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Germinal immunogenetics as a predictive factor for immunotherapy

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1 **Abstract**

2 Clinical response to checkpoint inhibitors-based (CPIs) therapies can vary among
3 tumor types and between patients. This led to a significant amount of pre-clinical and
4 clinical research into biomarker identification. Biomarkers have been found to cover
5 both the tumor itself and the tumor microenvironment. Entering host-related
6 parameters into the equation should provide a valuable strategy for identifying not
7 only factors predictive of treatment efficacy but also of treatment-related toxicity. It is
8 clear that germline variants can offer efficient and easily-assessable indicators (blood
9 DNA) to enlarge the spectrum of predictive markers for CPI-based treatment. A major
10 issue concerns the real functional significance of the reported single-nucleotide
11 polymorphisms (SNPs) linked to CPI-treatment outcome. Powered calculations
12 should lead to an optimal trade-off between sample size and allele frequency. New
13 molecular technologies and new analytical methods should provide opportunities to
14 bridge the knowledge gap between SNP-CPI treatment associations and the
15 functional impact of these SNPs.

16 **Key words:** Immunotherapy, Check-point inhibitors, predictive factors, germinal
17 immunogenetics

18

19 **1. Immunotherapy-predictive factors-current status in brief**

20 Immunotherapy using the so-called checkpoint inhibitors (CPI) has now reached a
21 high level of clinical evidence in terms of durable antitumor activity and acceptable
22 safety across a spectrum of solid and hematologic malignancies (Ribas and Wolchok
23 2018; Sharma and Allison 2015). The fact that clinical response to CPI-based
24 therapies can vary among tumor types and between patients has given rise to
25 considerable pre-clinical and clinical research into biomarker identification that may
26 allow greater accuracy in predicting response and resistance to treatment, as
27 recently reported in the excellent review article by Havel and colleagues (Havel,
28 Chowell, and Chan 2019). These biomarkers have been found to cover both the
29 tumor itself and the tumor microenvironment. Expression of PD-L1 has been reported
30 to be predictive of response to CPI targeting PD-1 in several cancers (Ansell et al.
31 2015; Garon et al. 2015; Havel, Chowell, and Chan 2019; Reck et al. 2016). As T
32 cells recognize immunogenic antigens, it has been shown that tumor antigenicity,
33 such as tumor mutational burden (TMB) or neoantigen load, could be associated with
34 response to CPI (Cristescu et al. 2018; Rizvi et al. 2015). Linked or not to TMB,
35 tumor microsatellite status has been identified as a predictor of CPI antitumor
36 efficacy with a link between the presence of microsatellite instability and enhanced
37 response rate (Le et al. 2015). Interestingly, and logically, a multifactorial approach
38 combining these biomarkers was recently reported (Ott et al. 2019). The biomarker
39 profile covered both the tumor microenvironment and the tumor characteristics
40 including a T-cell-inflamed gene expression profile (GEP), PD-L1 expression and
41 TMB. However, the study was undertaken retrospectively (Keynote – 028 clinical
42 trial) and covered multiple tumor types. It was shown that high levels of TMB, PD-L1
43 expression and T-cell-inflamed GEP, assessed separately or in combination, were
44 able to predict clinical response to pembrolizumab. More precisely, the highest
45 likelihood of clinical efficacy conferred by pembrolizumab was found in tumors
46 exhibiting both high TMB and elevated levels of inflammation translated by GEP or
47 PD-L1 (Ott et al. 2019). This study calls for prospective confirmation in order to
48 ensure greater precision regarding the strength of the relationships within individual
49 cancer types. Such a multifactorial approach also ensures its wide clinical scale
50 applicability in daily practice although the elevated intrinsic cost may constitute a
51 significant hurdle in clinical practice.

52 On the other hand, predictive markers are very scarce and even absent as
53 regards side-effects associated with CPI treatment practice. Although toxicity related
54 to CPI use is relatively rare and reversible, its severity is nevertheless challenging,
55 with an approximate 1% of treatment-related deaths reported in a recent meta-
56 analysis (Wang et al. 2018). This review underscores the risk of death due to
57 complications associated with CPI-based therapy as it is present in adjuvant and
58 maintenance therapy strategies (Antonia et al. 2017; Weber et al. 2017). Globally,
59 patients who died of toxic effects were older and patient sex had no influence on the
60 risk of lethal toxic events. Clearly, more reliable predictors are needed to identify the
61 few patients at high risk of toxic death under CPI treatment. On the other hand, there
62 is compelling evidence that some patients under CPI undergo deterioration of their
63 clinical status as a result of the applied therapy itself. This paradoxical phenomenon,
64 called hyperprogression, has recently been well reviewed by Champiat and
65 coworkers (Champiat et al. 2018). Hyperprogression needs to be acknowledged and
66 patients at risk should be identified to improve the management of CPI-based
67 therapy (Champiat et al. 2018). The review also stressed that, among a panel of
68 biomarkers covering PD-L1 status, TMB and lymphocyte infiltration score, none
69 appeared to be appropriate for the detection of hyperprogressive disease at
70 individual level (Champiat et al. 2018).

71 There is cumulative evidence that pharmacodynamics reactions (both
72 response and toxicity) to conventional anti-cancer therapy, including chemotherapy
73 and targeted therapy, may be linked to intrinsic genomic characteristics generally
74 referred to as pharmacogenetics (Ciccolini et al. 2015; Hertz and McLeod 2013). To
75 date, as summarized above, most research into predicting the clinical efficacy of CPI
76 treatment has focused on tumor-immune phenotype and somatic genomic features.
77 However and surprisingly enough, it is currently unclear how host germline genetics
78 may affect response to immunotherapy by CPI. Host-related parameters entered into
79 the equation should provide a valuable strategy for the identification not only of
80 factors predictive of treatment efficacy but also of treatment-related toxicity. In
81 addition, the present review article will examine the interactions between host and
82 CPI-based treatment outcome related to age, sex, microbiota and, notably, germline
83 genetics.

84 **2. Predicting CPI treatment outcome through host characteristics**

85 *2.1. Main host factors unrelated to germline genetics*

86 There is cumulative evidence supporting the role of the microbiome in the modulation
87 of response to CPI treatment across cancer types (Gopalakrishnan et al. 2018;
88 Havel, Chowell, and Chan 2019). It is clear that insights have recently been gained
89 into the influence of the microbiome on immunity and cancer (Abt et al. 2012). Trials
90 aimed at manipulating the gut microbiome are currently being developed to enhance
91 response to cancer immunotherapy (Gopalakrishnan et al. 2018). However, the
92 usefulness of microbiome profiling in patients treated by CPI remains unclear. A likely
93 major difficulty in this context is the vast complexity of the body-wide human
94 microbiome, particularly outside the gut. Other difficulties in this context are
95 populations in different geographical areas and with differing lifestyles (Pasolli et al.
96 2019). This problem highlights the need to capture microbial molecular mechanisms
97 that can be causal in microbiome-associated health conditions in general and in CPI-
98 treatment responses in particular.

99 An interesting meta-analysis has recently reported a possible association
100 between gender and CPI-treatment outcome (Wallis et al. 2019). The study covered
101 23 randomized clinical trials including 9322 men and 4399 women. In brief, meta-
102 analysis of study-level differences in response to treatment by CPI failed to reveal
103 statistically significant differences between males and females. However, this
104 question regarding the influence, or not, of gender on CPI treatment efficacy remains
105 controversial and open to debate since other authors have drawn the conclusion that
106 there is a significant advantage in favor of males (Conforti et al. 2018). It is possible
107 that differences in treatment outcomes between men and women may result from
108 difficulties in detecting interfering factors such as life-style, comorbidities, and the
109 presence or not of autoimmune diseases (Wallis et al. 2019).

110 Patient age is a host characteristic which cannot be ignored in the context of
111 immunity in general and regarding clinical efficacy of immunotherapy by CPI in
112 particular. However, little is known about age-related differences in patient response
113 efficacy/toxicity to CPI therapy. An age-related impact in lung cancer patients treated
114 by CPI was investigated in a recent report by King-Kallimanis and coworkers (King-
115 Kallimanis et al. 2018). Examining ten of the most commonly reported adverse
116 events (AE) under immunotherapy, the most frequently reported AE was fatigue,

117 which was slightly more common in patients aged 70 and older. On the other hand,
118 Casaluze and coworkers, also investigating the use of CPI in lung cancer,
119 demonstrated that the elderly population drew greater benefit from CPI, although with
120 contrasting results according to the type of CPI applied (Casaluze et al. 2018). The
121 interaction between aging and individual immunologic status is complex (Alpert et al.
122 2019). Nevertheless, it can potentially impact key mechanisms governing the
123 responsiveness of CPI treatment in terms of efficacy and toxicity (Castelo-Branco and
124 Soveral 2014). For instance, Kugel and coworkers recently reported that melanoma
125 tumors from older individuals had higher CD8+: FoxP 3 ratios, thus supporting the
126 increased response rate of elderly patients to anti-PD1 (Kugel et al. 2018). Clearly, a
127 better understanding of changes in the aging immune system and their impact on
128 CPI use would be helpful to improve immunotherapy management in advanced age.

129 *2.2. Factors related to germline genetics*

130 Current knowledge in genomic technologies has shed light on the identification of
131 germline DNA alterations possibly associated with treatment outcome under CPI
132 therapy. This vast area of investigation is providing a favorable context in terms of
133 clinical applicability (research into whole genomic DNA) and compares well with more
134 costly and laborious sequencing on available tumor samples. In this second part of
135 the review, we attempt to gather complementary elements which constitute both the
136 background (mainly links between individual SNPs and autoimmune diseases) and
137 current developments (clinical reports on germinal immunogenetics and CPI therapy)
138 including our own contribution in this field. **It should be noted that several of the**
139 **quoted studies are based on a limited number of patients with several SNPs. Such a**
140 **methodological context may limit the clinical impact of the report data. The recent**
141 **recommendations from the PAMM group of the EORTC point on the necessity to**
142 **apply strict rules as concerns clinical pharmacogenetics (Robert et al. 2014).** This
143 includes the studied population with the number of studied cases, the assessment of
144 diagnosis and treatments received. The recommendation also included the analyzed
145 polymorphisms with mentioned to be made to an easy identification in the main
146 databases. The authors also pointed to the applied statistical methods with a clear
147 references to the Bonferroni correction, for instance.

148 Autoimmune diseases are characterized by inflammation and tissue damage
149 largely attributable to general deregulation of immunity cells (Chen et al. 2018). In

150 this respect, similar mechanisms of cell immunity deregulation can be the origin of
151 autoimmune diseases and of excessive reactivity conferred by immunotherapy by
152 CPI. Interestingly, single-nucleotide polymorphisms (SNPs) in key immune regulatory
153 genes have been reported to be associated with auto-immune syndromes (Chen et
154 al. 2018; Molineros et al. 2013; Visscher et al. 2017). Auto-immune diseases with
155 variants and gene discovery were recently pointed to as an example of GWAS
156 success (Visscher et al. 2017). It was thus logical to examine possible connections
157 between these individual SNP distributions and immunotherapy treatment outcome.
158 Several recent reports have pinpointed such links. Regarding response to treatment,
159 a study by Lima and coworkers (Lima et al. 2015) examined **in 204 patients** the role
160 of functional polymorphisms in immune response genes as potential biomarkers of
161 BCG therapy in bladder cancer. Their approach merged an initial evaluation of
162 separate genetic variants and subsequent assessment of their combinations (Lima et
163 al. 2015). The focus was placed on 42 functional SNPs in 38 genes of molecules
164 potentially implicated in BCG immunotherapy mechanisms of action. They found that
165 several SNPs in cytokines, chemokines genes and their receptors carried a risk of
166 recurrence after BCG treatment. Interestingly, the authors included SNP-related data
167 in a global predictive approach and established a predictive score of BCG
168 immunotherapy outcome combining clinicopathological characteristics and a range of
169 genetic polymorphisms. Focusing on CPI treatment helps reveal this type of
170 relationship between SNPs-treatment-related effects in terms of both response to
171 treatment and toxicity. There is evidence showing a connection between the efficacy
172 of monoclonal antibody therapy and polymorphisms of their target itself, as recently
173 shown for CD52 **(2 SNPs)** and alemtuzimab in a group of 108 kidney graft recipients
174 (Oko et al. 2009). Considering more broadly the field of therapeutic monoclonal
175 antibodies and regarding herceptin and HER2 in breast cancer, our group has
176 previously reported on the Ile655Val genetic polymorphism for the risk of developing
177 trastuzumab-related cardiotoxicity **in a group 61 patients** (Beauclair et al. 2007). Also,
178 in a group of **52** colorectal cancer patients treated by cetuximab-irinotecan, we
179 previously demonstrated that the maximum toxicity grade was linked to the EGFR-
180 191C>A polymorphism (Etienne-Grimaldi et al. 2012). In this context of target
181 polymorphisms and as concerns CPI, Nomizo and coworkers suggested the
182 hypothesis that germline PD-1/PD-L1 SNPs might be potential predictive markers for
183 response to nivolumab in advanced non-small-cell lung cancer (NSCLC) patients

184 (Nomizo et al. 2017). In this study, five PD-L1 SNPs and two PD-1 SNPs were
185 genotyped in 50 NSCLC patients under nivolumab. The G-allele for PD-L1
186 *rs2282055* and the C-allele of PD-L1 *rs4143815* were found to be associated with
187 improved clinical response (Nomizo et al. 2017). On the other hand, other authors
188 based on 152 advanced melanoma patients and 7 SNPs, have shown CTLA4 gene
189 polymorphisms to be associated with anti-CTLA4 therapy (Breunis et al. 2008).

190 HLA class I and class II molecules play a central role in controlling the
191 specificity of antigen presentation (Havel, Chowell, and Chan 2019; Kelly and
192 Trowsdale 2019). The fact that some immune-mediated adverse events under CPI
193 are related to characteristics of well-defined autoimmune diseases linked to HLA risk
194 alleles (Jin et al. 2019; Paternoster et al. 2015) has logically led investigators to
195 explore whether HLA gene polymorphisms might be associated with CPI-related
196 toxicity (Chowell et al. 2018; Hasan Ali et al. 2019). Hassan Ali and coworkers
197 performed HLA haplotyping with complete HLA class I and class II sequencing in a
198 group of 102 patients under CPI (Hasan Ali et al. 2019). They found a significant
199 association between HLA-DRB1*11:01 and pruritus, while a significant association
200 was demonstrated between HLA-DQB1* 03:01 and colitis. However, this study was
201 built on a mix of cancer locations (NSCLC and melanoma) receiving heterogeneous
202 treatments (anti-CTLA4 alone, anti-PD1 alone, a combination of both). This may limit
203 the impact of the findings and requires confirmation studies on larger and clearly-
204 defined groups of patients taking into account treatment and cancer-type. HLA
205 genotype was also recently investigated regarding a possible link with response to
206 CPI-based treatment (Chowell et al. 2018). In this study, the authors effectively
207 characterized the sets of patients according to the type of CPI and tumor location. In
208 brief, the study covered a group of 1535 advanced patients on whom HLA-I
209 genotyping was performed. In two independent melanoma cohorts, patients with the
210 HLA-B44 supertype had extended survival. In contrast, the HLA-B62 genotype was
211 associated with poor outcome. While these reported data may have potential
212 implications for predicting response to CPI, the genetic complexity of the HLA system
213 is such that an easy and generalizable germinal genetic-based tool is difficult to
214 design on the currently available data.

215 *2.3. Personal implication*

216 We recently applied a global germinal immunogenetic approach in an attempt
217 to predict treatment outcome (toxicity and response) in patients under CPI (Refae et
218 al. 2018; Refae et al. 2019). The setting of potentially relevant SNPs was based on
219 an extensive literature search for genes implicated in immune reaction,
220 immunotherapy response and autoimmune diseases (Figure 1). Candidate SNPs
221 with minor allele frequency of $\geq 5\%$ in Caucasians according to SNPpedia
222 (<http://www.snppedia.com>) and Ensemble databases (<http://Ensemble.org>) were
223 selected. This led to the constitution of a custom panel of 86 genes and 166
224 associated SNPs. High-throughput genotyping of germinal DNA was performed by
225 MassArray (Agena Bioscience®). In a group of 48 patients with NSCLC (Refae et al.
226 2018), a composite score of favorable alleles (zero to five) was found to be markedly
227 associated with progression-free-survival. On a larger group of 94 patients (Refae et
228 al. 2019), it was possible to distinguish between an association with response rate
229 conferred by tumor environment-related gene polymorphisms (CCL2, NOS3, IL1RN,
230 IL12B, CXCR3, IL6R) and grade 3-4 adverse event prediction, which was more
231 closely linked to target-related SNPs (UNG, IFNW1, CTLA-4, PD-L1, IFNL4). It is
232 certain that these promising results based on multi-SNP predictive signatures need
233 larger prospective series (in progress) to reveal their full clinical significance and
234 applicability.

235 **3. Advantages and limits**

236 Germinal immunogenetics, as summarized above for the main current applications in
237 the field of CPI-based treatment, has established its potential clinical usefulness.
238 Germinal immunogenetics constitutes an ideal source of additional information in the
239 area of predictive biomarkers for immunotherapy by CPI, which are generally
240 centered on the tumor itself or on its environment. It is clear that germline variants
241 can provide efficient and easily assessable indicators (blood DNA, at any time) in
242 order to enlarge the range. Is germinal immunogenetics to be ranked at the same
243 decisional level as molecular and cellular predictive biomarkers for immunotherapy
244 by CPI? Probably not, and rightly so. The initial go/no go step, as exemplified by RAS
245 mutation testing in colorectal cancer with anti-EGFR treatment, can be translated to
246 biological predictive parameters for CPI-based therapy with PD-L1 expression,
247 mutational load, microsatellite instability and tumor T cell infiltrate. Once a decision to
248 treat is taken, additional information regarding patient characteristics is useful. This

249 additional information may be supplied by germinal immunogenetics, thus involving
250 several potential risks, i.e. the risk of the patient being a lesser responder and the
251 risk of him/her being predisposed to adverse events. This second step of dose
252 adjustment is based on the individual germinal immunogenetic profile. Clearly, the
253 two steps, with predictive markers on one hand and germinal immunogenetics on the
254 other, may be ideally complementary (Table 1). However, it is important to take into
255 account certain limitations in the ability of germinal polymorphisms to provide
256 accurate predictions in patients receiving CPI-based therapy. These limitations of
257 germinal polymorphism assessment concern not only CPI-based therapy but also the
258 general field of anticancer treatment. For instance, the pharmacogenetics of
259 anticancer agents has largely proven its clinical utility (DPD and fluoropyrimidines,
260 UGT1A1 for irinotecan) (Henricks et al. 2018; Paez et al. 2019). However, this
261 predictive tool suffers from several inherent drawbacks: the small number of cases
262 on which links between pharmacogenetics and pharmacodynamics are generally
263 established and the lack of independent validation on larger cohorts. The recently
264 reported study by Bins and coworkers is an illustration for CPI-based therapy. The
265 authors assessed the association between seven SNPs in four genes and toxicity
266 under CPI (Bins et al. 2018). A multivariate analysis in an exploration cohort revealed
267 that homozygous variant patients for PDCD1 B04C>T ran a lower risk of toxicity.
268 However, in a prospective validation group this link was no longer observed (Bins et
269 al. 2018). Relatively few prospective controlled trials in which the clinical usefulness
270 of gene polymorphisms was firmly established have been published as concerns
271 DPD (Henricks et al. 2018) and UGT1A1 (Paez et al. 2019).

272 Another important issue concerns the precise functional significance of the reported
273 SNPs linked to treatment outcome. This lack of information may be explained by the
274 complexity of the investigations needed. Generally, only *in silico* simulations using
275 dedicated software are undertaken to shed light on this important issue of the
276 functional impact of reported predictive SNPs. Table 2 illustrates the main free
277 software programs available in this context. These programs generate hypotheses
278 for future experimental investigations in order to test the biological functionality of the
279 alleles of interest. An illustration of this strategy is found in the study by Chen and
280 coworkers (Kugel et al. 2018). The authors identified a variant of IgG1 with a Gly
281 396→Arg (hlgG1-G396R), which positively correlated with systemic lupus
282 erythematosus. Interestingly, the authors generated mice carrying the G396R

283 homozygous genotypes. They were able to show that the variant impacted the
284 phosphorylation of the ITT motif leading to an alteration of tyrosine kinase signaling
285 on antigen binding.

286 A clear distinction between a true predictive marker and a prognostic factor should
287 also be defined. In this regard, Rendleman and coworkers reported on the link
288 between IL10 *rs3024493* and clinical outcomes in a population sample of 1022
289 melanoma patients (Rendleman et al. 2015). They found a significant association of
290 this IL10 gene polymorphism with melanoma survival while no mention of applied
291 CPI-based treatment was made in this study. Thus, there would appear to be a
292 potential risk in concluding that this IL10 gene polymorphism has a predictive value in
293 melanoma patients treated by CPI whereas it only has intrinsic prognostic value
294 independently of an applied therapy. Similarly, Liu and coworkers (Liu et al. 2018)
295 recently reported on the prognostic value of CTLA-4 *rs231775* in patients with renal
296 carcinoma. Patients were treated by antiangiogenic therapy with sunitinib and not by
297 CPI-based treatment. This finding highlights to the need to understand the biological
298 significance of the disclosed alleles in order to establish more clearly their potential
299 link with the drug mechanism of action.

300 **4. Perspectives**

301 It is clear that an understanding of mechanisms underlying the inter-individual
302 variability of immunotherapy sensitivity remains a key challenge for personalized
303 medicine. The identification of reliable immunotherapy biomarkers that provide
304 insights into biological and genetic sources of response variability will be critical to
305 guide personalized-medicine approaches.

306 The statistical power to establish clinical genetic associations should be
307 revisited, as recently stressed by Visscher and coworkers (Visscher et al. 2017).
308 Carefully-powered calculations should lead to an optimal trade-off between sample
309 size, allele frequency and effect size. A GWAS catalogue from 2008 to 2016 revealed
310 a SNP-trait discovery timeline with an increasing number of SNP-related traits
311 (Welter et al. 2014). New molecular technologies and innovative analytical methods
312 should provide opportunities to bridge the knowledge gap between SNP-CPI
313 treatment associations and the functional impact of these SNPs and the gene level.
314 The design of novel computational methods incorporating machine learning and
315 bioinformatic techniques should make available tools particularly suitable for

316 predicting immunosensitivity at individual level and for identifying SNP-related
317 biological mechanisms (Oh et al. 2017). The huge power of the emerging
318 CRISPR/cas9-based technologies (Karimian et al. 2019) could offer real
319 opportunities by assisting in the design of appropriate biological models to test the
320 functional impact of the SNPs discovered in germinal immunogenetic studies
321 investigating CPI-based therapy. At this level, a dual approach associating cellular
322 and animal models appears to be particularly relevant to ensure adequate
323 exploration of functional impacts following SNP discovery (Winters, Murray, and
324 Winslow 2018). It must also be borne in mind, in most cases, that the molecular
325 mechanisms by which non-coding genetic variants disrupt gene expression remain
326 unclear. In this respect, it is important to mention the DICE project (database of
327 immune cell expression, expression quantitative trait loci[eQTL] and epigenomics)
328 which is shedding more light on eQTL and the transcriptomic data human immune
329 system (Schmiedel et al. 2018).

330 **Author's contributions**

331 All authors have been participated in the writing and involved in critical revision of this
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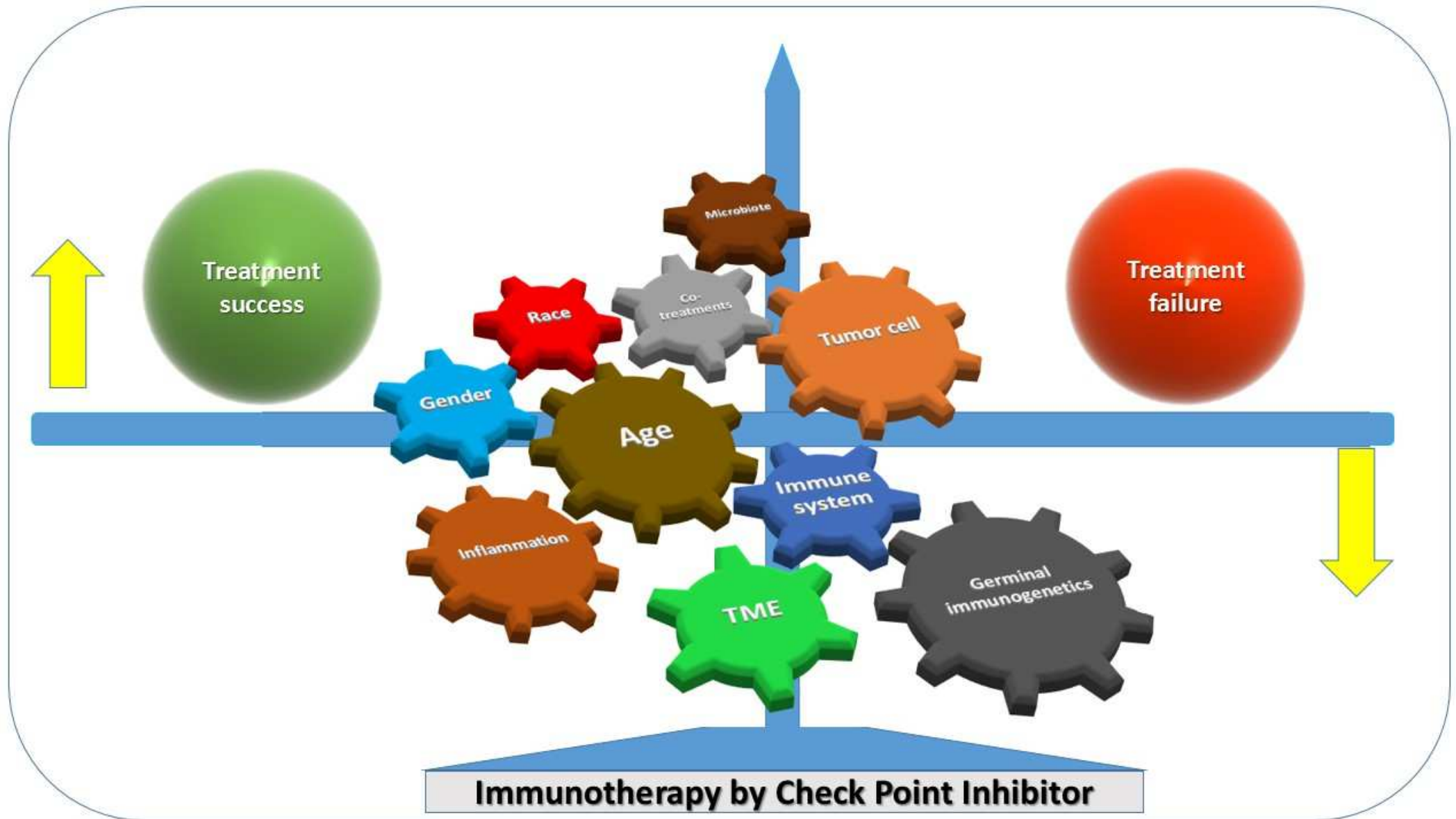


Figure 1: Germinal immunogenetics wheel within the CPI response machinery. SNPs (germinal immunogenetics) hold a place in the global machinery linked to the response to CPI. They can interfere with the immune system itself but also with the microbiota, the tumoral microenvironment (TME) and the tumor. Other potential influencing factors may (non-exclusively) implicate race, sex, age and inflammation.

Table 1: A tentative global approach for optimizing CPI-based treatment

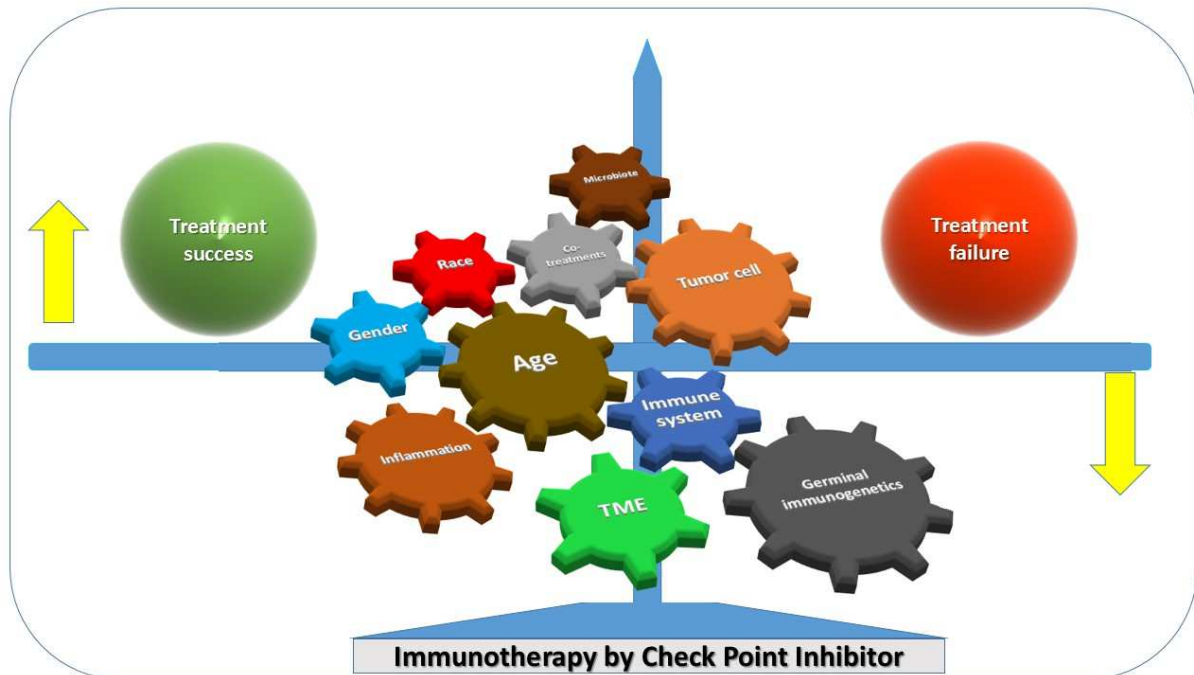
THE CURRENT APPROACH		THE COMPLEMENTARY PART OF THE HOST	
MARKERS	Tumor and environnement-related	MARKERS	Germinal immunogenetics (SNP score)
	- Target expression (PD-L1)		- Tumor-related factors (PD-L1, CTLA-4, IDO, HLA...)
	- Tumor mutational load		- Microenvironment-related (INF, TCR...)
	- Tumor T cell infiltrate (quantitative, qualitative)		↓
	- MSS / MSI		Risk Score Calculation
DECISIONS	- Go/No Go	DECISIONS	- Individual dose adjustment
	- Combine with CPI (plus chemotherapy, plus TKIs...)		- Schedule adaptation
			- PK survey incorporation

Table 2: Free available tools to analyze SNPs

NAME	Link	Description
HAPLOREG	https://pubs.broadinstitute.org/mammals/haploreg/haploreg.php	Explores annotations of the noncoding genome at variants on haplotype blocks, such as candidate regulatory SNPs at disease-associated loci. HaploReg returns SNPs in LD with query SNPs, their frequency in 4 populations from 1000 Genomes Phase1, and also tells you what evidence ENCODE has found for regulatory protein binding, chromatin structure, the chromatin state of the region, and putative transcription factor binding motifs that are altered by the variant.
ENSEMBL	https://www.ensembl.org/index.html	Gives the location of the variant on the gene
GTEX	https://gtexportal.org/home/	The Genotype-Tissue Expression (GTEx) project is an ongoing effort to build a comprehensive public resource to study tissue-specific gene expression and regulation. Samples were collected from 53 non-diseased tissue sites across nearly 1000 individuals, primarily for molecular assays including WGS, WES, and RNA-Seq. The GTEx Portal provides open access to data including gene expression, QTLs, and histology images.
REGULOMEDB	http://www.regulomedb.org/index	RegulomeDB is a database that annotates SNPs with known and predicted regulatory elements in the intergenic regions of the H.Sapiens genome. Known and predicted regulatory DNA elements include regions of DNAase hypersensitivity, binding sites of transcription factors, and promoter regions that have been biochemically characterized to regulation transcription. Sources of these data include public datasets from GEO, the ENCODE project, and published literature.
SNIPMIR	http://www.genomique.info:8080/merge/index?action=MISNP	Tests the gain/loss of microRNA binding induced by a SNP

Graphical abstract

Germinal immunogenetics as a predictive factor for immunotherapy



Clinical response to checkpoint inhibitors-based (CPIs) therapies can vary among tumor types and between patients according to several factors.

Entering host-related parameters (germinal immunogenetics) into the biomarker panel of CPI should provide a valuable strategy for identifying not only factors predictive of treatment efficacy but also of treatment-related toxicity.

A major issue concerns the real functional significance of the reported single-nucleotide polymorphisms (SNPs) linked to CPI-treatment outcome.