VIRTUAL ESMO congress 2020

LBA25

Results from the phase II biomarker driven trial with nivolumab (N) and ipilimumab or VEGFR tyrosine kinase inhibitor (TKI) in naïve metastatic kidney cancer (m-ccRCC) patients (pts): The BIONIKK trial

Y. Vano[1], R.T. Elaidi[2], M. Bennamoun[3], C.M. Chevreau[4], D. Borchiellini[5], D. Pannier[6], D. Maillet[7], M. Gross-Goupil[8], C. Tournigand[9], B. Laguerre[10], P. Barthélémy[11], F. Joly[12], G. Gravis[13], S. Caruso[14], C-M. Sun[15], V. Verkarre[16], W-H. Fridman[15], J. Zucman-Rossi[14], C. Sautès-Fridman[15], S. Oudard[17]

[1] Medical Oncology, Hôpital Européen Georges Pompidou, AP-HP Centre – Université de Paris, Paris, France; Centre de Recherche des Cordeliers, INSERM, Université de Paris, Sorbonne Université, Paris, France, Paris, France, [2] Medical Oncology, ARTIC - Association pour la Recherche de Thérapeutiques Innovantes en Cancérologie; Hôpital Européen Georges Pompidou, AP-HP Centre – Université de Paris, Paris, France, Paris, France, [3] Medical Oncology, Institut Mutualiste Montsouris, Paris, France, [4] Medical Oncology, Institut Universitaire du Cancer -Toulouse- Oncopole, Toulouse, France, [5] Medical Oncology, Centre Anticancer Antoine Lacassagne, Nice, France, [6] Medical Oncology, Centre Oscar Lambret, Lille, France, [7] Medical Oncology, Centre Hospitalier Lyon Sud, Pierre Bénite, France, [8] Medical Oncology, Centre Hospitalier Universitaire de Bordeau - Hôpital Saint-André, Bordeaux, France, [9] Medical Oncology, Centre Hospitalier Universitaire Henri-Mondor, Créteil, France, [10] Medical Oncology, Centre Eugene - Marquis, Rennes, France, [11] Medical Oncology, Hôpitaux Universitaires de Strasbourg/ Institut de Cancérologie Strasbourg Europe, Strasbourg, France, [12] Medical Oncology, Centre François Baclesse, Caen, France, [13] Medical Oncology, Institut Paoli Calmettes, Institut Paoli-Calmettes, Aix-Marseille Université, Marseille, France, [14] Functional Genomics of Solid Tumors, Centre de Recherche des Cordeliers, INSERM, Université de Paris, Sorbonne Université, Paris, France, Paris, France, [15] Inflammation, Complement and Cancer, Centre de Recherche des Cordeliers, INSERM, Université de Paris, Sorbonne Université, Paris, France, [16] Pathology, Hôpital Européen Georges Pompidou, AP-HP Centre – Université de Paris, Paris, France[17] Medical Oncology, Hôpital Européen Georges Pompidou, AP-HP Centre – Université de Paris; Immunotherapy and Anti-Angiogenic Therapy in Oncology, Université de Paris, INSERM, PARCC, Paris, France

Background

Nivolumab-ipilimumab (NI) and sunitinib/pazopanib (TKI) are indicated in m-ccRCC pts with IMDC intermediate/poor and good risk groups, respectively. Based on unsupervised analysis of genes expressed in m-ccRCC, we identified 4 groups (ccrcc1-4) with immune and angiogenic high/low features which could allow to better identify responders to either N, NI or TKI. We here report final analysis results of the BIONIKK trial.

Methods

BIONIKK is an open-label, French multicenter randomized phase 2 trial evaluating N vs. NI vs. TKI in upfront m-ccRCC according to ccrcc1-4 (35-gene signature, CITsig). ccrcc1,4 and ccrcc2,3 pts were randomized to receive N vs. NI and NI vs. TKI respectively. Primary endpoint (PE): objective response rate (ORR, RECIST1.1) per treatment and group. Secondary endpoints: progression-free survival (PFS), overall survival (OS) and tolerability. 150 pts were expected in target cohort (TC). An additional cohort was included to assess inter-platform variability.

Results

From 06/2017 to 07/2019: screened=308, randomized=202 (ALL), evaluable for PE=187 with TC=154. No correlation between ccrcc1-4 and IMDC risk groups (p=0.14). ORR (TC): N=30%, NI=44%, TKI=50%, with differences according to ccrcc1-4 (table1). ORR for NI were comparable across all groups. In ccrcc1 ORR for N was half that of NI while both were comparable in ccrcc4. In ccrcc2, ORR for TKI was as high as for NI. After a median (m) FU of 16 months (mo), mPFS (TC, mo): N=4.9, NI=10.4, TKI=NR, with again observed differences according to ccrcc1-4. OS data are not mature (events:16%). No new safety signal emerged compared to published data. CITsig in frozen and FFPE samples will be presented at the meeting.Table: LBA25

ccrcc groups	1		4		2		3	
	N	NI	N	NI	NI	TKI	NI	TKI
N= (ALL, 202)	*43*	*41*	*18*	*18*	*37*	*36*	*5*	*4*
N= (TC, 154)	*29*	*33*	*14*	*17*	*29*	*26*	*4*	*2*
ORR, % (TC)	21	39	50	53	48	54	25	0
CR	0	6	7	12	14	0	0	0
PR	21	33	43	41	34	54	25	0
SD	34	37	7	18	34	31	50	100
PD	45	24	43	29	18	15	25	0

Conclusions

We demonstrate for the 1st time in m-ccRCC pts that gene expression signatures may enable to enrich response rates. An extensive translational program is planned to identify new biomarkers.

Clinical trial identification

EudraCT: 2016-003099-28; NCT029609. Release date: November 10, 2016.

Legal entity responsible for the study

Association pour la Recherche des Thérapeutiques Innovantes en Cancérologie.

Funding

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Disclosure

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Chevreau: Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Bristol Myers Squibb; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Ipsen; Honoraria (self), Advisory/Consultancy: Novartis. D. Borchiellini: Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Bristol Myers Squibb; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Pfizer; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Novartis; Honoraria (self), Advisory/Consultancy: Ipsen; Travel/Accommodation/Expenses: Roche; Honoraria (self), Advisory/Consultancy: MSD. D. Pannier: Travel/Accommodation/Expenses: Bristol Myers Squibb; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: AstraZeneca; Honoraria (self), Advisory/Consultancy: Bayer; Honoraria (self), Advisory/Consultancy: Janssen. D. Maillet: Honoraria (institution), Advisory/Consultancy, Travel/Accommodation/Expenses: Janssen; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Bristol Myers Squibb; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Pfizer; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: AstraZeneca; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: MSD; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Sanofi; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Novartis; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Ipsen. M. Gross-Goupil: Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Bristol Myers Squibb; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Pfizer; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: MSD; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Roche; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: AstraZeneca; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Novartis; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Ipsen. C. Tournigand: Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Bristol Myers Squibb; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Sanofi; Honoraria (self), Advisory/Consultancy, Travel/Accommodation/Expenses: Novartis; Honoraria (self), Research grant/Funding (self): Roche; Honoraria (self), Research grant/Funding (self): MSD; Honoraria (self), Travel/Accommodation/Expenses: Bayer; Honoraria (self), Research grant/Funding (self): Amgen. B. Laguerre: Honoraria (self): Bristol Myers Squibb; Honoraria (self): Ipsen; Honoraria (self): MSD; Honoraria (self): Roche; Travel/Accommodation/Expenses: Pfizer. P. Barthélémy: Advisory/Consultancy, Travel/Accommodation/Expenses: Bristol Myers Squibb; Advisory/Consultancy, Travel/Accommodation/Expenses: Pfizer; Travel/Accommodation/Expenses: MSD; Advisory/Consultancy, Travel/Accommodation/Expenses: Janssen; Advisory/Consultancy, Travel/Accommodation/Expenses: Sanofi; Advisory/Consultancy, Travel/Accommodation/Expenses: Roche; Advisory/Consultancy: Novartis; Advisory/Consultancy, Travel/Accommodation/Expenses: Ipsen; Advisory/Consultancy, Travel/Accommodation/Expenses: Astellas; Advisory/Consultancy: Eusa Pharma. F. Joly: Honoraria (institution), Advisory/Consultancy, Travel/Accommodation/Expenses: Bristol Myers Squibb; Honoraria (institution), Advisory/Consultancy, Travel/Accommodation/Expenses: Pfizer; Honoraria (institution), Advisory/Consultancy, Travel/Accommodation/Expenses: MSD; Advisory/Consultancy, Travel/Accommodation/Expenses: Roche; Honoraria (institution), Advisory/Consultancy, Travel/Accommodation/Expenses: AstraZeneca; Honoraria (institution), Advisory/Consultancy: Astellas; Honoraria (institution), Advisory/Consultancy, Travel/Accommodation/Expenses: Janssen; Honoraria (institution), Advisory/Consultancy: Bayer; Advisory/Consultancy, Travel/Accommodation/Expenses: GSK; Advisory/Consultancy, Travel/Accommodation/Expenses: Sanofi; Advisory/Consultancy, Travel/Accommodation/Expenses: Ipsen; Advisory/Consultancy: Clovis. G. Gravis: Honoraria (institution), Advisory/Consultancy, Travel/Accommodation/Expenses: Bristol Myers Squibb; Honoraria (institution), Advisory/Consultancy, Travel/Accommodation/Expenses: Pfizer; Honoraria

(institution), Travel/Accommodation/Expenses: MSD; Advisory/Consultancy, Travel/Accommodation/Expenses: AstraZeneca; Honoraria (institution): Astellas; Honoraria (institution), Advisory/Consultancy, Travel/Accommodation/Expenses: Janssen; Honoraria (institution), Advisory/Consultancy: Bayer; Advisory/Consultancy, Travel/Accommodation/Expenses: Sanofi; Advisory/Consultancy, Travel/Accommodation/Expenses: Ipsen. S. Oudard: Honoraria (self): Bristol Myers Squibb; Honoraria (self): Pfizer; Honoraria (self): Novartis; Honoraria (self): Merck; Honoraria (self): Sanofi; Honoraria (self): Astellas; Honoraria (self): Janssen. All other authors have declared no conflicts of interest.