high-risk and which patient is at low-risk of adverse outcomes. Calibration is the agreement between the observed and predicted outcomes for individual patients.¹¹ Model performance should be judged at external validation prior to clinical use. Non-validated models are at a risk of overestimating predictive ability, a risk known as optimism.¹¹ This is especially important in a heterogeneous disease such as iCCA.¹²

A recent systematic review demonstrated that the majority of prognostic models in high-impact journals do not follow methodological recommendations, limiting their applicability and reliability.¹³ To determine the external validity of prognostic models in patients with resected iCCA, a systematic review to identify all externally validated prognostic models for survival was performed. Furthermore, this article sought to identify common prognostic factors across models, and assess methodological quality of the studies in which the models were developed.

Methods

This study was part of the VALidated surgIcal moDels of hepATobiliary malignanciEs (VALIDATE) effort, to index and appraise all validated surgical models for survival after hepatobiliary malignancies (hepatocellular carcinoma, colorectal liver metastasis, pancreatic duct adenocarcinoma, pancreatic neuroendocrine tumors, distal, perihilar and intrahepatic cholangiocarcinoma). The PRISMA Statement was followed for the reporting of this systematic review (www.prisma-statement.org). A comprehensive search of Embase, Medline, Web of Science, the Cochrane database, and Google Scholar was performed, using the search terms provided in Appendix A1. The last search was conducted on July 18th, 2019. Eligible studies performed an external validation of one or more prognostic models for diseasefree survival (DFS) or overall survival (OS) among patients who underwent a resection for iCCA. All studies written in the English language and published after 1990 were considered. Nonoriginal articles (i.e. reviews or expert opinions) were excluded. Studies with prognostic models containing prognostic factors that are not used in clinical practice (e.g., RNA/DNA sequencing data or liquid biopsies) were also excluded. Studies were excluded if no model performance measures were reported.¹⁴ Studies with patients treated with transplantation, ablation, or other techniques other than resection were excluded. Studies focused on recurrence of iCCA were excluded.

Validation studies

Three reviewers (SB, BGa and BB) independently assessed the abstracts of all studies identified by the search. Eligibility was determined by reviewing the full manuscript of potentially relevant studies. Disagreement among the reviewers was resolved by discussion. Descriptive, methodological, and outcome data from each validation study were extracted using a standard form by two reviewers (SB and BGa) and independently validated by a third reviewer (JV). If a validation study validated more than one prognostic model, data was extracted for each validated model.

Performance of the prognostic models at external validation was evaluated by discrimination and calibration. Discrimination was assessed using the area under the curve (AUC) of the receiver operating characteristic (ROC), Harrell's concordance index (cindex), the Brier score, or a similar measure.^{11,15} Because the cindex was the most commonly reported discrimination measure, it was used as the principal measure of external validity. The cindex is the probability that for two random patients, the patient with the worst *predicted* survival had the worst *observed* survival. A c-index of 0.5 indicates no predictive discrimination and a value of 1.0 indicates perfect separation of patients with different outcomes.¹⁵ For binary outcomes, i.e. studies in which time to event is disregarded, the AUC equals the c-index.¹⁵ An AUC or cindex below 0.6 was considered poor quality, while a c-index between 0.6 - 0.7 was considered moderate quality, and a c-index above 0.7 was considered good quality. Calibration is the agreement between observed outcomes and predictions for individual patients. Calibration was assessed using the calibration plot, intercept and/or slope. Because most models do not provide an estimate of OS or DFS, assessment of the calibration of the models in validation studies was difficult. Survival curves were also used to grossly compare prognosis per risk group in the validation study with prognosis and model estimates in the development study.

Development studies

The included validation studies performed an external validation of one or more prognostic models. Using the reference lists of these studies, the corresponding publications describing the original studies in which the prognostic model was developed were identified. To determine the methodological quality of these models, a review by participants of the Cochrane Prognostic Studies group and the CHARMS checklist were used as a guideline.^{13,16} Based on this review a quality assessment considering cohort description, statistical analysis, reporting of results, and model performance was systematically performed. For all reported characteristics one point could be earned, except for statistical selection of prognostic factors. The total score per model is the sum of the individual points.

Statistical analysis

Analyses were conducted using the *meta* package for R 3.5.1 (cran.r-project.org). Pooled hazard ratios (HR) with 95% confidence intervals (95% CI) were calculated by using the inverse variance method from the HR estimates in the final models. Random effects models were used as heterogeneity between included populations was assumed. C-indices were pooled on the probability scale using inverse variance weighting and random

effects meta-analysis.¹⁷ In case of overlapping studies, the smallest study was excluded from pooling. Studies that reported no confidence bounds or standard error for their c-index or HR could not be included in pooled analysis.

Results

Validation studies

Electronic searches identified 10,282 results (Fig. 1). Of the fulltext articles, 13 external validation studies for prognosis in iCCA met the inclusion criteria (Table 1). The median number (interquartile range (IQR)) of patients in which models were validated was 126 (82–367). Three studies included more than 500 patients.^{18–20}

Included models

The 13 validation studies validated 18 different prognostic models (Table 1; listed separately Appendix A2). Ten prognostic models were validated in only one study. The 18 prognostic models were validated 23 times for DFS and 52 times for OS. Two models were only validated for OS,^{21,22} two only for DFS,^{23,24} and the other models for both outcomes. In twelve prognostic models,^{10,21–31} statistical methods were used for model development; six models were expert opinion or consensus based.^{32–37} One prognostic model was developed for mixed iCCA and hepatocellular carcinoma.²⁴ Ten models^{21,25,27,30,32,33,35–38} could be applied in the preoperative setting; the other eight models required pathological prognostic factors that are only available after resection.



Figure 1 Prisma flow diagram of the VALIDATE effort, to find studies that validate prognostic models after resection of HPB cancer

Table 1 External validation studies of prognostic models for iCCA. Models in red have a poor performance (i.e. c-index < 0.6), in yellow a moderate performance (0.6–0.7), and in green a good performance (>0.7). The method of the PNI development study was unknown as it was not available in English. Studies that reported no confidence bounds or standard error for their c-index could not be included in pooled analysis

Outcome	Model	Validation studies	Total Patients	Pooled C- index (95%Cl)	Range	l ²	Consensus or Statistical	Quality Points /17	Calibration Curve/Kaplan Meier
DFS	AJCC 6 ^{th 32}	41	54		0.68		С		None
	AJCC 7 ^{th 33}	18,23,24, 41	1528	0.58 (0.53-0.63)	0.52-0.66	74%	С		КМ
	AJCC 8 ^{th 34}	41, 59	208		0.61-0.73		С		КМ
	BCLC 35	39	99		0.57		С		KM
	CLIP 25	39	99		0.59		S	9	KM
	Hyder ²⁶	18	1054		0.52		S	11	KM
	LCSGJ 36	18, 41, 59	1262	0.59 (0.52-0.66)	0.56-0.70	83%	С		KM
	mGPS ²⁷	39	99		0.52		S	8	KM
	Nathan ²⁸	18	1054		0.58		S	9	КM
	Okabayashi ²⁹	18	1054		0.56		S	6	KM
	Okuda ³⁰	39	99		0.56		S	6	KM
	PECAR score 24	24	101		0.61		S	10	CC
	PNI 37	39	99		0.51		N/A		KM
	Renji ²³	23	106		0.65		S	9	СС
	SHPBSJ 31	18	1054		0.56		S	6	KM
	Wang ¹⁰	18	1054		0.61		S	13	KM
OS	AJCC 6 ^{th 32}	10, 22, 41, 60	919	0.62 (0.58-0.67)	0.60-0.67	0%	С		КМ
	AJCC 7 ^{th 33}	10, 18, 20, 22, 40, 41, 60, 61	2329	0.62 (0.59-0.64)	0.59-0.68	45%	С		КМ
	AJCC 8 ^{th 34}	19, 20, 41, 59	1216	0.61 (0.51-0.72)	0.56-0.67	84%	С		KM
	BCLC 35	39	99		0.61		С		KM
	CLIP 25	39	99		0.58		S	9	KM
	Fudan ²¹	40	188		0.55		S	8	KM
	Hyder ²⁶	18, 40	1242	0.61 (0.58-0.64)	0.59-0.63	0%	S	11	СС
	LCSGJ 36	10, 18, 41, 59-61	2051	0.64 (0.61-0.66)	0.61-0.68	38%	С		KM
	mGPS ²⁷	39	99		0.46		S	8	KM
	Nathan ²⁸	10, 18, 61	1717	0.62 (0.57-0.67)	0.59-0.64	73%	S	9	KM
	Okabayashi ²⁹	10, 18, 60, 61	1843	0.61 (0.58-0.64)	0.59-0.67	26%	S	6	KM
	Okuda ³⁰	39	99		0.55		S	6	KM
	PNI 37	39	99		0.60		N/A		KM
	SHPBSJ 31	18	1054		0.61		S	6	KM
	Wang ¹⁰	10, 18, 40	1243	0.70 (0.65-0.76)	0.65-0.76	51%	S	13	CC
	Yeh 22	22	105	0.68 (0.55-0.83)	0.64-0.79	64%	S	11	CC

Consensus based models included various editions of the American Joint Committee on Cancer (AJCC) TNM staging for iCCA.^{32–34} Consensus based models for HCC including the Barcelona Clinic Liver Cancer (BCLC),³⁵ and the prognostic nutritional index (PNI) were validated in patients with mixed iCCA and HCC tumors.³⁹

Prognostic factors

The most common prognostic factors in models for iCCA are shown in Table 2. Lymph node metastases had the most severe impact on survival (pooled HR 2.20, 95% CI 1.74–2.78),^{10,22} followed by multiple tumors (HR 1.63, 95% CI 1.26–2.11),^{21,26} and vascular invasion (HR 1.44, 95% CI

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Table 2 Model prognostic factors

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	Imaging / Pathology					Clinical	Laboratory				Other			
	Tumor Size	Tumor Number	Vascular	Involvement of	Invasion of	Regional Lymph	Distant	Child-Pugh	Carbohydrate	Carcino-	C-reactive	Lymphocyte	Albumin	Other
			Invasion	Visceral	Adjacent Organs	Node	Metastases		Antigen 19-9	embryonic	Protein	Count		factors ^b
				Peritoneum		Metastases				antigen				
AJCC TNM 6th Edition	а	а	а			а	а							
AJCC TNM 7th Edition		а	а	а	а	а	а							
AJCC TNM 8th Edition	а	а	а	а	а	а	а							
BCLC	а	а	а			а	а	а						
CLIP	а	а	а					а						а
FUDAN	а	а							а					а
Hyder	а	а	а			а								а
LCSGJ	а	а	а	а		а	а							
mGPS											а		а	
Nathan		а	а		а	а	а							
Okabayashi		а	а			а	а							
Okuda	а												а	а
PECAR score ⁺			а			а								а
PNI												а	а	
Renji	а					а		а						а
SHPBSJ	а	а	а			а	а							
Wang	а	а	а		а	а			а	а				
Yeh	а		а			а				а				а
Models including factor	12	12	13	3	5	13	8	3	2	2	1	1	3	7

a Model designed for mixed hepatocellular/intrahepatic cholangiocarcinoma.

b Other prognostic factors include gender, age, symptoms, mucobilia, hepatholithiasis, tumor boundary on radiology, resection margin, growth pattern, differentiation, hepatitis B surface antigen, cirrhosis, alkaline phosphatase, gamma glutamyltransferase, bilirubin, alfa foetoprotein. Details in Appendix A3.

1.05–1.96).^{10,22} The HR per centimeter tumor size increase was 1.08 in one model.¹⁰ Two studies included demographic factors, such as age and sex.^{24,26} Laboratory investigations that were used included carbohydrate antigen 19-9 (CA 19-9),^{10,21} carcinoembryonic antigen (CEA),^{10,22} alfa fetoprotein (AFP),²⁵ c-reactive protein (CRP),²⁷ lymphocyte count,³⁷ and albumin.^{27,30,37} Most models used different cut-offs when categorizing prognostic factor values, limiting pooled analyses (Appendix A3).

Performance of models at validation – discrimination

The performance of 18 models was assessed in 75 external validations (Table 1). For DFS, 11 models performed poorly at pooled external validation with an AUC or c-index below 0.6 and 5 models had moderate performance with a c-index between 0.6 and 0.7, For OS, four models performed poorly and eleven models had a moderate performance. Only the Wang model reached a good performance for OS (c-index: 0.70) at pooled validation using seven prognostic factors: tumor size, tumor number, vascular invasion, invasion into adjacent organs, lymph node metastases, CA 19-9 and CEA (Fig. 2a).¹⁰ The Wang model was validated in three external cohorts from China (n = 82; c - 1)index: 0.75),¹⁰ the U.S. (n = 188; c-index 0.72),⁴⁰ and Europe, China and North America (n = 1054; c-index: 0.67).¹⁸ Yeh's model showed good discrimination (0.79) in one small validation cohort (n = 38), and comparatively low (0.64) in another (n = 67)²² All AJCC (American Joint Committee on Cancer) staging systems had a poor or moderate performance (Fig. 2b c). In one study, the 8th edition AJCC staging systems reached a c-index of 0.73.41 The LCSGJ, the Japanese consensus model, performed equally modest (0.64; Fig. 2d).³⁶

Performance of models at validation - calibration

Kaplan-Meier survival estimates of the different risk groups were reported in 55/75 (73%) validations. In contrast, calibration

plots or tables, for comparing predicted with observed survival for individual patients were only reported in six validation studies (8%) of four prognostic models. Calibration was not reported at all in 18 (24%) validations. The Wang model demonstrated good calibration in an external validation study performed by the same authors.¹⁰ Reasonable calibration at external validation was noted for the Wang and Hyder models.⁴⁰

Quality assessment of development studies

The quality of six model development studies was not formally evaluated, because the prognostic models were expert or consensus based.^{32–37} Quality assessment was performed for the 12 studies that used statistical modeling. The cohort was well described in all studies (Table 3; studies listed in Appendix A2). All studies were retrospective. Ten studies dichotomized or categorized continuous prognostic factors resulting in loss of information. Interaction was evaluated in two studies. Six studies had more than 15 events per variable (EPV) in the multivariable analysis, and one study had EPV <5. Handling of missing data was not adequately reported in eight studies. Statistical methods for variable selection were accurately described in only six studies. Six studies evaluated discrimination. Five studies evaluated calibration. External validation was reported in four development studies. The points score per model is appended to Table 1. The median number of points achieved was 9/17 (IQR: 8-10). The model by Wang and colleagues outperformed the other models with a score of 13/17.

Discussion

This review identified 18 validated prognostic models for survival of patients after resection of iCCA.^{38,42,43} All but one of the prognostic models had a poor to moderate performance (c-statistic < 0.7) for OS on external validation and eight were

Study	C-index	SE		95%-CI Weight
Buettner, S.	0.67	0.0210		0.67 [0.63; 0.71] 46.3%
Doussot, A.	0.72	0.0408		0.72 [0.64; 0.80] 25.8%
Wang, Y.	0.75	0.0383		0.75 [0.68; 0.82] 27.9%
Random effects mo	del			0.70 [0.65; 0.76] 100.0%
Heterogeneity: I ² = 51%	$%, τ^2 = 0.0011,$	p = 0.13		
(a)			0.6 0.7 0.8	
Study	C-index	SE		95%-CI Weight
Jing C	0.67	0.0316	÷	0.67 [0.61; 0.73] 49.8%
Sasaki K	0.56	0.0309 <		0.56 [0.50; 0.62] 50.2%
Random effects mo		_		0 61 [0 51: 0 72] 100 0%
Heterogeneity: $I^2 = 84\%$	$_{6}^{6}, \tau^{2} = 0.0050,$	p = 0.01		
			0.6 0.7 0.8	
(b)				
Study	C-index	SE		95%-Cl Weight
Ali, S.M.	0.62	0.0408		0.62 [0.54; 0.70] 7.5%
Buettner, S.	0.64	0.0210		0.64 [0.60; 0.68] 18.2%
Doussot, A.	0.63	0.0230		0.63 [0.59; 0.67] 16.5%
Yeh, C.	0.68	0.0370		0.68 [0.61; 0.75] 8.7%
Yeh, C.	0.64	0.1290 <	•	- 0.64 [0.39; 0.89] 0.9%
Yeh, C.	0.59	0.0090		0.59 [0.57; 0.61] 31.3%
Liu L	0.59	0.0224		0.59 [0.55; 0.64] 16.9%
Random effects mo	del	0.00		0.62 [0.59; 0.64] 100.0%
Heterogeneity: $I = 45\%$	$\%, \tau = 0.0004,$	p = 0.09	06 07 08	
(c)			0.0 0.1 0.0	
Study	C-index	SE		95%-Cl Weight
Ali, S.M.	0.65	0.0408		0.65 [0.57; 0.73] 10.5%
Buettner, S.	0.63	0.0120		0.63 [0.61; 0.65] 45.4%
Jing C	0.68	0.0281		0.68 [0.63; 0.74] 18.8%
LiuL	0.60	0.0224		0.60 [0.56; 0.65] 25.4%
Random effects mo	del		\diamond	0.64 [0.61; 0.66] 100.0%
Heterogeneity: I ² = 38%	%, $\tau^2 = 0.0003$,	p = 0.19		
(d)			0.6 0.7 0.8	

Figure 2 Forest plots of the c-index of the most relevant models for overall survival. (a) Wang model, (b) AJCC TNM 8th Edition, (c) AJCC TNM 7th Edition, (d) LCSGJ

validated only in small cohorts (n < 500). Only the Wang model had a good pooled performance score of 0.70 and good calibration at multiple validations.¹⁰ The Wang model requires seven prognostic factors: tumor size, tumor number, vascular invasion, invasion into adjacent organs, lymph node metastases, CA 19-9, and CEA.¹⁰ Performance of models predicting DFS was worse compared to models predicting OS, presumably because studies

were retrospective and follow-up was not protocolized. Methodological quality of the development studies was poor, with the Wang model as one of few exceptions.

Most patients with iCCA and their treating physicians are interested in individual prognosis. Assessment of prognosis is often based on informal assessment of one or more key prognostic factors, for example, lymph node status and the number of

Cohort description	Number of Studies	iCCA (n=8)	Mixed iCCA & HCC (n=4)	Total (n=12)
	Prospective Cohort	0	0	0
	Inclusion Criteria Clear	8	4	12
	Baseline Characteristics	7	4	11
	Recruitment Dates	8	4	12
	Follow-Up Reported	7	1	8
Analyses	Outcome Definition	3	4	7
	Interaction Tested	2	0	2
	Continuous Predictors Used	2	0	2
	15 Events per variable	3	3	6
	Missing Data Reported	0	0	0
Results	Adequate Handling of Missing Data	3	1	4
	Statistical Variable Selection	8	2	10
	Clear Method for Variable Selection	3	3	6
	Univariable Results Presented	6	3	9
Performance	Multivariable Results Presented	7	2	9
	Calibration Analyzed	4	1	5
	Discrimination Analyzed	5	1	6
	Validity Assessment	5	2	7
	External Validity Assessment	3	1	4

Table 3 Methodological quality of studies that developed prognostic models for iCCA. Quality was assessed for the cohort description, analyses, results, and performance analyses. The numbers in the table are the counts of studies that handled each quality item adequately

tumors. Prognostic models are a formal method of bringing together all independent prognostic factors for the most accurate prognosis. In the era of electronic patient records, a complex equation for individual prognosis should not be a hurdle to be replaced by a simplified but inaccurate staging system or risk score. Unfortunately, individual prognosis of even the best prognostic model remains inaccurate; patients may still have an OS that is much better or worse than predicted. To some extent this leaves room for improvement of the best prognostic models, but uncertainty will always remain because of the stochastic nature of disease.⁴⁴

Six of the 18 prognostic models for iCCA patients were based on expert opinion or consensus, rather than statistical analyses. The AJCC staging system is the best-known consensus based staging system for iCCA with three validated editions (6th, 7th, and 8th). It aims to determine prognosis for patients and physicians as well as advice on the best treatment.³⁴ The 8th edition continues to adhere to anatomical prognostic factors; T-stage is determined by the number of tumors, the size of the largest tumor, the presence of vascular invasion, perforation of the visceral peritoneum, and direct extrahepatic invasion; N-stage by regional lymph node involvement; and M-stage by distant metastases.³⁴ The performance of all three AJCC staging systems was moderate at best. Five out of seven prognostic factors in the Wang model, however, are also present in the 8th edition of the AJCC staging system. The Wang model has improved the AJCC staging by adding two nonanatomic factors (CA 19-9 and CEA) and used statistical analysis to determine the weight of each risk factor.

Poor methodological quality of the model development studies also contributed to poor performance. The four studies that described their statistical variable selection process, employed stepwise selection of prognostic factors, which leads to high variability of included prognostic factors in small studies.¹¹ Dichotomizing continuous prognostic factors at arbitrary cutoffs contributes to bias and less power.⁴⁵ In theory, only one definition or categorization of a risk factor is ideal per outcome and subpopulation. Furthermore, information on missing data and the way it was handled was lacking in all studies and in 8/12 studies, respectively. Commonly, regression analyses were performed with complete cases only, reducing statistical power and potentially introducing selection bias.^{11,46,47} Six out of twelve studies had <15 EPV. Quality recommendations for prognostic models are available in the TRIPOD statement for transparent reporting of a multivariable prediction model for individual prognosis.⁴⁸ Organizations such as the AJCC have also developed strict guidelines for endorsement of prediction models.⁴⁹

Performance of prognostic models was often good in small development cohorts, but poor when models were validated in a larger external dataset. This might partially be remedied by employing proper internal validation methods, most notably

bootstrapping^{14,50} and internal-external cross-validation (e.g., in multicenter studies patients of each hospital are left out once in a sub analysis).^{50,51} These methods were employed only in a third of the included development studies. Small cohort size is also a problem for external validation. The median validation cohort was only about 100 patients, while each year about 4000 patients are diagnosed with iCCA in the U.S. alone.^{52,53} A consequence of the small sample size of validation cohorts is the observed variation in model performance between external validations. This variation resulted in a high I² score at pooled analyses of model performance of validation studies.

Future research should focus on collaborative development of prognostic models. The current tendency is to develop new prognostic models rather than validating existing models. This is reflected by the publication of 18 different models. Furthermore, authors should validate existing models in large cohorts from different settings, such as different hospitals in different care systems. Subsequently, models should be recalibrated if existing models have suboptimal performance (discrimination or calibration) at external validation with large cohorts. Recalibration is a simple form of model updating. It means readjusting the baseline hazard and hazard ratios of independent prognostic factors. Only in the event that validation and recalibration fail, should new models be developed.^{11,42} New prognostic models for resected iCCA should explicitly report whether they are applicable in the preoperative setting or only after resection, because they require factors available after pathological exam of the resected specimen. Prognostic models with readily available patient and tumor characteristics (e.g., age and tumor stage) are important as a benchmark for novel prognostic biomarkers.^{54,55} The Wang model is the current benchmark for novel prognostic biomarkers for iCCA. Expensive measurement of a novel biomarker is only useful for prognostication, if it improves on the Wang model. Novel biomarkers, however, may also aim to predict response to treatment. For example, targeted treatments for iCCA patients with genomic alterations in IDH and FGFR are currently evaluated.^{56–58} The main value of such biomarkers is to determine treatment benefit rather than prognosis.

This study has several limitations. It only assessed externally validated prognostic models. Consequently, recent promising prognostic models that have not yet been validated may have been excluded. Secondly, calibration of models is difficult to quantify and summarize; consequently, only a general description of calibration was presented. Pooled hazard ratio estimates for prognostic factors are hampered by methodological quality in the published studies. Finally, all prognostic models were validated in retrospective cohorts that inherently have missing data. Validation studies rarely included all eligible consecutive patients.

Out of 18 prognostic models for iCCA, the Wang model, consisting of tumor size, tumor number, vascular invasion, invasion into adjacent organs, lymph node metastases, CA 19-9 and CEA, performed best on external validation. Most models have poor methodological quality and poor performance on

external validation. Future research should focus on external validation of existing models in large cohorts from different settings, rather than developing new models in small cohorts. The best prognostic model can then be incrementally improved by adding novel biomarkers.

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None

Conflict of interest

None declared.

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Further Reading

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Appendix A1. Search terms

Embase.com

(('nomogram'/de OR (nomogram*):ab,ti) OR ((((prediction/de OR prognosis/de OR survival/exp OR mortality/exp OR 'tumor recurrence'/exp OR recurrence/de OR 'cancer prognosis'/exp OR 'predictive validity'/de) AND (model/exp OR 'proportional hazards model'/de OR 'algorithm'/de)) OR ((predict* NEAR/6 (model* OR surviv* OR mortalit* OR recurren* OR algorithm*))):ab,ti) AND (validity/exp OR 'validation study'/de OR 'validation process'/de OR 'receiver operating characteristic'/de OR 'area under the curve'/de OR 'reproducibility'/de OR (validat* OR validit* OR (discriminat* NEAR/3 (perform* OR power*)) OR roc OR rocs OR (receiver* NEAR/3 operat* NEAR/3 (characteristic* OR curve*)) OR (area* NEAR/3 curve*) OR auc OR aucs OR concordan* OR calibrat* OR reproducib*):ab,ti))) AND ('digestive system tumor'/exp OR 'intestine resection'/exp OR 'liver resection'/ exp OR 'pancreas resection'/de OR ((('digestive system' OR hepat* OR intrahepat* OR gastrointestin* OR liver OR pancrea* OR hpb OR billiar*) NEAR/3 (tumor* OR tumour OR neoplas* OR cancer OR carcino* OR adenocarcino* OR resect*)) OR hepatectom* OR pancreatectom* OR whipple OR pancreaticoduodenectom* OR cholangiocarcinom*):ab,ti) AND ('surgery'/exp OR 'surgery':lnk OR (surg* OR operative* OR operation* OR resect* OR hepatectom* OR pancreatectom* OR whipple OR pancreaticoduodenectom*):ab,ti) NOT ([animals]/lim NOT [humans]/lim)

Medline ovid

(("nomograms"/OR (nomogram*).ab,ti.) OR ((((survival/OR exp mortality/OR mortality.xs. OR "recurrence"/OR "Neoplasm Recurrence, Local"/OR "prognosis"/) AND (exp "Models, Theoretical"/OR "Algorithms"/)) OR ((predict* ADI6 (model* OR surviv* OR mortalit* OR recurren* OR algorithm*))).ab,ti.) AND ("Reproducibility of Results"/OR "Validation Studies"/OR "Validation Studies as Topic"/OR "ROC Curve"/OR "Area Under Curve"/ OR (validat* OR validit* OR (discriminat* ADJ3 (perform* OR power*)) OR roc OR rocs OR (receiver* ADJ3 operat* ADJ3 (characteristic* OR curve*)) OR (area* ADJ3 curve*) OR auc OR aucs OR concordan* OR calibrat*).ab,ti.))) AND (exp "Gastrointestinal Neoplasms"/OR "Hepatectomy"/OR "Pancreatectomy"/OR ((("digestive system" OR hepat* OR intrahepat* OR gastrointestin* OR liver OR pancrea* OR hpb OR billiar*) ADJ3 (tumor* OR tumour OR neoplas* OR cancer OR carcino* OR adenocarcino* OR resect*)) OR hepatectom* OR pancreatectom* OR whipple OR pancreaticoduodenectom* OR cholangiocarcinom*).ab,ti.) AND (exp "Surgical Procedures, Operative"/OR "surgery".xs. OR (surg* OR operative* OR operation* OR resect* OR hepatectom* OR pancreatectom* OR whipple OR pancreaticoduodenectom*).ab,ti.) NOT (exp animals/NOT humans/)

Cochrane

(((nomogram*):ab,ti) OR ((((predict* NEAR/6 (model* OR surviv* OR mortalit* OR recurren* OR algorithm*))):ab,ti)

AND ((validat* OR validit* OR (discriminat* NEAR/3 (perform* OR power*)) OR roc OR rocs OR (receiver* NEAR/3 operat* NEAR/3 (characteristic* OR curve*)) OR (area* NEAR/3 curve*) OR auc OR aucs OR concordan* OR calibrat* OR reproducib*):ab,ti))) AND (((('digestive system' OR hepat* OR intrahepat* OR gastrointestin* OR liver OR pancrea* OR hpb OR billiar*) NEAR/3 (tumor* OR tumour OR neoplas* OR cancer OR carcino* OR adenocarcino* OR resect*)) OR hepatectom* OR pancreatectom* OR whipple OR pancreaticoduodenectom* OR cholangiocarcinom*):ab,ti) AND ((surg* OR operative* OR operation* OR resect* OR hepatectom* OR OR pancreatectom* OR whipple pancreaticoduodenectom*):ab,ti)

Web of science

TS=((((nomogram*)) OR ((((predict* NEAR/5 (model* OR surviv* OR mortalit* OR recurren* OR algorithm*)))) AND ((validat* OR validit* OR (discriminat* NEAR/2 (perform* OR power*)) OR roc OR rocs OR (receiver* NEAR/2 operat* NEAR/2 (characteristic* OR curve*)) OR (area* NEAR/2 curve*) OR auc OR aucs OR concordan* OR calibrat* OR reproducib*)))) AND (((("digestive system" OR hepat* OR intrahepat* OR gastrointestin* OR liver OR pancrea* OR hpb OR billiar*) NEAR/2 (tumor* OR tumour OR neoplas* OR cancer OR carcino* OR adenocarcino* OR resect*)) OR hepatectom* OR pancreatectom* OR whipple OR pancreaticoduodenectom* OR cholangiocarcinom*)) AND ((surg* OR operative* OR operation* OR resect* OR hepatectom* OR pancreatectom* OR whipple OR pancreaticoduodenectom*)) NOT ((animal* OR rat OR rats OR mouse OR mice OR murine) NOT (human* OR patient*)))

PubMed publisher

(("nomograms"[mh] OR (nomogram*[tiab])) OR ((((survival [mh] OR mortality[mh] OR mortality[sh] OR "recurrence"[mh] OR "Neoplasm Recurrence, Local"[mh] OR "prognosis"[mh]) AND ("Models, Theoretical"[mh] OR "Algorithms"[mh])) OR ((predict*[tiab] AND (model*[tiab] OR surviv*[tiab] OR mortalit*[tiab] OR recurren*[tiab] OR algorithm*[tiab])))) AND ("Reproducibility of Results"[mh] OR "Validation Studies"[mh] OR "Validation Studies as Topic"[mh] OR "ROC Curve"[mh] OR "Area Under Curve"[mh] OR (validat*[tiab] OR validit*[tiab] OR (discriminat*[tiab] AND (perform*[tiab] OR power*[tiab])) OR roc OR rocs OR (receiver*[tiab] AND (operating[tiab]) AND (characteristic*[tiab] OR curve*[tiab])) OR (area*[tiab] AND curve*[tiab]) OR auc OR aucs OR concordan*[tiab] OR calibrat* [tiab])))) AND ("Gastrointestinal Neoplasms"[mh] OR "Hepatectomy"[mh] OR "Pancreatectomy"[mh] OR ((("digestive system" OR hepatic*[tiab] OR hepato*[tiab] OR hepatob*[tiab] OR hepatoc*[tiab] OR intrahepat*[tiab] OR gastrointestin*[tiab] OR liver OR pancreas*[tiab] OR pancreat*[tiab] OR hpb OR billiar* [tiab]) AND (tumor*[tiab] OR tumour OR neoplas*[tiab] OR cancer OR carcino*[tiab] OR adenocarcino*[tiab] OR resect*

[tiab])) OR hepatectom*[tiab] OR pancreatectom*[tiab] OR whipple OR pancreaticoduodenectom*[tiab] OR cholangiocarcinom*[tiab])) AND ("Surgical Procedures, Operative"[mh] OR "surgery"[sh] OR (surg*[tiab] OR operation*[tiab] OR operative*[tiab] OR resect*[tiab] OR hepatectom*[tiab] OR pancreatectom*[tiab] OR whipple OR pancreaticoduodenectom* [tiab])) NOT (animals[mh] NOT humans[mh]) AND publisher [sb]

Google scholar

nomogram|nomograms "liver|pancreas|pancreatic|hepatic|hpb surgery|resection"|hepatectomy|hepatectomies|pancreatectomy| pancreaticoduodenectomy|pancreatectomies|pancreaticoduodenectomies|whipple.

Appendix A2. Included models

Based on Statistical Analysis

- 1. CLIP. A new prognostic system for hepatocellular carcinoma: a retrospective study of 435 patients: the Cancer of the Liver Italian Program (CLIP) investigators. Hepatology 1998; 28(3): 751-5.
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Consensus Based Models

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Appendix A3. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10. 1016/j.hpb.2020.07.007.