

British Journal of Cancer (2016) 115, 281–289 | doi: 10.1038/bjc.2016.212

Keywords: prognostic score; nomogram; overall survival; locally advanced pancreatic cancer; chemotherapy

# Prognostic nomogram and score to predict overall survival in locally advanced untreated pancreatic cancer (PROLAP)

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**Background:** The management of locally advanced pancreatic cancer (LAPC) patients remains controversial. Better discrimination for overall survival (OS) at diagnosis is needed. We address this issue by developing and validating a prognostic nomogram and a score for OS in LAPC (PROLAP).

**Methods:** Analyses were derived from 442 LAPC patients enrolled in the LAP07 trial. The prognostic ability of 30 baseline parameters was evaluated using univariate and multivariate Cox regression analyses. Performance assessment and internal validation of the final model were done with Harrell's C-index, calibration plot and bootstrap sample procedures. On the basis of the final model, a prognostic nomogram and a score were developed, and externally validated in 106 consecutive LAPC patients treated in Besançon Hospital, France.

**Results:** Age, pain, tumour size, albumin and CA 19-9 were independent prognostic factors for OS. The final model had good calibration, acceptable discrimination (C-index = 0.60) and robust internal validity. The PROLAP score has the potential to delineate three different prognosis groups with median OS of 15.4, 11.7 and 8.5 months (log-rank P < 0.0001). The score ability to discriminate OS was externally confirmed in 63 (59%) patients with complete clinical data derived from a data set of 106 consecutive LAPC patients; median OS of 18.3, 14.1 and 7.6 months for the three groups (log-rank P < 0.0001).

**Conclusions:** The PROLAP nomogram and score can accurately predict OS before initiation of induction chemotherapy in LAPC-untreated patients. They may help to optimise clinical trials design and might offer the opportunity to define risk-adapted strategies for LAPC management in the future.

Received 18 February 2016; revised 15 June 2016; accepted 20 June 2016; published online 12 July 2016

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Pancreatic cancer (PC) is one of the leading causes of cancer-related mortality worldwide, with 5-year relative survival of only 8%. The predicted death rates have progressively increased over the past years (Siegel  $et\ al$ , 2016). This unfavourable trend emphasises the importance of giving priority to research in PC prevention and treatment. Number of deaths by PC in 2014 in the European Union (EU) has been estimated to 82 300 cases equally distributed in men and women. By analogy, a similar prediction has been reported for women with breast cancer ( $N=89\,300$ ) (Malvezzi  $et\ al$ , 2014).

Most PCs are unresectable due to the presence of either distant metastases or locoregional metastases, including vascular invasion (locally advanced PC: LAPC). At the time of diagnosis, up to 35% of patients with PC present with locally advanced disease (Philip, 2011). The management of those patients is still controversial, specifically the role of radiotherapy remains uncertain (Huguet *et al*, 2007; Krishnan *et al*, 2007; Chauffert *et al*, 2008; Loehrer *et al*, 2011; Philip, 2011; Hajj and Goodman, 2015).

Currently, there is a lack of staging system and consensus regarding specific risk profile for overall survival (OS) in LAPC, which can lead to confusion in research strategies development and potentially inappropriate management of patients. Given this aspect and the current interest in precision medicine, there is a need for prognostic tools to optimise patients' selection for appropriate treatment therapy in order to achieve more personalised management. Specifically, more accurate prediction of OS at diagnosis may help to ensure well-balanced arms in clinical trials and to a better management patient care in the future. Ultimately, such a tool may lead to improve patient's health-related quality of life (HRQoL), chemotherapy (CT) cost-effectiveness ratio, and design of future clinical trials.

Nomograms have been increasingly used for survival prediction in different cancer settings as an alternative to traditional TNM staging system or a new standard (Balachandran *et al*, 2015). Unfortunately, no single study evaluating a nomogram for survival prediction in LAPC patients is available.

We aimed to develop and validate a new prognosis model, nomogram and score for OS using a broad spectrum of parameters currently available at baseline. This model was developed based on a large cohort of LAPC patients enrolled in the phase III LAP07 trial and validated in patients encountered in daily clinical practice.

# **PATIENTS AND METHODS**

**Patients.** The development cohort was obtained from an international, multicentre, randomised phase III LAP07 trial (ClinicalTrials.gov NCT00634725). The complete design and trial procedures of the LAP07 study was previously described (Hammel *et al*, 2016). Briefly, the LAP07 study assessed whether chemoradiotherapy

(CRT) administered to LAPC patients whose tumour has been controlled after 4 months of gemcitabine alone or plus erlotinib induction CT increases OS compared with continuation of the same CT. In this trial, CRT did not increase OS compared with the continuation of CT alone. Demographics, cancer history, clinicopathological, biological and radiological parameters at baseline as well as treatment outcomes were collected.

The external validation cohort included 106 consecutive LAPC patients treated at the University Hospital of Besançon, France between January 2003 and December 2013.

Main eligibility and exclusion criteria along with treatment and procedures for the development and validation cohorts are specified in Supplementary Appendix A1.

**Follow-up.** In the development cohort, patients were observed at 2, 4, 7, 9 and 11 months and every 2 months thereafter. At each follow-up visit, a detailed clinical history and a complete physical

examination were carried out. Database was locked on 23 February 2014.

In the validation cohort, patients were treated using standard clinical protocols. A radiological evaluation was performed every 3 months. Database was locked on 13 November 2015.

**Statistical analysis.** The primary analysis was performed on the LAP07 intent to treat population. Mean (s.d.) values and frequency (percentage) were provided for the description of continuous and categorical variables, respectively. Means and proportions were compared using Student's t-test and  $\chi^2$ -test (or Fisher's exact test, if appropriate), respectively.

In the development cohort, OS was calculated from the date of study randomisation to the date of death from any cause. Patients last known to be alive were censored at the time of their last follow-up assessment (Bonnetain *et al*, 2014). In the external validation cohort, the starting point for OS was the date of diagnosis of LAPC. OS was estimated using the Kaplan–Meier method and described using median or rate at specific time points with 95% confidence intervals (95% CI). Follow-up was calculated using a reverse Kaplan–Meier estimation when feasible (Schemper and Smith, 1996).

Cox-proportional-hazard models were performed to estimate the hazard ratio (HR) and 95% CI for factors associated with OS. The association of the baseline parameters with OS was first assessed using univariate Cox analyses, and then those with P < 0.10 were entered into a final multivariate Cox regression model. Significantly skewed continuous variables, such as neutrophil count, total bilirubin, alkaline phosphatase, aspartate transaminase, alanine aminotransaminase, lactate dehydrogenase, albumin and cancer antigen 19.9 (CA 19-9), were normalised by logarithmic transformation. Hazard proportionality was checked by plotting log-minus-log survival curves and by the cumulative martingale process plots. Log-linearity assumption for continuous variables was also checked graphically by making a categorical variable. For continuous variables involved in the final multivariate model, a fractional polynomial method was applied to validate the transformation used and to assess the relationship between predictors and survival. In the absence of clinical hypothesis and/or documentation in the literature, no interaction term was considered in the model construction.

Accuracy of the final model was verified regarding two parameters: discrimination and calibration. The predictive value and the discrimination ability (that is, the ability to separate patients with different prognosis) of the final model were evaluated with the Harrell's concordance index (C-index) (Harrell *et al*, 1996). One thousand random samples of the population were used to derive 95% CI for the C-statistic. Calibration and goodness of fit refers to the ability to provide unbiased survival predictions in groups of similar patients. These were assessed by visual examination of calibration plot and tested with an extension of the Hosmer–Lemeshow test for survival data. Internal validation of the final multivariate model was performed with a bootstrap sample procedure.

The final model was used to derive a nomogram allowing the estimation of median and individual post-diagnosis OS probabilities at 6, 12, 24 and 48 months. For estimation at population level, a prognostic score was constructed and weighted with  $\beta$ -coefficients estimations in the final model, and normalised between 0 and 5. To give a reasonable spread of risk, we chose to work on two and three prognostic risk groups. In such way, different cut points for the risk score from the development set were explored. These were based on the optimal cut point (Hothorn and Lausen, 2003) and Cox's (Cox, 1957) methods for the two- and three-risk groups approach, respectively. Median and tertiles were also considered. The discrimination abilities of the different prognostic scores produced were assessed with the Harrell's concordance index (C-index) by considering risk groups classification.

Patients' baseline key characteristics were compared between prognostic risk groups using Fisher-exact test and the Kruskal-Walis test for categorical and quantitative parameters, respectively.

To explore the performance of the final model, sensitivity analyses were performed by forcing the treatment assigned at first randomisation (gemcitabine  $\nu s$  gemcitabine plus erlotinib) to enter into the model and by including baseline histological grade and systolic blood pressure; two parameters that were not initially selected in the multivariate analysis process due to their high rate of missing data. To assess potential bias arising from missing data for parameters involved in the multivariate final model on their significance (P-value) and estimates ( $\beta$  and its standard error), a multiple imputation procedure with a Markov chain Monte Carlo method was performed using SAS MI and MIANALYZE procedure.

The final multivariate and the prognostic score discrimination abilities were confirmed in an external validation cohort and evaluated with the Harrell's concordance index (C-index) with survival predictions from the model and from risk groups classification, respectively. To identify risk groups and to determine their survival profile, the same development cohort-derived risk predictive algorithm was applied.

All analyses were performed using SAS version 9.3 (SAS Institute) and R software version 2.15.2 (R Development Core Team; http://www.r-project.org). Values of P < 0.05 were considered statistically significant and all tests were two-sided. Details on the interpretation of important statistical concepts are given in Supplementary Appendix A2.

# **RESULTS**

Patient characteristics. A total of 442 LAPC patients treated in the LAP07 trial between February 2008 and December 2011 formed the development cohort. The median follow-up time was 34.3 months (95% CI, 27.6–43.7). Overall, 106 LAPC patients treated in the University Hospital of Besançon between January 2003 and December 2013 were included in the external validation cohort. Patient baseline characteristics according to the cohort set are summarised in Table 1. As expected, given its daily clinical nature the validation cohort differed from the LAP07 population with respect to, age, histological grade, WHO-PS, tumour size and treatment regimens.

	Development set cohort– LAP07 trial (N = 442)	External validation set cohort-University Hospital of Besançon cohort (N=106)	Р	
Age, years <sup>a</sup>	63.5 ± 9.6	67.1 ± 10.2	0.0007	
Gender, N (%) Male Female	228 (52%) 214 (48%)	57 (54%) 49 (46%)	0.7456	
Localisation, N (%) Head/head and body Other (body and/or tail) Unknown	302 (69%) 138 (31%) 2	71 (70%) 31 (30%) 4	0.9059	
Grading, N (%) Well differentiated Moderately differentiated Poorly differentiated Missing	107 (48%) 75 (34%) 41 (18%) 219	9 (26%) 17 (50%) 8 (24%) 72	0.05556	
Lymph nodes, N (%) Yes No Missing	179 (41%) 258 (59%) 5	_ _ _ _		
WHO-PS, N (%) 0 1 2 3 Missing	197 (46%) 203 (47%) 31 (7%) 0 (0%) 11	31 (30%) 59 (56%) 14 (13%) 1(1%) 1	0.004892	
RECIST tumour size (mm) <sup>a</sup> Missing	44.0 ± 18.0 20	38.3 ± 14.7	0.00385	
RECIST tumour size (mm), N (%)  <30 30–50  ≥50  Missing	66 (16%) 226 (54%) 130 (31%) 20	22 (23%) 56 (58%) 19 (20%) 9	0.04676	
Vascular invasion, N (%) Superior mesenteric artery Coeliac trunk Hepatic artery No Missing	144 (33%) 188 (43%) 25 (6%) 79 (18%) 6	- - - - -		
Median follow-up time, months (95% CI)	34.3 (27.6–43.7)	All patients were followed until death (maximum time observed = 76.6) except five patients alive with a median follow-up equal to 10		

Abbreviations: CI = confidence interval; NA = not available; PS = performance status; WHO = World Health Organization. Bold values refer to significant P-values reflecting statistical significant difference for the parameter considered between the 2 cohorts.

<sup>a</sup>Plus-minus values are means ± s.d.

**Prognostic factors for OS.** Only 8 out of 30 evaluated baseline parameters were associated with OS in the univariate Cox analyses with a P < 0.1. These were age, histological grade, performance status (the World Health Organization scale), systolic blood pressure, pain, albumin level, tumour size and CA 19-9 (Table 2). The multivariate Cox analysis (N = 358) showed five

independent risk factors for OS: age; pain; albumin; tumour size; and CA 19-9 (Table 3).

Performance assessment and internal validation of the final model. The multivariate model exhibited acceptable discrimination ability (C-index 0.60; 95% bootstrap percentile CI, 0.57–0.64)

Demographic parameters	·	Number of	Number of			
Age at Inclusion, years				HR	95% CI	Р
Section   Comparison   Compar	Demographic parameters					
Maile	Age at inclusion, years	442	379	1.013	1.003–1.024	0.0148
Female   214	Sex					
Pathological parameters  Primary tumour site  Head-head and body  302 260 1  Head-head and body  302 260 1  138 117 0.951 0.764-1.183 0.6519  Linkinown  2 117 0.951 0.764-1.183 0.6519  Linkinown  1 2 117 0.951 0.764-1.183 0.6519  Linkinown  2 1 1.106 0.799-1.530 —  Moderately differentiated  75 62 1.106 0.799-1.530 —  Moderately differentiated  75 62 1.106 0.799-1.530 —  Proorly differentiated  75 62 1.106 0.799-1.530 —  Moderately differentiated  75 92 2 1					— 0.748_1.120	— 0 3897
Primary turour site    Head-head and body   302   260   1		214	101	0.713	0.740-1.120	0.3077
Head-head and body						<u> </u>
Histological grade		302	260	1		
Histological grade  Well differentiated			117	0.951	0.764–1.183	0.6519
Well differentiated		2				
Moderately differentiated		407	00	4		
Poorly differentiated   41					0 700_1 530	_
Regional lymph node invasion   No						0.0021
No				-		
Yes         179         152         0.954         0.776-1.174         0.6584           Arterial involvement         10         7         1         —         —           Yes         430         370         0.635         0.299-1.345         0.2352           Missing         2         —         —         —         —         —           2 Inclaid parameters         PSFWHO)         —	Regional lymph node invasion					
Missing   S					— 0 77/ 1 174	0 (504
Arterial involvement No 10 7 1 7 Yes 430 370 0.635 0.299-1.345 0.2352 Missing 2					U.//6-1.1/4 —	
No						
Missing         2         —         —         —         —           Clinical parameters           SPS (WHO)         10         197         162         1         — <td></td> <td>10</td> <td>7</td> <td>1</td> <td>_</td> <td>_</td>		10	7	1	_	_
PS (WHO)			370	0.635	0.299–1.345	0.2352
PS (WHO)  0		2		_		_
0 197 162 1	•					
1 203 179 1.252 1.012-1.550 — 2 31 30 1.731 1.171-2.558 0.0092 Missing 11 — — — — — — — — — Systolic blood pressure, mmHg 252 222 1.011 1.003 to 1.019 0.0048 Diastolic blood pressure, mmHg 260 222 1.006 0.997-1.015 0.2176  Diarrhoea  No 408 351 1 — — — — — —  Yes 31 27 0.763 0.516-1.129 0.1763  Missing 3 — — — — — — — — —  Pain No 186 155 1 — — — — —  Pain No 186 155 1 — — — — —  Yes 253 223 1.199 0.976-1.472 0.0834  Missing 3 — — — — — — — — —  Jaundice  No 387 334 1 — — — — — —  Sady Mass Index, kg m - 2 434 372 0.993 0.968-1.019 0.5831  Body Mass Index, kg m - 2  Noranal weight (18.5-25) 249 216 1 — — — —  Noranal weight (18.5-25) 249 216 1 — — — —  Noranal weight (18.5-25) 249 216 1 — — — —  Noranal weight (18.5-25) 37 32 1.041 0.718-1.510 0.0982  Missing 8 7 0.994 0.632-1.409 0.982  Brecentage of weight loss 385 329 1.009 0.993-1.025 0.2653  Biological parameters  Haematological function  Neutrophils, mm² (log-value) 437 374 1.473 0.818-2.654 0.1973 1.481 co.1975  Neutrophils, mm² (log-value) 437 374 1.473 0.818-2.654 0.1973 1.481 co.1976.		107	162	1		
Missing     11     —     —     —     —       Systolic blood pressure, mmHg     252     222     1.011     1.003 to 1.019     0.0048       Diardicel blood pressure, mmHg     260     222     1.006     0.997-1.015     0.2176       Diardicel Blood pressure, mmHg     260     222     1.006     0.997-1.015     0.2176       No     408     351     1     —     —       Yes     31     27     0.763     0.516-1.129     0.1763       Missing     3     —     —     —     —       Pain     No     186     155     1     —     —       Yes     253     223     1.199     0.976-1.472     0.0834       Missing     3     —     —     —     —       Jaurdice     Jaurdice     Jaurdice     Jaurdice     Jaurdice     Jaurdice     Jaurdice       No     387     334     1     —     —     —       Body Mass Index, kgm²     4     —     —     —     —       Body Mass Index, kgm²     434     372     0.993     0.968-1.019     0.5831       Body mass index, kgm²²     434     372     0.993     0.968-1.019     0.5831       Body mass					1.012–1.550	_
Systolic blood pressure, mmHg  252  222  1.011  1.003 to 1.019  0.0048  Diastolic blood pressure, mmHg  260  222  1.006  0.997-1.015  0.2176  0.2176  Diarrhoea  No  408  351  1  ——————————————————————————————	2		30	1.731	1.171–2.558	0.0092
Diastolic blood pressure, mmHg   260   222   1.006   0.997-1.015   0.2176     Diarrhoea	Missing	11	_	_	_	_
Diarrhoea	Systolic blood pressure, mmHg	252	222	1.011	1.003 to 1.019	0.0048
No     408     351     1     —     —       Yes     31     27     0.763     0.516-1.129     0.1763       Missing     3     —     —     —     —       Pain     No     186     155     1     —     —       Yes     253     223     1.199     0.976-1.472     0.0834       Missing     3     —     —     —     —       Jaundice     —     —     —     —     —       No     387     334     1     —     —       Yes     51     44     0.971     0.709-1.331     0.8550       Missing     4     —     —     —     —       Body Mass Index, kg m⁻²     434     372     0.993     0.968-1.019     0.5831       Body mass index, kg m⁻²     249     216     1     1     0.078-1.510     0.044     0.078-1.025     0.1944     0.632-1.409     0.9822       Normal weight (18.5-25)     249     216     1     0.979-1.025     0.2653       Percentage of weight loss     38     32     1.041     0.718-1.510     0.632-1.409     0.9822       Missing     8     27     0.944     0.632-1.409     0.993-1.025     0.2653<	Diastolic blood pressure, mmHg	260	222	1.006	0.997–1.015	0.2176
Yes     31     27     0.763     0.516-1.129     0.1763       Missing     3     -     -     -     -     -       Pain     186     155     1     -     -     -       Yes     253     223     1.199     0.976-1.472     0.0834       Missing     3     -     -     -     -     -     -       Jaundice     387     334     1     -	Diarrhoea					
Missing     3     —     —     —     —       Pain     No     186     155     1     —     —       Yes     253     223     1.199     0.976-1.472     0.0834       Missing     3     —     —     —     —     —       Jaundice     —     —     —     —     —     —     —       No     387     334     1     —     —     —     —       Yes     51     44     0.971     0.709-1.331     0.8550       Missing     4     —     —     —     —     —     —       Body Mass Index, kg m <sup>-2</sup> 434     372     0.993     0.968-1.019     0.5831       Body mass index, kg m <sup>-2</sup> 249     216     1     1     1       Underweight (18.5-25)     249     216     1     0.718-1.510     0.718-1.510       Overweight (25-30)     114     97     0.979     0.770-1.244     0.632-1.409     0.9822       Wissing     8     3     2     1.009     0.993-1.025     0.2653       Percentage of weight loss     385     329     1.009     0.993-1.025     0.2653       Biological parameters       Haemaglobin, g dl <sup>-1</sup> <					— 0 E14 1 120	0 1742
Pain  No  186  186  155  1  — — — — — — — — — — — — — — —					U.310=1.127 —	
No     186     155     1     —     —       Yes     253     223     1.199     0.976-1.472     0.0834       Missing     3     —     —     —     —       Jaundice     —     —     —     —       No     387     334     1     —     —       Yes     51     44     0.971     0.709-1.331     0.8550       Missing     4     —     —     —     —     —       Body Mass Index, kg m⁻²     —     —     —     —     —     —       Normal weight (18.5-25)     249     216     1     —     —     —       Underweight <18.5						
Missing     3     —     —     —     —       Jaundice       No     387     334     1     —     —       Yes     51     44     0.971     0.709-1.331     0.8550       Missing     4     —     —     —     —       Body Mass Index, kgm <sup>-2</sup> 434     372     0.993     0.968-1.019     0.5831       Body mass index, kgm <sup>-2</sup> —     —     —     —     —     —       Normal weight (18.5-25)     249     216     1     —     —     —       Normal weight (25-30)     114     97     0.979     0.770-1.244     O.718-1.510     Overweight (25-30)     114     97     0.979     0.770-1.244     O.632-1.409     0.9822       Missing     8     —     —     —     —     0.9822       Missing     8     —     —     0.993-1.025     0.2653       Biological parameters       Haematological function     Neutrophils, mm³ (log-value)     437     374     1.473     0.818-2.654     0.1973       Haemoglobin, gdl <sup>-1</sup> 442     379     0.954     0.887-1.025     0.1976		186	155	1	_	_
Jaundice			223	1.199	0.976–1.472	0.0834
No     387     334     1     —     —       Yes     51     44     0.971     0.709-1.331     0.8550       Missing     4     —     —     —     —       Body Mass Index, kg m⁻²     434     372     0.993     0.968-1.019     0.5831       Body mass index, kg m⁻²     2     249     216     1       Normal weight (18.5-25)     249     216     1       Underweight <18.5		3	_	_	_	_
Yes     51     44     0.971     0.709-1.331     0.8550       Missing     4     -     -     -     -     -       Body Mass Index, kg m <sup>-2</sup> 434     372     0.993     0.968-1.019     0.5831       Body mass index, kg m <sup>-2</sup> 2     249     216     1       Normal weight (18.5-25)     249     216     1       Underweight <18.5						
Missing     4     —     —     —     —     —       Body Mass Index, kg m <sup>-2</sup> 434     372     0.993     0.968-1.019     0.5831       Body mass index, kg m <sup>-2</sup> 28     37     32     1.041     0.718-1.510       Underweight (18.5-25)     249     216     1     0.718-1.510       Overweight (25-30)     114     97     0.979     0.770-1.244       Obese ≥ 30     34     27     0.944     0.632-1.409     0.9822       Missing     8     27     0.944     0.632-1.409     0.9822       Percentage of weight loss     385     329     1.009     0.993-1.025     0.2653       Biological parameters       Haematological function       Neutrophils, mm³ (log-value)     437     374     1.473     0.818-2.654     0.1973       Haemoglobin, gdl⁻¹     442     379     0.954     0.887-1.025     0.1976					0.700 1.221	0.0550
Body Mass Index, kg m <sup>-2</sup> Body mass index, kg m <sup>-2</sup> Normal weight (18.5–25)  Underweight <18.5  Overweight (25–30)  Obese ≥ 30  Missing  Percentage of weight loss  Biological parameters  Haematological function  Neutrophils, mm³ (log-value)  Neutrophils, mm³ (log-value)  Haemoglobin, g dl −¹  Variable Mass Index, kg m <sup>-2</sup> 249  216  1  1  0.718–1.510  0.718–1.510  0.770–1.244  0.977  0.979  0.770–1.244  0.9822  0.9822  1.009  0.993–1.025  0.2653				U.97 I	U.709=1.331 —	U.055U
Body mass index, kg m <sup>-2</sup> 249     216     1       Normal weight (18.5–25)     249     216     1       Underweight <18.5			372	0.993	0.968–1.019	0.5831
Normal weight (18.5–25)     249     216     1       Underweight <18.5			-	<del>-</del>		
Underweight <18.5	Normal weight (18.5–25)	249	216	1		
Obese≥30 Missing     34 27 0.944 0.632–1.409 0.9822       Missing     8       Percentage of weight loss     385 329 1.009 0.993–1.025 0.2653       Biological parameters       Haematological function Neutrophils, mm³ (log-value)       Haemoglobin, g dl⁻¹     437 374 1.473 0.818–2.654 0.1973 0.954 0.887–1.025 0.1976	Underweight < 18.5					
Missing         8						0.0000
Percentage of weight loss 385 329 1.009 0.993–1.025 0.2653  Biological parameters  Haematological function  Neutrophils, mm³ (log-value) 437 374 1.473 0.818–2.654 0.1973  Haemoglobin, g dl -1 442 379 0.954 0.887–1.025 0.1976			21	0.944	0.032-1.409	0.9822
Biological parameters  Haematological function  Neutrophils, mm³ (log-value)  Haemoglobin, g dl <sup>-1</sup> Neutrophils, description  Neutrophils, mm³ (log-value)  437  437  374  1.473  0.818–2.654  0.1973  0.954  0.887–1.025  0.1976			329	1.009	0.993-1.025	0.2653
Haematological function       Neutrophils, mm³ (log-value)     437     374     1.473     0.818–2.654     0.1973       Haemoglobin, g dl⁻¹     442     379     0.954     0.887–1.025     0.1976						
Neutrophils, mm³ (log-value)         437         374         1.473         0.818-2.654         0.1973           Haemoglobin, g dl⁻¹         442         379         0.954         0.887-1.025         0.1976	<u> </u>					
Haemoglobin, g dl <sup>-1</sup> 442 379 0.954 0.887–1.025 0.1976	Neutrophils, mm <sup>3</sup> (log-value)	437	374	1.473	0.818–2.654	0.1973
Platelets, mm <sup>3</sup> 438 376 1.000 1.000—1.000 0.1442	Haemoglobin, g dl <sup>-1</sup>	442	379	0.954	0.887-1.025	0.1976
	Platelets, mm <sup>3</sup>					

	Number of	Number of			
	patients	events	HR	95% CI	P
Biochemical					
Creatinine, $\mu$ mol I <sup>-1</sup>	440	377	0.996	0.990-1.002	0.2153
Creatinine clearance rate, ml min - 1	313	263	1.000	0.996-1.005	0.9169
Potassium, mmol I <sup>- 1</sup>	422	363	0.985	0.784-1.237	0.8950
Total bilirubin, $\mu$ mol I <sup>-1</sup> (log-value)	440	377	1.028	0.769-1.375	0.8517
Alkaline phosphatase, UII <sup>-1</sup> (log-value)	432	371	1.147	0.789-1.667	0.4727
Aspartate transaminase, UII <sup>-1</sup> (log-value)	438	375	1.297	0.832-2.021	0.2510
Alanine aminotransferase, UII <sup>-1</sup> (log-value)	436	373	0.866	0.623-1.205	0.3930
Lactate dehydrogenase, UII <sup>-1</sup> (log-value)	313	268	1.089	0.599-1.983	0.7792
Albumin, g l <sup>-1</sup>	393	336	0.963	0.944-0.982	0.0002
Proteinuria, g l <sup>-1</sup>	313	272	0.988	0.968-1.007	0.2152
Hypercalcemia, mmol I <sup>-1</sup>	347	301	1.885	0.755-4.707	0.1748
CA 19-9, UI (log-value)	411	359	1.171	1.057–1.296	0.0025
Radiological parameters					
Tumour size, mm	422	362	1.008	1.002–1.015	0.0081

Abbreviations: CI = confidence interval; HR = hazard ratio; PS = performance status; WHO = World Health Organization. Bold values refer to P-values < 0.1 highlighting parameters involved in the final multivariate construction as described in the statistical section.

	Number of patients	Number of death	HR	95% CI	P	Internal validation BCA HR 95%	Max scores in nomogram
Age at diagnosis, years	358	307	1.013	1.000-1.025	0.0478	1.000-1.025	43
Pain							
No Yes	155 203	130 177	1 1.292	- 1.023–1.632	0.0317	1.046–1.657	16
Albumin, g l <sup>-1</sup>	358	307	0.963	0.942-0.984	0.0006	0.942-0.988	96
Tumour size, mm	358	307	1.008	1.001–1.015	0.0214	1.000–1.016	100
CA 19-9, UI (log-value)	358	307	1.172	1.047-1.311	0.0056	1.039–1.306	80

and a good calibration at 6, 12, 24 and 48 months (P = 0.99, P = 0.55, P = 0.30, and P = 0.08, respectively). The calibration plots showed an optimal agreement between model prediction and actual observation for predicting OS probability at 6, 12, 24, and 48 months (Figure 1).

In the internal validation, uncertainties around HR measured with the bootstrapping procedure (Table 3) reflected the robustness of the final model.

**Sensitivity analyses.** In the sensitivity analysis, the performance of the final model was investigated by forcing the allocated treatment (gemcitabine *vs* gemcitabine plus erlotinib). Associations remained unchanged (Supplementary Appendix Table A1A).

After adjustment of the final model for histological grading and systolic blood pressure, main associations of the final multivariate model remained unchanged except for CA 19-9 (Supplementary Appendix Table A1B).

The final multivariate model was based on 358 (81.0%) patients (complete-subject analysis) for whom the five parameters were available. A multiple imputation analysis based on 1000 imputed data sets for all the variables provided similar results to the complete-subject analysis in term of significance for the association (P-value) and for coefficient estimations ( $\beta$  and SE) (Supplementary Appendix Table A1C).

**Prognostic nomogram for OS.** Nomogram integrating all significant independent factors for OS was built (Figure 2). An illustration and details on the nomogram development are provided in Supplementary Appendix A3.

Prognostic score for death-risk stratification. A PROLAP (PRognostic score for Overall survival in LAPC) score ranging from 0 to 5 based on the final model was calculated for each patient. All factors included in the score were weighted according to the  $\beta$ -parameter

estimation issued from the final Cox model. The contribution of each individual factor was summed to generate a raw score that was finally applied to normalisation between 0 and 5. This score construction and equation are provided as Supplementary Appendix A3.

On the basis of an optimal cut point determined by Hothorn and Lausen method (Supplementary Appendix Figure A1) patients were categorised into two-risk groups with significantly different prognostic profiles (Figure 3A): a low-risk group (N=242, score < 2.455) and a high-risk group (N=116, score  $\geq 2.455$ , HR = 2.01 95% CI, 1.58–2.56; P<0.0001). The median OS was 14.7 and 9.4 months for the low-risk group and the high-risk group, respectively (P<0.0001).

Considering that the prognostic score assumes a normal distribution (mean = 2.27; s.d. = 0.39) for the three-risk groups approach, Cox demonstrated that the loss of information from grouping would be minimised by selecting cut points equal to 2.291 and 2.720. Such grouping achieved a clear separation of the Kaplan–Meier curves (Figure 3B). The median OS was 15.3, 11.7 and 8.5 months for the low, intermediate and the high-risk groups, respectively (P < 0.0001).

Results for classification of patient's into two- and three-risk groups related to the median and tertiles approach are provided in Supplementary Appendix Figure A2. These, however, were not selected as the main result given the low efficiency of this approach.

Baseline characteristics of patients according to the risk groups. For the two-risk group approach, in the high-risk group, 75% of patients presented with pain, were older, with moderate albumin level and had tumour of large size. In contrast, in the low-risk group, 48% of patients reported pain, were younger, had normal albumin levels and had tumour of small size (Supplementary Appendix Table A1A). A similar trend across groups was observed in the three-risk groups approach (Supplementary Appendix Table A1B).

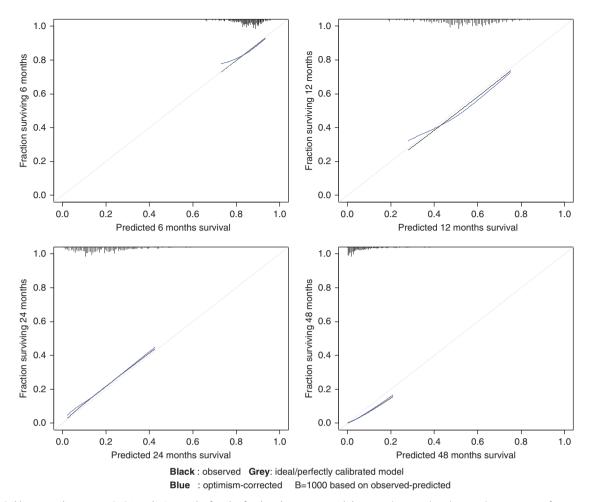


Figure 1. Calibration plots at 6, 12, 24 and 48 months for the final multivariate model. Vertical axis is the observed proportion of patients surviving at time of interest.

Agreement between nomogram prediction and the PROLAP score. Given that the prognostic nomogram and score were built from the same multivariate final model parameters, they can be connected. Characterisation of risk groups with the total number of points derived from the nomogram is provided in the Kaplan–Meir curves (Figure 3A and B).

Predictive value of treatments on OS according to the risk groups. In the two- and three-risk group approaches, there were no differential effects on OS of the gemcitabine-erlotinib combination across groups. In addition, no significant OS difference was observed in favour of CRT over CT across groups.

Interestingly, a total of 121 (68%) low-risk, 85 (62%) intermediate-risk and 19 (44%) high-risk patients reached the second randomisation (P = 0.0027). A similar significant trend was also observed in the two-risk group analysis. Detailed results are provided in Supplementary Appendix A4.

Validation of the discriminatory ability of the PROLAP score. A total of 63 (59%) of patients from the external validation cohort had all the information required to be eligible for the score calculation using five baseline parameters (pain, CA 19-9, albumin, tumour size and age). Similar characteristics at diagnosis and outcomes were observed between eligible and non-eligible patients (Supplementary Appendix Table A2).

Overall, the final multivariate model identified in the development set exhibited a better discrimination ability in the validation cohort (C-index 0.68; 95% bootstrap percentile CI, 0.59–0.77).

In the two-risk group approach, the discrimination ability of the risk score algorithm developed in the main analysis was externally confirmed, with median OS estimated to 17.1 months for the low-risk group and 9.2 months for the high-risk group (HR = 2.3; 95% CI, 1.3 to 4.2; log-rank P = 0.003; Figure 3C) and with a better C-index estimation (0.61; 95% CI 0.54 to 0.68) than in the development cohort.

Similarly in the three-risk group approach, the discrimination ability of the risk score was externally confirmed, with median OS estimated to 18.3 months for the low-risk group, 14.1 months for the intermediate-risk group and 7.6 months for the high-risk group (log-rank P<0.0001; Figure 3D) and with a better C-index estimation (0.68; 95% CI 0.59–0.76) than in the development cohort.

# **DISCUSSION**

Currently, there is no efficient prognostic staging system that could help to estimate OS at diagnosis in LAPC patients. On the basis of the largest phase III clinical trial of LAPC, we established a novel easy-to-use survival prediction model built on five key parameters (age, albumin, tumour size, CA 19-9 and pain) and provided a prognostic nomogram and score.

Nomograms are an important component of modern medical decision-making (Balachandran *et al*, 2015). The main goal of such staging systems is to provide the most accurate predictions for specified end points. In this way, parameters to consider should be easily available and measurable. The proposed nomogram fulfils these requirements and produces individual survival estimations in LAPC patients. The baseline prognostic score can be considered as a complementary tool for clinical practice by producing a classification

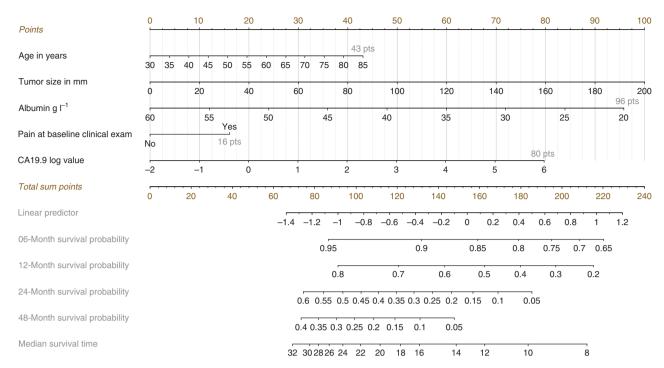


Figure 2. Prognostic nomogram to predict individual overall survival probability in patients with locally advanced pancreatic cancer. Points are assigned for each risk factor by drawing a line upward from the corresponding values to the 'point' line. The total sum of points for four risk factors is plotted on the 'total points' line. A line is drawn down to read the corresponding predictions of 6-, 12-, 24- and 48-month-survival probability and median survival time. For example, a patient with the following characteristics–63 years old (26 points), tumour measurement equal to 105 mm (53 points), albumin at 40.9 g l<sup>-1</sup> (46 points), CA 19-9 at 89 (log-value = 1.95; 39 points) and the presence of pain at baseline clinical exam (16 point) will have a total points of 180, which corresponds to 6-, 12-, 24- and 48-month-survival probabilities of 80% (95% CI 71–86), 40% (95% CI 25–55), 7% (95% CI 2–17) and 1% (95% CI 0–4) and a predicted median survival time of 10.5 months (95% CI 8.75–13.5). An online web-based application smartphone compatible was developed that provides individualised survival estimates from the nomogram: http://www.umqvc.org/en/tool/prolap.html.

of the patients into well-identified death-risk populations. We have developed an open-access web site smartphone compatible to automatically compute the prognostic nomogram and score estimations. (http://www.umqvc.org/en/tool/prolap.html).

The present work revealed a considerable heterogeneity among LAPC patients regarding their OS-risk profiles. The recognition of risk groups with different prognostic outcomes may offer the opportunity to define risk-adapted strategies for LAPC management in the future. Indeed, while our analysis was based on OS, but not on progression-free survival, we accurately identified patients more likely not to be eligible for the second randomisation. Overall, 32% of the low-risk, 38% of the intermediate-risk and 56% of the high-risk patients failed to reach the second randomisation due to progression.

Our study supports the role of the nomogram and/or the PROLAP score as tools to be used both for patient selection and/or for patients' stratification in future clinical trials. These may help to reduce heterogeneity among treatment arms in terms of risk profile and thus better estimate the treatment effect. Indeed, if patients from the risk groups identified are distributed unequally among arms this difference can lead to a distortion in the outcome analysis. It seems therefore reasonable to recommend pre-planned subgroup analyses according to the level of such a score in future trials.

It is worth noting that two of the five factors included in our model, pain and albumin are objective surrogates for measurement of HRQoL (Burris *et al*, 1997). The importance of these parameters in the model and the recognition of HRQoL as an additional prognostic value for OS in metastatic disease (Gourgou-Bourgade *et al*, 2013) and in other tumour types (Diouf *et al*, 2014; Fiteni *et al*, 2016; Paquette *et al*, 2016) suggest that HRQoL needs to be evaluated in the future prognostic models for LAPC.

Our study has several strengths. The score was constructed in the framework of a large international multicentre trial with a broad spectrum of parameters available at diagnosis. Moreover, discrimination, calibration and internal validation underlined satisfactory performance and validity of the model. We built our model in a rigorous methodological framework respecting a recent recommended checklist for nomograms (Balachandran et al, 2015) and providing a transparent reporting of the multivariate model as suggested in the TRIPOD statement (Collins et al, 2015). The internal validation ensured a reliable performance for patients similar to those of the development cohort. Our prognostic score was fully externally replicated in the 'real-world' patients encountered in daily clinical practice: different centres; clinicians; treatments; and periods. This external validation population is quite different to the development set and underlines the robustness of our results in the clinical setting. A validation in a larger cohort of patients will be performed with the International Pancreas Database Program ARCAD metabase, which is currently under development. Finally, the five parameters identified in our study reflect the general condition of the patient and disease activity and therefore provide clinically relevant information in LAPC. These factors are admitted prognostic factors in LAPC patients by clinicians and accordingly enhance the relevance of the tools developed.

The present study has also several limitations. The role of pain status could be further refined by its assessment at diagnosis before administration of analgesic or by documenting whether the patient was receiving opioids or not at the time of assessment. In case of baseline cholestasis, the CA 19-9 level should be better estimated after biliary drainage whenever possible in order to minimise overestimation. Despite the broad spectrum of parameters analysed and the acceptable performance of the score, we recognise

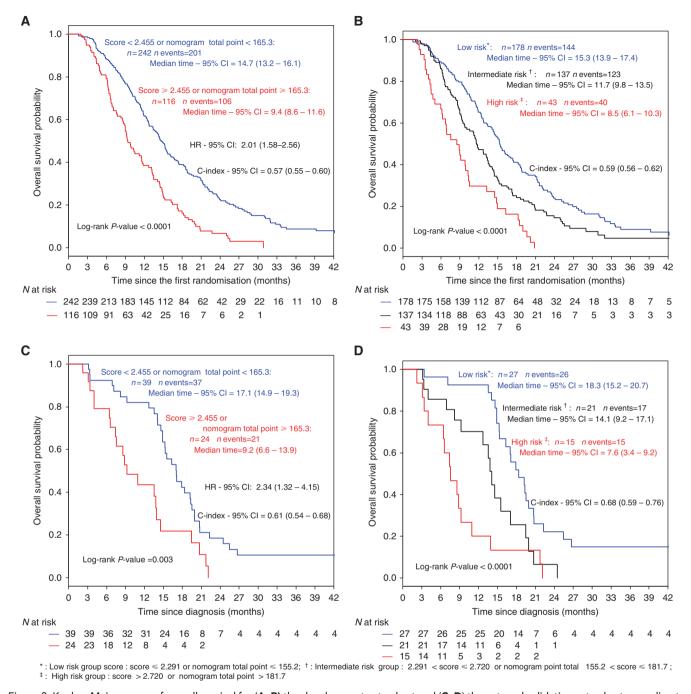


Figure 3. Kaplan–Meier curves of overall survival for (**A**, **B**) the development set cohort and (**C**, **D**) the external validation set cohort according to prognostic score group for the Hothorn & Lausen optimal cut point (**A**, **C**) and Cox's methods (**B**, **D**) for the two- and three-risk groups approach, respectively. An online web-based smartphone compatible application was developed that provides risk-group classification for OS from the PROLAP score: http://www.umqvc.org/en/tool/prolap.html.

that additional potentially relevant variables such as a neutrophil to lymphocyte ratio could not be assessed and merit future consideration (Proctor *et al*, 2012; Stotz *et al*, 2013; Goldstein *et al*, 2015) given that novel biologic insights have recently been validated through the pancreatic genome project (Bailey *et al*, 2016).

In conclusion, we present here a novel OS prediction model based on five key independent prognostic factors at the time of diagnosis. This allowed us to develop and externally validate the first prognostic staging system for OS in LAPC and then to provide functional tools at individual (nomogram) and population (score) levels: http://www.umqvc.org/en/tool/prolap.html. In this study, we revealed considerable heterogeneity among LAPC patients regarding their OS-risk profiles with the recognition of clearly different risk groups.

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The prognostic nomogram and the score proposed may help to optimise clinical trials design and might offer the opportunity to define risk-adapted strategies for LAPC management in the future.

### **ACKNOWLEDGEMENTS**

We thank Florian Limousin (graphic designer and independent web developer in Pearlweb society) for the web development application support. The LAP07 trial was supported in part by a grant from Roche. Data from the INTERNATIONAL INTERGROUP STUDY LAP07 (France: GERCOR, FFCD & FNCLCC (PRODIGE)-SFRO; Belgium: BGDO; Australia: AGITG; Sweden: Nordic Group).

# **CONFLICT OF INTEREST**

PA and TA have received honoraria and consulting fee from Roche. PH has received consulting fee from Roche. FB has received honoraria and research funding from Roche. The remaining authors declare no conflict of interest.

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