

Anti-LAG-3: A change in the paradigm of advanced melanoma treatment

Anti-LAG-3: uma mudança de paradigma no tratamento do melanoma avançado

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ABSTRACT

Melanoma is the deadliest skin cancer globally. It arises from the malignant transformation of melanocytes through multiple complex pathways. While cutaneous melanoma, originating from the epidermis, is the most common form, other rarer subtypes also exist. The complex physiopathology of melanoma, characterized by a high mutational load and metastatic potential, when correlated with the hallmarks of cancer, clearly demonstrates its predisposition to immunotherapy.

Immunotherapy has significantly improved clinical outcomes, with the median survival of patients with advanced melanoma increasing from 6 months to 6 years following treatment with immune checkpoint inhibitors. However, the high risk of toxicity, particularly with the current standard combination therapies, and problems related to relapse or resistance to treatment, remain a major concern, with some mechanisms yet to be fully elucidated. Therefore, the discovery of new molecules targeting alternative immune checkpoints (ICs) has become one of the leading approaches.

This review, focusing on lymphocyte-activation gene 3 (LAG-3), characterizes this novel IC at the structural and molecular level, as well as describes its mechanism of action. Moreover, it highlights key clinical trials involving anti-LAG-3 molecules, including the landmark RELATIVITY-047 study, which led to the approval of relatlimab, the first anti-LAG-3 monoclonal antibody, in combination with nivolumab, as a first-line treatment for advanced melanoma. By reporting these promising clinical results, which demonstrate that this novel combination therapy is safer and as effective as other first-line therapies, this review points to a paradigm shift in the treatment of advanced melanoma.

Keywords: melanoma, immunotherapy, anti-LAG-3, relatlimab, clinical trials.

RESUMO

O melanoma é o cancro de pele mais mortal do mundo. Este resulta da transformação maligna dos melanócitos através de múltiplas vias de sinalização complexas. Embora o melanoma cutâneo, com origem na epiderme, seja a forma mais comum, existem outros subtipos mais raros. A complexa fisiopatologia do melanoma, caracterizada por uma elevada carga mutacional e potencial metastático, quando correlacionada com os *hallmarks* do cancro, transparece de forma evidente a sua predisposição para o tratamento com imunoterapia. A imunoterapia melhorou significativamente o prognóstico clínico, com a sobrevivência média dos doentes com melanoma avançado a aumentar de 6 meses para 6 anos, após o tratamento com inibidores dos *checkpoints* imunológicos. No entanto, o elevado risco de toxicidade, em particular com as atuais terapias combinadas padrão, e os problemas relacionados com recaídas ou com a resistência ao tratamento, continuam a ser um grande desafio, havendo alguns mecanismos ainda por elucidar. Por conseguinte, a descoberta de novas moléculas que visam *checkpoints* imunológicos alternativos tornou-se uma das principais abordagens. Este artigo, centrado no gene de ativação de linfócitos 3 (LAG-3), caracteriza este inovador *checkpoint* imunológico a nível estrutural e molecular, descrevendo também o seu mecanismo de ação. Além disso, destaca os principais ensaios clínicos que envolvem moléculas anti-LAG-3, incluindo o estudo de referência RELATIVITY-047, que levou à aprovação do relatlimab, o primeiro anticorpo monoclonal anti-LAG-3, em combinação com o nivolumab, como tratamento de primeira linha para o melanoma avançado. Ao destacar estes resultados clínicos promissores, que demonstram que esta nova terapêutica combinada é mais segura e tão eficaz como outras terapêuticas de primeira linha, esta revisão aponta para uma mudança de paradigma no tratamento do melanoma avançado.

Palavras-chave: melanoma, imunoterapia, anti-LAG-3, relatlimab, ensaios clínicos.

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INTRODUCTION

Immunotherapy represents one of the most promising and effective strategies in melanoma treatment¹. By harnessing the patient's immune system, this approach strengthens the ability to recognize, target and destroy cancer cells, leading to notable improvements in clinical outcomes^{2,3}.

Advanced melanoma, whether unresectable or metastatic, is among the most immunogenic tumors, owing to its high mutational burden⁴. This characteristic and its significant metastatic potential and resistance to conventional therapies make it a perfect candidate for immunotherapy treatment⁵.

Immunotherapy, particularly through immune checkpoint inhibitors (ICIs), has revolutionized the treatment of advanced melanoma, and has shown efficacy in managing a wide range of other tumors as well⁶. The importance of ICIs within the clinical paradigm was further underscored by the awarding of the 2018 Nobel Prize in Physiology or Medicine to James P. Allison and Tasuku Honjo, for their groundbreaking discovery of cancer therapy via inhibition of negative IC regulation⁴.

This review aims to provide a comprehensive description of melanoma, by linking its physiopathology with the principal hallmarks of cancer, and to present an overview of ICIs immunotherapy in the treatment of this disease, emphasizing the benefits of the emerging anti-lymphocyte-activation gene 3 (LAG-3) therapy, as evidenced in the latest clinical trials.

To this end, a search was carried out on search engines such as PubMed® and ScienceDirect®, using the following terms,

individually or in combination: “melanoma”, “classification” “physiopathology”, “hallmarks of cancer”, “immune checkpoint inhibitors”, “anti-CTLA-4”, “anti-PD-1”, “anti-LAG-3” and “clinical trials”.

Melanoma

Characterization and Epidemiology

Melanoma is a malignant tumor characterized by the uncontrolled proliferation of melanocytes, melanin-producing cells that play a vital role in the pathogenesis of this skin cancer⁷. Depending on its location, different types of melanomas can be identified. Cutaneous, mucosal and ocular (uveal) are the most important⁸.

Cutaneous melanoma, which originates in the basal layer of the epidermis, is the most common type of melanoma⁹. Studies conducted by the International Agency for Research on Cancer (IARC) predict that the number of new cases of cutaneous melanoma per year will increase by more than 50% between 2020 and 2040. Consequently, it is anticipated that annual new cases will exceed 500.000, with mortality rates rising by more than two-thirds, reaching nearly 100.000 deaths per year¹⁰.

Conversely, mucosal and ocular melanomas are less common but generally have a worse clinical prognosis¹¹. Following cutaneous melanoma, ocular melanoma, particularly that which originates in the uvea (ocular choroid, ciliary body and iris) is the second most common type^{12,13}. It represents 3-5% of all melanomas and is considered the most common primary intraocular malignancy¹⁴. Mucosal melanoma arises from melanocytes present in the mucous membranes of the respiratory, gastrointestinal and

genitourinary tracts, and this rare condition accounts for approximately 1% of melanoma cases¹⁵.

Despite melanoma representing only 1% of all skin cancers, it is the deadliest skin cancer worldwide¹⁶. According to GLOBOCAN, the web database of the IARC, around 330.000 new cases of melanoma were diagnosed globally, and nearly 60.000 people died from the disease in 2022¹⁷. It is expected that these figures will continue to rise, as the incidence of melanoma is growing rapidly, faster than other cancers, making it a major public health problem¹⁸.

The European scenario mirrors this trend. Based on the latest 2022 data from the European Cancer Information System (ECIS), melanoma is the 6th most frequently occurring cancer in Europe¹⁹. With incidence rates being higher in men than in women, melanoma is also one of the most common cancers among young adults^{20,21}.

In Portugal, there are approximately 1.500 new cases of melanoma every year²². The age-standardized incidence and mortality rates are 10.2/100000 individuals and 2.5/100000 individuals, respectively, making it the 18th most common and the 20th deadliest cancer¹⁹.

Physiopathology of Melanoma

The physiopathology of melanoma is complex and characterized by intricate molecular dynamics. It arises due to multiple genetic changes, with ultraviolet (UV) being considered the primary mutagenic risk factor. Beyond UV exposure, other risk factors, including the number of nevi, genetic susceptibility and family history of melanoma have been linked to melanoma progression²³.

Regarding melanocytic neoplasms, two different types can be considered: a benign one, termed melanocytic nevi, and a malignant one, referred to as melanoma²⁴.

The progression from benign to malignant is not linear but can be conceptualized into five stages: melanocytic nevi, dysplastic nevi, melanoma *in situ*, invasive melanoma and metastatic melanoma²⁵. This progression between stages involves an interaction of both genetic factors and UV-induced damage⁵.

Melanocytic Nevi

Melanocytic nevi are benign proliferations of melanocytes²⁵. Depending on whether they develop at or after birth, melanocytic nevi can be congenital or acquired, respectively²⁶.

Despite being considered the first stage of melanoma progression, not all melanomas pass through this phase. As a matter of fact, only about 30% of melanomas derive from a pre-existing benign precursor melanocytic nevus²⁷. These skin lesions are, therefore, quite stable and are more likely to regress than to progress to melanoma²⁵. However, there seems to be a relationship between the number and size of melanocytic nevi and the risk of developing melanoma²⁸.

Concerning their genesis, these benign neoplasms originate mainly from mutations in the v-Raf murine sarcoma viral oncogene homolog B1 (*BRAF*)²⁷. This genetic modification, which occurs in around 50% of melanomas and 70% of benign nevi, constitutively activates the mitogen-activated protein kinase (MAPK) pathway, causing oncogenic proliferation^{29,30}. *BRAF*^{V600E} mutation is the most common and involves the su-

stitution of valine (V) for glutamic acid (E) at codon 600³¹.

However, BRAF^{V600E} mutation alone, in most cases, is not enough to evolve into malignant stages³². This can be explained by a phenomenon called oncogene-induced senescence (OIS). OIS is a powerful tumor-suppressive mechanism that can be enabled after oncogenic-activating genomic modifications, such as BRAF^{V600E} mutations³³. It leads to the overexpression of certain tumor suppressor proteins, including p16, which control the cell division process³³. Therefore, melanoma progression from a benign stage to a malignant one does not occur frequently. Nevertheless, some melanocytic nevi can develop into intermediate lesions, known as dysplastic nevi³⁴.

Dysplastic Nevi

Dysplastic nevi are pigmented lesions with benign and malignant histopathological features²⁵. These intermediate neoplasms were first reported by Clark and colleagues in 1978. Since then, there has been a debate about its definition and importance in the clinical evaluation of melanoma³⁵.

Although in most cases they are stable lesions that tend to regress over time, it remains a melanoma risk factor³⁵. In addition, dysplastic nevi are known to have a higher mutational load than benign lesions and a lower mutational load than malignant lesions²⁵. Indeed, it has different mutations from the previous stage. Besides the mutations involving the MAPK pathway, such as BRAF or neuroblastoma RAS viral oncogene homolog (NRAS) mutations, genetic modifications in the telomerase reverse

transcriptase (*TERT*) promoter and hemizygous alterations of cyclin-dependent kinase inhibitor 2A (*CDKN2A*) gene have also been identified²⁵.

These genetic alterations are critical for melanoma progression. *NRAS* mutations disrupt the MAPK pathway, leading to sustained cell proliferation⁸. Mutations in the *TERT* promoter induce the transcription of telomerase, allowing cells to avoid senescence³⁶. *CDKN2A* encodes the p14 and p16 proteins, both of which play key roles in the regulation of cell division³⁷.

Melanoma in situ

The term “melanoma *in situ*” (MIS) is used to describe a horizontal (radial) growth phase of melanocytes entirely within the epidermis²⁵. These lesions are staged as Tis, according to the tumor, node, metastasis (TNM) system developed by the American Joint Committee on Cancer (AJCC). Briefly, this system is based on three key points. The first concerns the primary tumor (T) and assesses its thickness and the presence or absence of ulcerations. The second key point is related to the lymph node (N) involvement and describes how many lymph nodes contain melanoma cells. Lastly, the metastasis (M) category is used to classify melanoma according to whether it has metastasized³⁸.

Once melanoma has been classified according to the TNM system, it can be further categorized into five stages (0, I, II, III, IV). Therefore, melanoma *in situ* can also be referred to as stage 0 melanoma³⁹.

As expected, MIS has a higher frequency of mutations compared to intermediate lesions. Several studies using assays

with greater sensitivity have detected a higher frequency of mutations affecting the MAPK signaling pathway, predominantly in the *BRAF*, neurofibromin 1 (*NF1*) and *NRAS* genes²⁵. Besides this, mutations in the *TERT* promoter also play an important role in the pathogenesis of MIS⁴⁰.

These lesions can persist for years before progressing to invasive melanoma, suggesting that additional mutations are required, along with the ability to evade the immune system²⁵.

Invasive Melanoma

Unlike MIS, which remains confined to the epidermis, melanoma becomes invasive when tumor cells spread to other tissues, such as the dermis or submucosa²⁵. Invasive melanoma typically grows in a vertical pattern and most often originates from MIS. Consequently, it has a significant probability of metastasizing⁴⁰.

Invasive melanoma is characterized by a high mutational load, with copy-number alterations being prevalent⁴¹. One of the most critical mutations is the biallelic inactivation of *CDKN2A*, as it marks the transition to invasive melanomas⁴⁰. Moreover, other genetic alterations, such as deletion of phosphatase and tensin homolog (*PTEN*) tumor suppressor gene and *BRAF* mutations are detected. Amplifications of the murine double minute 2 (*MDM2*), *TERT* and yes-associated protein 1 (*YAP1*) genes, along with mutations in the switch/sucrose non-fermentable (SWI/SNF) chromatin remodeling complex can also be detected and exert a significant impact at this stage^{25,41}. Indeed, the *MDM2* gene encodes the *MDM2* protein, an impor-

tant regulator of p53 activity⁴². *YAP1*, encoded by the *YAP1* gene, controls cell growth and proliferation⁴³. Mutations within the SWI/SNF complex, specifically AT-rich interaction domain 2 (*ARID2*) and AT-rich interaction domain 1A (*ARID1A*), impair its tumor suppressor activity²⁵.

Metastatic Melanoma

According to the National Cancer Institute, a cancer is considered metastatic when cancer cells spread from the site of the original (primary) tumor and form a new tumor in other organs or tissues of the body⁴⁴.

Metastasis can be categorized into three types: locoregional, regional, and distant. Locoregional metastasis is classified as satellites or intransit metastasis; regional metastasis involves the lymph nodes; and distant metastasis can affect skin, lung, brain and other sites⁴¹. Interestingly, the primary sites where melanoma metastasis commonly occurs include lymph nodes, lungs, liver, bones, and brain³⁴.

Undoubtedly, genetic changes persist, with metastatic melanoma showing a higher rate of mutations and chromosomal aberrations. This increased mutational burden includes a significant incidence of *BRAF* and *NRAS* activating mutations⁴¹.

Additionally, mutations have been identified in the *CDKN2A* and EPH receptor A3 (*EPHA3*) genes, as well as in tumor suppressor genes, including tumor protein p53 (*TP53*) and retinoblastoma, although rare and *PTEN*. Point out that these mutations are strongly related to exposure to UV radiation⁴¹.

Pathways to Melanoma

Not all types of melanomas undergo every stage of progression. Some may derive from a melanocytic or dysplastic nevi, while others may arise *de novo*⁹. Moreover, melanoma may manifest as melanoma *in situ* or progress to invasive forms. Its etiology is also diverse, as not all cases are attributed to intense UV exposure, and the genetic mutations underlying melanoma development vary. Since cutaneous melanoma is the most common form, melanoma is often classified in the literature into four primary types: superficial spreading melanoma, nodular melanoma, lentigo maligna melanoma, and acral lentiginous melanoma. However, this classification oversimplifies the complexity of melanoma. To address this complexity, in 2018, the World Health Organization (WHO)

classified nine different evolutionary pathways for the genesis of cutaneous, mucosal and uveal melanomas. This classification was based on UV radiation exposure, expressed by cumulative sun damage (CSD), genetic alterations and clinical and pathological characteristics of the precursor lesions^{28,45}.

Considering the main etiological factor (CSD), melanomas can be clustered into two groups²³:

- Melanomas typically associated with CSD (low or high-CSD);
- Melanomas not consistently associated with CSD (no CSD).

Table 1 provides a summary of the differences among the nine pathways. Note that nodular cutaneous melanoma occupies a special place in this classification because all or most of these pathways refer to it.

Table 1. Classification of melanoma according to its pathway (Adapted from^{8,23})

UV Exposure		Pathway	Melanoma Subtype	Common Mutations	
Melanomas typically associated with CSD	Low-CSD	I	Superficial Spreading Melanoma	<i>BRAFV600</i> ^b <i>CDKN2A</i> ^a <i>NRAS</i> ^b	<i>TERT</i> ^d <i>PTEN</i> ^a <i>TP53</i> ^a
	High-CSD	II	Lentigo Maligna Melanoma	<i>NRAS</i> ^b <i>BRAF non-V600E</i> ^b <i>KIT</i> ^b <i>TERT</i> ^d	<i>NF1</i> ^a <i>CDKN2A</i> ^a <i>PTEN</i> ^a <i>TP53</i> ^a <i>RAC1</i> ^b
		III	Desmoplastic Melanoma	<i>NF1</i> ^a <i>NFKBIE</i> ^d	<i>NRAS</i> ^b <i>PIK3CA</i> ^b

Table 1. Classification of melanoma according to its pathway (Adapted from^{8,23}) (cont.)

	UV Exposure	Pathway	Melanoma Subtype	Common Mutations	
Melanomas not consistently associated with CSD		IV	Spitz Melanoma	HRAS ^b ALK ^e CDKN2A ^a	NTRK1 ^e NTRK3 ^e
		V	Acral Melanoma	KIT ^b NRAS ^b BRAF ^b HRAS ^b KRAS ^b	NTRK3 ^e ALK ^e NF1 ^a CDKN2A ^a TERT ^f CCND1 ^d
		VI	Mucosal Melanoma	KIT ^b NRAS ^b KRAS ^b BRAF ^b NF1 ^b CDKN2A ^a	SF3B1 ^a CCND1 ^d CDK4 ^d MDM2 ^d
		VII	Melanomas arising in congenital nevi	NRAS ^b	BRAFV600E ^b
		VIII	Melanomas arising in blue nevi	GNAQ ^b GNA11 ^b CYSLTR2 ^b	BAP1 ^a EIF1AX ^c SF3B1 ^c
		IX	Uveal Melanoma	GNA11 ^b GNAQ ^b CYSLTR2 ^b PLCB4 ^b	BAP1 ^a EIFAX ^c SF3B1 ^c

Abbreviations: CSD - Cumulative Sun Damage; UV - Ultraviolet.

^a Loss-of-Function Mutation; ^b Gain-of-Function Mutation; ^c Change-of-Function Mutation; ^d Amplification; ^e Rearrangement

^f Promoter Mutation.

Hallmarks of Melanoma

Hallmarks of cancer refer to a series of essential functional abilities that human cells acquire as they progress from a normal state to a neoplastic growth state. These capabilities are crucial for enabling cells to develop into malignant tumors. As such, it is a key tool for unraveling the

vast complexity of cancer phenotypes and genotypes into a provisional set of underlying principles⁴⁶.

According to the most recent literature, 14 hallmarks of cancer are now recognized, as illustrated in Figure 1⁴⁶. This chapter explores the most significant hallmarks of cancer in melanoma development.



Figure 1. Hallmarks of Cancer (With permission from⁴⁶).

Genomic Instability and Mutation

This enabling characteristic plays a significant role in tumor progression, as it is responsible for the phenotypic variation in melanoma⁴⁷. Genomic instability increases the mutation rate, potentially acting as the main trigger for other hallmarks of cancer^{47,48}. As previously analyzed, the genesis of several melanoma subtypes of melanoma is positively related to exposure to UV radiation, making it one of the main factors leading to this genomic instability⁴⁸.

The mutations resulting from these genetic alterations are diverse but will be included under other cancer hallmarks, considering their molecular characteristics.

Evading Growth Suppressors

To grow uncontrollably, tumor cells must evade anti-growth signals. These signals are mediated by tumor suppressor proteins, such as the p53 - the “guardian of the genome” - and the retinoblastoma protein (pRB)⁴⁸. In melanoma, *CDKN2A* is the most inactivated tu-

mor suppressor gene. As mentioned, it encodes the tumor suppressor proteins p16 and p14³⁷.

The primary role of the p16 protein is to bind and inhibit the cyclin-dependent kinases CDK4 and CDK6. This action prevents these kinases from phosphorylating the pRB, resulting in cell cycle arrest at the G1/S checkpoint and promoting cell senescence. When the *CDK2NA* gene is mutated, p16 loses its function. As a result, CDK4 and CDK6 are not inhibited and phosphorylate pRB, allowing the cell cycle to progress from G1 to S phase. This mutation, thus, supports melanoma progression, by promoting melanocytes proliferation, delaying senescence and initiating invasion^{37,48}.

On the other hand, the p14 protein antagonizes MDM2-mediated ubiquitination, thereby preventing p53 degradation³⁷. MDM2 negatively regulates p53, by promoting its ubiquitination and subsequent proteasome-mediated degradation⁴⁹. If the *CDK2NA* gene is mutated, p14 protein cannot inhibit the activity of MDM2, leading to p53 inactivation. Consequently, cells evade apoptosis and proliferate indefinitely, sustaining the development of melanoma.

Despite the importance of both proteins as tumor growth suppressors, most *CDKN2A* mutations are p16-dependent, so p16 appears to be more prominent than p14³⁷.

Sustaining Proliferative Signaling

The most important trait of cancer cells is their ability to maintain chronic proliferation. This is achieved by constantly activating signaling pathways that promote cell growth and division⁵⁰.

Sustaining proliferative signaling in melanoma is primarily achieved by a *BRAF* mutation. Other driver mutations, such as *NRAS* mutation can also be present (15%-20% of melanomas), making it the second most frequent mutation type. Both mutations interfere with the MAPK pathway^{30,51}.

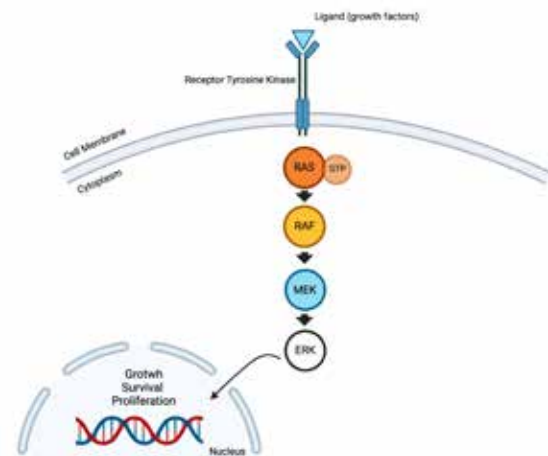
MAPK Pathway

The MAPK pathway regulates vital cellular functions, namely proliferation, growth, survival and apoptosis^{8,30}.

This signaling pathway is active under normal conditions but is overactivated in melanoma⁸. It comprises cytoplasmic serine/threonine and tyrosine kinases, including rat sarcoma virus (RAS), rapidly accelerated fibrosarcoma (RAF), mitogen-activated protein kinase (MEK), and extracellular signal-regulated kinase (ERK). RAS is a GTPase with three isoforms encoded by the Harvey rat sarcoma viral oncogene homolog (*HRAS*), *NRAS*, or Kirsten rat sarcoma viral oncogene homolog (*KRAS*), while RAF is a protein kinase that includes three isoforms encoded by the A-Raf proto-oncogene, serine/threonine kinase (*ARAF*), *BRAF* and C-Raf proto-oncogene, serine/threonine kinase (*CRAF*)³⁰. MEK is a dual specificity kinase that activates ERK, a serine/threonine protein kinase that transmits mitogen signals and, upon activation, translocates to the nucleus and regulates transcription factors activity and gene expression⁵².

Typically, the activation process begins when growth factors bind to tyrosine kinase receptors. This event triggers the activation of Ras family proteins, specifically the monomeric G proteins. Consequently, this initiates a cascade that

activates RAF serine/threonine kinases, which in turn activate MEK. Active MEK then dually phosphorylates ERK, enabling its translocation to the nucleus, where it activates transcription factors, thereby intensifying the transcription of genes involved in cell growth, proliferation, survival and migration^{8,53}. The MAPK pathway and its activation cascade is represented in Figure 2.



Abbreviations: ERK - Extracellular Signal-Regulated Kinase; GTP - Guanosine Triphosphate; MEK - Mitogen-Activated Protein Kinase; RAF - Rapidly Accelerated Fibrosarcoma; RAS - Rat Sarcoma Virus

Figure 2. MAPK Pathway (Created in BioRender).

BRAF Mutation

BRAF mutation, especially *BRAF*^{V600E}, is the most prominent driver of constitutive activation of the MAPK pathway in melanoma.

The primary cause of *BRAF*^{V600E} mutation remains a topic of debate, notably because it does not exhibit a UV signature mutation. It is characterized by a T to A transversion, atypical of the UV radiation-induced DNA damage, which generally causes C to T or CC to TT transversions at dipyrimidine sites. Several theories have been proposed to

explain the emergence of the *BRAF*^{V600E} mutation. These include its possible role as a minor direct byproduct of UV radiation, errors in DNA polymerases following UV exposure or indirect UV damage mediated by reactive oxygen species (ROS)^{25,27}.

However, it is known that *BRAF* mutation increases its biochemical activity. Thus, phosphorylation and activation of MEK will occur more frequently, which in turn activates ERK, leading to excessive cell proliferation⁸.

NRAS Mutation

NRAS mutation is the most common mutation in the RAS genes in melanoma but it occurs less frequently than in other solid tumors⁸. Q61R mutation, which results from the substitution of glutamine (Q) for arginine (R) at position 61, is the most frequent *NRAS* mutation in this skin cancer⁵⁴.

Unlike *BRAF* mutations, which exclusively activate the MAPK signaling pathway, some evidence proposes that *NRAS* mutations can initiate both the MAPK and phosphatidylinositol 3 kinase (PI3K) pathways. Furthermore, *NRAS* and *BRAF* mutations are seldom found together, suggesting that a mutation in either gene is sufficient to activate the MAPK pathway⁸.

As expected, this genetic change leads to constitutive activation of the downstream RAF-MEK-ERK signaling pathway, which promotes cell proliferation and survival.

Enabling Replicative Immortality

Cancer cells have the unique ability to replicate indefinitely, which is essential for tumor development. Unlike normal

cells, which can only divide a limited number of times before stopping due to the shortening of telomeres (Hayflick Limit), cancer cells can bypass this restriction. Normally, when telomeres, the protective DNA sequences at the ends of chromosomes, become too short, cells cease dividing and either enter senescence or die⁵⁰.

However, melanoma is associated with the upregulation of the *TERT* gene. The telomerase complex includes a catalytic subunit, the *TERT*, and the telomerase RNA component (TERC)⁴⁸. Normally, telomerase is silent in most human somatic cells, being expressed only during development⁵⁵. Nevertheless, mutations in the promotor of the *TERT* gene upregulate its transcriptional activity and expression, resulting in increased telomerase activity. Thereby, this upregulation maintains telomere length and overcomes the telomere-induced senescence barrier, granting cancer cells the ability to proliferate indefinitely, which promotes cell immortalization and the development of melanoma³⁶.

Activating Invasion and Metastasis

Metastasis allows cancer cells to spread throughout the body, resulting in a poor prognosis. Indeed, metastatic melanoma is the deadliest form of the disease.

Successful metastasis is accomplished through five steps: invasion, intravasation, circulation, extravasation, and colonization at secondary tumor sites⁵⁶.

To metastasize, cancer cells must undergo numerous changes. Among these, the epithelial-to-mesenchymal transition (EMT) is particularly important. This genetic and epigenetic-based process is critical for cell invasion and metasta-

sis and is described as a phenomenon in which epithelial tumor cells acquire mesenchymal phenotypic properties⁵⁷. However, melanoma is not an epithelial tumor, since melanocytes arise from the neural crest. Therefore, according to accumulating evidence, melanoma experiences a complex phenomenon called phenotype switching, which results in an EMT-like process⁵⁶. During this process, melanoma cells lose adhesive factors, switching from a proliferative, differentiated and stationary, epithelial-like state to an invasive, dedifferentiated and metastatic, mesenchymal-like state⁵⁸⁻⁵⁹. Normally, melanocytes are connected to basal keratinocytes by adhesion molecules, such as E-cadherins. However, during this transition, E-cadherins are replaced by N-cadherins. This modification contributes to the migration of melanoma cells, as N-cadherins support their survival and increase contact with other cells, promoting migration and proliferation³⁴⁻⁶⁰.

Notably, this transition is not permanent. Some evidence has demonstrated that cells can switch back to a mesenchymal state after undergoing EMT, in a process called mesenchymal-to-epithelial transition (MET). Melanoma cells, through their ability to switch phenotypes, undergo a MET-like process that promotes the spread of cancer to other organs, as the cells return to a more proliferative state⁵⁷.

Avoiding Immune Destruction

The immune system is essential for survival, defending the host against various pathogens and cancer cells. Notwithstanding, cancer cells develop ways to evade detection and destruction by manipulating multiple immune pathways.

T Cells Dysfunction

T cells are an essential component of the acquired immune response. Based on the type of glycoprotein expressed on their membrane surface, two types of T cells can be discerned: CD4+ T cells, commonly referred to as helper T cells (Th), and CD8+ T cells, also known as cytotoxic T cells (Tc)⁶¹. Both play an important role in preventing melanoma progression. While CD4+ T cells release cytokines to induce or suppress other immune cells, CD8+ T cells kill infected and tumor cells⁶².

Melanoma cells disrupt the effective immunological activity of T cells to evade immune system control. One of the most prominent immune pathways affected involves the abnormal expression of IC molecules. ICs are proteins expressed on the surface of immune cells, such as T cells, that recognize and bind to partner proteins expressed on other cells, including antigen-presenting cells (APCs) and tumor cells. This interaction sends an “off” signal to the T cells, suppressing their activation and hindering their immune and effector functions⁶³.

Under normal conditions and immunological homeostasis, this transmission of inhibitory signals occurs to prevent overreaction and autoimmunity⁶⁴. Nevertheless, in melanoma, the immunological homeostasis is disturbed, and the overexpression of IC receptors and their ligands on immune and tumor cells, results in immune inhibition rather than tumor cell death. Numerous ICs have been studied and others are currently under investigation. LAG-3 is the focus of the latest ICI therapy.

Regarding immune suppression, regulatory T cells (Tregs) are fundamental. Tregs are a subtype of CD4+ T cells

whose primary function is to regulate the immune system by suppressing other immune cells⁶⁵. Tregs, like IC, are critical for maintaining self-tolerance. In melanoma, these immunosuppressive T cells are increased in the TME⁶⁵. Tregs release immunosuppressive cytokines, such as interleukin 10 (IL-10), IL-35, and transforming growth factor-beta (TGF- β), that suppress immune cell activity and release cell membrane soluble mediators, such as granzymes and perforin, which induce T cell apoptosis^{65,66}. Melanoma cells can also increase the expression of IC receptors on the surface of Tregs, once again leading to the escape of the immune system. On the other hand, Tregs interfere with metabolic pathways within the TME, by depleting ATP. This reduces the proliferation of effector T cells and suppresses the activity of dendritic and myeloid cells⁶⁵.

Dendritic Cells

Antigen processing and presentation is a critical step for T cell activation and proliferation, making it a key process during an immune response. It is mediated by professional APCs, such as dendritic cells (DCs), B cells and macrophages. These cells recognize, process and present antigens to T cells through the major histocompatibility complex (MHC). CD4+ T cells recognize the antigen in complex with MHC class II (MHC II) and CD8+ T cells recognize the antigen only when it is presented via MHC class I (MHC I).

During melanoma progression, the proper function, maturation and migration of DCs are significantly disrupted. Accordingly, tumor and associated immune cells produce vascular endothelial

growth factor (VEGF), which suppresses DCs maturation and migration via the signal transducer and activator of transcription 3 (STAT-3) pathway^{67,68}.

Additionally, Tregs and tumor cells release high levels of TGF- β , and IL-10⁶⁸. These immunosuppressive cytokines interfere with the maturation and migration of DCs to the lymph nodes by negatively regulating the expression of MHC II and the co-stimulatory B7 molecules (CD80/CD86)^{66,68}. This results in defective antigen presentation, which is crucial for T cell activation⁶⁶.

Moreover, antigen presentation by melanoma cells is also disturbed. Melanoma cells can present their antigens to active CD8+ T cells via MHC I, located on the surface of their membrane. As a result of epigenetic changes, melanoma cells downregulate and mask MHC I, making them less recognizable to the immune system^{66,67}.

Myeloid-Derived Suppressor Cells

Myeloid-derived suppressor cells (MDSCs) are a subset of myeloid cells with immunosuppressive functions. Due to their ability to inhibit an adequate immune response and promote cancer metastasis, several reports have shown a negative correlation between high levels of MDSCs and survival⁶⁹.

MDSCs express negative IC molecules and produce cytokines, namely TGF- β and IL-10, as well as prostaglandin E2 (PGE2), and exosomes. These elements contribute to the dysfunction of T and natural killer (NK) cells, while also promoting the induction of Tregs. Additionally, MDSCs facilitate the dissemination of cancer cells by promoting angiogenesis and supporting the processes of EMT and MET⁷⁰.

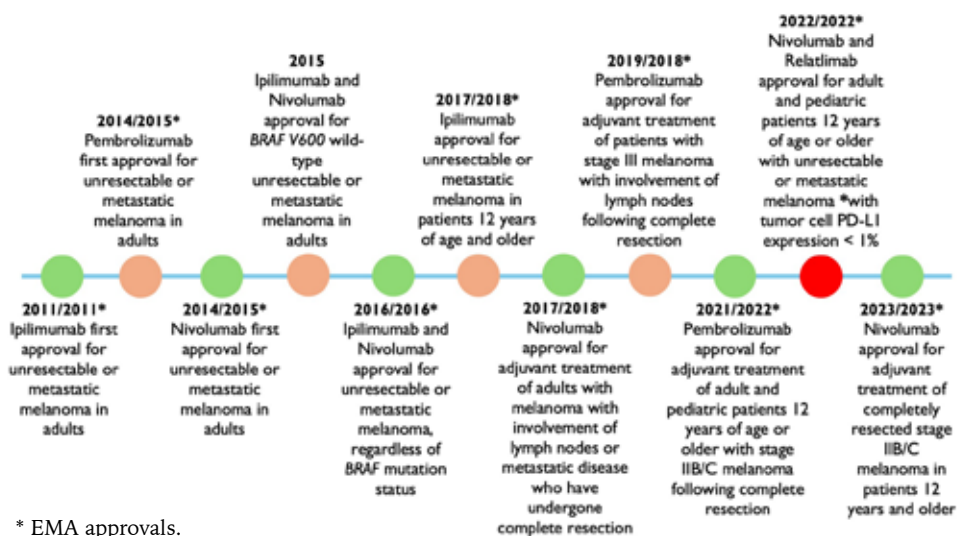
Another immune escape mechanism orchestrated by MDSCs involves their differentiation into tumor-associated macrophages (TAMs) and the subsequent oscillation between M1 or M2 macrophages⁶⁶. The M1 phenotype, mediated by Th1 polarization of TAMs, has anti-tumor properties. M1 macrophages exert their anti-tumor properties by secreting pro-inflammatory cytokines, ROS, and nitric oxide (NO). In addition, they act as effective APCs, thereby enhancing the adaptive anti-tumor immune response. On the other hand, M2 polarization, which is induced by Th2 and predominates in melanoma patients, inhibits T cell activity by activating Tregs and promotes melanoma progression^{66,69}. This switch from M1 to M2 macrophages occurs as melanoma progresses to more advanced stages, supporting tumor immune invasion⁶⁶.

Immune Checkpoint Inhibitors

Over the past decade, there have been major advances in the treatment of melanoma, largely due to the growing development of immunotherapy. The

introduction of the first ICI in 2011, as illustrated in Figure 3, changed the therapeutic paradigm and gave patients renewed hope. ICIs have proven effective in increasing both progression-free survival (PFS) and overall survival (OS) in several patients, establishing them as a key option in melanoma treatment⁷¹. As a matter of fact, according to the American Society of Clinical Oncology (ASCO) guidelines, ICIs are the mainstay of first-line treatment for advanced melanoma⁷². The recent approval of the first LAG-3 blocking antibody by the Food and Drug Administration (FDA) and the European Medicines Agency (EMA), in 2022 (Figure 3), has brought a breath of fresh air to advanced melanoma immunotherapy, and made the decision for first-line ICI therapy, which previously relied on cytotoxic T-lymphocyte-associated protein 4 (CTLA-4) and programmed cell death protein 1 receptor (PD-1) inhibitors, more challenging⁷³.

This chapter will cover each of the ICI immunotherapies used in advanced stages of melanoma, with a particular focus on anti-LAG-3 immunotherapy.



* EMA approvals.

Figure 3. Timeline of FDA and EMA approvals of ICI-based immunotherapies for the treatment of melanoma⁷⁴⁻⁹⁴.

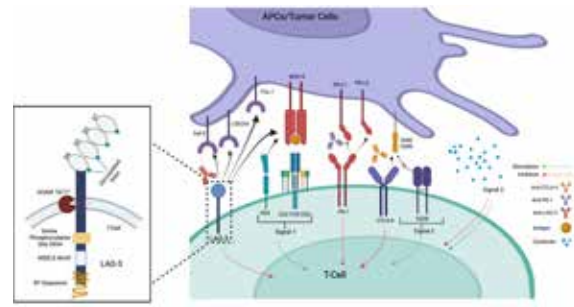
Anti-CTLA-4

CTLA-4 is a cell surface receptor expressed on T cells that plays a crucial role in immune homeostasis. It is constitutively activated in Tregs, whereas conventional T cells express high levels of this receptor only upon activation⁹⁵.

T cell activation depends on three major signals: antigen presentation and recognition, co-stimulation, and cytokines. The initial signal involves the binding of the T cell receptor (TCR) to the antigen-MHC complex presented by APCs and the interaction between CD4 co-receptor and MHC. This interaction, which upregulates CTLA-4 on T cells, is not sufficient for full T cell activation and a second signal is required. This second signal is mediated by the co-stimulatory interaction between CD28, expressed on T cells, and B7 molecules on APCs, and it is precisely in this process that CTLA-4 interferes. Cytokines, in turn, influence the polarization of naive T cells into different subtypes.

CTLA-4 acts as a competitive antagonist of the CD28 receptor, by inhibiting its co-stimulatory signal with its B7 ligands. Although both receptors bind to B7 molecules expressed on the surface of APCs, CTLA-4 has a higher affinity. Thus, by mediating a co-inhibitory signal through its interaction, CTLA-4 initiates a signaling cascade that results in the suppression of T cells activity⁷¹.

Anti-CTLA-4 monoclonal antibodies block the interaction between CTLA-4 and B7 molecules, allowing CD28 co-stimulation, which subsequently activates T cells and enhances the immune response against cancer cells⁹⁶. Figure 4 illustrates this mechanism.



Abbreviations: ADAM 10 - A Disintegrin and Metalloproteinase 10; ADAM 17 - A Disintegrin and Metalloproteinase 17; CTLA-4 - Cytotoxic T-Lymphocyte-Associated Protein 4; FGL-1 - Fibrinogen-Like Protein 1; Gal-3 - Galectin-3; LAG-3 - Lymphocyte-Activation Gene 3; LSECtin - Lymph Node Sinusoidal Endothelial Cell C-Type Lectin; MHC II - Major Histocompatibility Complex II; PD-1 - Programmed Cell Death Protein 1 Receptor; PD-L1 - Programmed Death-Ligand 1; PD-L2 - Programmed Death-Ligand 2; TCR - T Cell Receptor.

Figure 4. Overview of the mechanism of action of LAG-3, CTLA-4 and PD-1 with a focus on LAG-3 structure (Created in BioRender).

Ipilimumab, a fully human anti-CTLA-4 monoclonal antibody, was the first ICI approved by the FDA and the EMA in 2011. This approval was a game changer in melanoma therapy, marking a revolutionary breakthrough in cancer treatment. Since then, research into ICIs has continued, and immunotherapy is increasingly at the forefront of the treatment of many cancers.

Anti-PD-1

The receptor PD-1 is expressed on various immune cells, namely T cells, B cells and NK cells⁹⁶. PD-1 mediates a co-inhibitory signal by binding to its ligands, programmed death-ligand 1 (PD-L1) and programmed death-ligand 2 (PD-L2), leading to T cell inactivation⁷¹. PD-L1 and PD-L2 are widely expressed. While PD-L1 is expressed on T cells, B cells, DCs, and macrophages, as well as in non-lymphoid tissues among tumor cells or stromal elements in the TME,

PD-L2 is mainly expressed on DCs and monocytes but can also be expressed in other immune and non-immune cells^{71,96}. Melanoma cells can express both PD-1 ligands, which allow them to escape immune destruction⁹⁷.

In 2014, the FDA approved pembrolizumab, a humanized anti-PD-1 monoclonal antibody, for the treatment of advanced melanoma. In the same year, nivolumab, a fully human anti-PD-1 monoclonal antibody, was approved for the same therapeutic indications (Figure 3). Both antibodies work by binding to the PD-1 receptor, thereby blocking its inhibitory signaling and reactivating T cell function, as presented in the Figure 4⁹⁸.

To achieve better clinical outcomes, the combination of anti-CTLA-4 and anti-PD-1 monoclonal antibodies is widely employed. Indeed, the association of ipilimumab and nivolumab is one of the first-line treatments in advanced melanoma, as multiple studies have shown greater clinical outcomes, traduced by longer PFS and higher objective response rate (ORR), compared to monotherapy^{99,100}. In terms of median survival, the combination therapy showed striking results, extending patient survival from a mere 6 months to approximately 6 years³.

Remarkably, CheckMate 067, a phase III study that compared the safety and efficacy of nivolumab alone, nivolumab and ipilimumab dual therapy, or ipilimumab monotherapy, in previously untreated patients with unresectable stage III or IV melanoma, was the cornerstone for the extended approval of nivolumab and ipilimumab for the treatment of advanced melanoma regardless of *BRAF* mutation status¹⁰¹.

However, safety remains a major concern, as several immune-related adverse events (irAEs) have been reported among patients, many of which have led to premature discontinuation of treatment^{99,102}. These side effects, along with treatment tolerance and resistance, underscored the urgent need to develop new ICIs that target alternative pathways⁹⁹. Anti-LAG-3 has emerged as one of the most promising candidates¹⁰³.

Anti-LAG-3

First described in 1990 by Frédéric Triebel and colleagues, LAG-3 is an IC receptor expressed by activated T cells, NK cells, B cells, and DCs¹⁰³. LAG-3 is formed by 498 amino acids and is encoded by a gene located on human chromosome 12, adjacent and homologous to CD4¹⁰⁴. Structurally, it consists of 3 regions: transmembrane region, extracellular region, and cytoplasmic region. In the transmembrane-cytoplasmic region, LAG-3 is cleaved from the cell membrane by the action of A disintegrin and metalloproteinases 10 and 17 (ADAM10 and ADAM17). The extracellular region comprises four immunoglobulin superfamily domains (D1, D2, D3 and D4), which are essential for binding to ligands. Finally, the cytoplasmic region can be divided into 3 parts: the serine phosphorylation site S454, the KIEELE motif, and the glutamate-proline dipeptide repeat motif, known as EP sequence^{103,104}. Figure 4 illustrates the structure of LAG-3.

LAG-3 expression on T cells is upregulated by TCR stimulation or by cytokines, such as IL-2, IL-7 and IL-12^{105,106}. Regarding its ligands, LAG-3 interacts with MHC II, galectin-3 (Gal-3), lymph node sinusoidal endothelial cell C-type

lectin (LSEctin), fibrinogen-like protein 1 (FGL-1) and α -synuclein fibrils (α -syn), to dampen T cell functions¹⁰⁷. MHC II on APCs is the canonical ligand of LAG-3. Given the similarity between LAG-3 and CD4, and the fact that LAG-3 has a greater affinity for MHC II, it would be expected that one of the main inhibitory mechanisms of LAG-3 would be its competition with CD4. However, this remains controversial, since some studies revealed that LAG-3 does not block the interaction between MHC II and CD4^{103,108}. Rather, it is more likely that LAG-3, once combined with MHC II through its D1 domain, exerts its inhibitory effects via its cytoplasmic domain¹⁰³. Even though the exact mechanisms of this signaling are not fully understood, as a result of this negative regulation occurs a downregulation of T cell cytokine and granzyme production, CD4+ and CD8+ T cell activation and expansion are inhibited and Treg differentiation is increased^{104,108,109}.

Gal-3 was the second LAG-3 ligand to be described¹⁰⁶. It is expressed in melanoma cells and other cells within the TME, and its interaction with LAG-3, according to *in vitro* experiments, inhibits the secretion of interferon-gamma (IFN- γ) by CD8+ T cells, thus affecting an adequate immune response¹⁰³. Another potential LAG-3 ligand is LSEctin. LSEctin is expressed in melanoma cells, and by binding to the four glycosylated sites expressed in the extracellular region of LAG-3, suppresses T cell response and sustains tumor growth^{103,110}. FGL-1 is also an important ligand of LAG-3, and it is overexpressed in melanoma¹⁰⁶. Through its interaction with the D1 and D2 domains of LAG-3, FGL-1 mediates its immunosuppressive activity by inhibiting the activation of antigen-speci-

fic T cells^{103,110}. Besides, LAG-3 appears to interact with α -syn in the central nervous system, suggesting that LAG-3 may also play a role outside the immune system¹⁰³.

As far as melanoma is concerned, it is characterized by aberrant expression of LAG-3, with tumor-infiltrating lymphocytes (TILs) in the TME expressing high levels of this IC. This high expression enhances immune escape and melanoma growth¹⁰⁹. Therefore and considering all that have been discussed about the functions of LAG-3, it is expected that LAG-3 inhibition will restore the immunological functions of several immune cells and halt the progression of melanoma. Reflecting this, relatlimab, the first human LAG-3 blocking monoclonal antibody, was approved by the FDA and the EMA in 2022 for the treatment of unresectable or metastatic melanoma. Relatlimab binds to LAG-3 and inhibits its interaction with MHC II and other ligands, thereby not only enhancing T cell immune activity and cytokine release but also inhibiting Treg activity^{103,104}.

Interestingly, increasing evidence suggests that LAG-3 and PD-1 can be co-expressed in CD4+ and CD8+ TILs and synergistically mediate their immunosuppressive functions. In preclinical murine melanoma models, dual genetic knockout of both LAG-3 and PD-1 led to delayed tumor growth and increased survival rates^{73,110}. These data highlight that simultaneous targeting of both ICs may provide therapeutic benefits, potentially overcoming the resistance observed with single agent treatments⁷³. In fact, relatlimab was approved in combination with nivolumab under the trade name Opdualag[™], following a phase II/III clinical trial⁸³.

Clinical Trials

The approval of Opdualag™ was based on the RELATIVITY-047 clinical trial. Since then, numerous studies have been conducted to assess the efficacy and safety of this innovative dual immunotherapy, as well as to explore new molecules targeting LAG-3.

RELATIVITY-047

RELATIVITY-047 is a II/III phase, double-blind and randomized trial comparing the efficacy and safety of the combination of relatlimab and nivolumab *versus* nivolumab monotherapy, in 714 patients with previously untreated metastatic or unresectable melanoma¹¹¹. After a median follow-up of 13.2 months, the results turned out to be very promising, which supported its approval as a new first-line treatment option for advanced melanoma¹¹¹⁻¹¹². In fact, the study successfully met its primary endpoint, with the combination of relatlimab and nivolumab more than doubling the median PFS compared to nivolumab alone (10.1 months *versus* 4.6 months) and reducing the risk of melanoma progression by 25%. Notably, among the study subgroups, the combination therapy also reached longer PFS¹¹¹.

Regarding safety, the dual therapy was associated with a higher rate of treatment-related adverse events (TRAEs) of any grade, with these occurring in 81.1% of patients, compared to 69.9% of those treated with nivolumab alone. Grade 3-4 TRAEs were observed in 18.9% of patients receiving the combination *versus* 9.7% in the monotherapy group, with more patients discontinuing treatment due to these adverse events in

the combination group (8.5% vs 3.1%). The most common irAEs were hypothyroidism or thyroiditis, affecting 18.0% of patients treated with relatlimab and nivolumab and 13.9% of patients after nivolumab treatment¹¹¹.

Overall, adverse events were more frequent in the relatlimab and nivolumab group, nevertheless, no new or unexpected safety signals were associated with this novel combination treatment¹¹¹.

The secondary endpoints remained blinded, because the difference in OS did not reach statistical significance¹¹¹. Therefore, an updated report with a median follow-up of 19.3 months was conducted¹¹³. From this second follow-up, it was evident that OS rates at 12, 24, and 36 months were consistently better with combination therapy compared to monotherapy. Specifically, OS rates were 77.0% *versus* 71.6% at 12 months, 63.7% *versus* 58.3% at 24 months, and 55.8% *versus* 48.8% at 36 months, respectively. On the other hand, ORR was higher with the dual immunotherapy. In the updated analysis, ORR was 43.1% for relatlimab plus nivolumab group and 32.6% for the nivolumab therapy. Complete and partial responses were achieved in a greater percentage of patients with combination therapy. It should be noted that relatlimab combined with nivolumab continued to demonstrate a durable PFS advantage. This ongoing PFS benefit was observed alongside a stable safety profile compared to the initial report^{112,113}.

RELATIVITY-047 also assessed the health-related quality of life (HRQoL) of patients. The results showed that, although more adverse events were re-

ported with the combination therapy, overall tolerability was similar in both arms, supporting the dual PD-1 and LAG-3 inhibition as a viable first-line treatment¹¹⁴.

Lastly, it is important to highlight that these findings suggest a favorable safety profile and comparable efficacy when compared to reports from clinical trials involving dual checkpoint inhibition with CTLA-4 and PD-L1 inhibitors. However, as cross-trial comparisons should be made with caution, a head-to-head clinical trial comparing both therapeutic combinations in different key subgroups

may be of interest to gather more data and allow a clearer choice between the first lines of treatment. Moreover, such a trial could also play a decisive role in identifying and validating additional predictive biomarkers for these subgroups undergoing therapy. This is particularly significant given that these therapies are the most widely used in the treatment of advanced melanoma and there is currently a lack of reliable biomarkers in melanoma¹⁰²⁻¹¹⁵. An indirect comparative analysis between the RELATIVITY-047 and the CheckMate 067 clinical trials is presented in Table 2 below.

Table 2. Comparison of the efficacy and safety data of RELATIVITY-047 and CheckMate 067 clinical trials^{101,111,113,116}

Results	RELATIVITY-047		CheckMate 067		
	Relatlimab/ Nivolumab	Nivolumab	Ipilimumab/ Nivolumab	Nivolumab	Ipilimumab
Median PFS (months)	10.2	4.6	11.5	6.9	2.9
Median OS (months)	NR	34.1	NR	37.6	19.9
ORR (%)	43.1	32.6	57.6	43.7	19.0
2-year PFS (%)	38.5	29.0	43.0	37.0	12.0
2-year OS (%)	63.7	58.3	64.0	59.0	45.0
TRAEs of any grade (%)	81.1 (14.6*)	69.9 (6.7*)	95.5 (36.4*)	82.1 (7.7*)	86.2 (14.8*)
Grade 3-4 (%)	18.9 (8.5*)	9.7 (3.1*)	55.0 (29.4*)	16.3 (5.1*)	27.3 (13.2*)

Abbreviations: NR - Not Reached; ORR - Objective Response Rate; OS - Overall Survival; PFS - Progression Free Survival; TRAEs - Treatment-Related Adverse Events.

*Led to treatment discontinuation.

RELATIVITY-020

Despite therapeutic innovation in advanced melanoma, approximately 40% of patients continue to have no significant response, even with first-line immunotherapies. Thus, novel therapies, such as relatlimab and nivolumab, are crucial to improving outcomes and preventing disease progression¹¹⁷.

RELATIVITY-020, an open-label phase I/IIa, dose escalation and cohort expansion trial, assessed the efficacy and safety of the combination of relatlimab and nivolumab in 518 patients with advanced melanoma who had documented progression after immunotherapy. Two study cohorts, D1 and D2, were conducted. Each cohort was established according to the prior treatment received by the participants and followed distinct dosing regimens. Cohort D1 included only patients with one prior line of anti-PD-1 therapy, either alone or in combination with anti-CTLA4. In contrast, D2 allowed multiple lines of treatment, including patients who had received prior adjuvant or neoadjuvant anti-PD-1 therapies^{112,117}.

In terms of efficacy, the ORR observed was 12% and 9.2% in the D1 and D2 pooled, respectively. The median PFS was lower in cohort D1 compared to D2 (2.1 vs 3.2 months). Furthermore, the median duration of response (DOR), although not achieved in D1 group, was 12.8 months in D2 cohort. Finally, the median OS was 14.7 months in D1 group and 17.1 months in D2¹¹⁷.

Safety was measured by the rate of adverse events and was similar in both groups. As a matter of fact, the incidence of TRAEs of any grade was 67.5% in D1 cohort and 68.9% in D2 cohort.

Of these, 15% and 12.8% corresponded to grade 3-4 reactions in groups D1 and D2, respectively. Rash (7.3%) was the most frequent irAEs in D1 and D2 groups¹¹⁷.

Considering all these data, the combination therapy of relatlimab and nivolumab provided promising results in terms of efficacy and safety, regardless of the cohorts. Therefore, for patients who are refractory to previous PD-(L)1 inhibitor-containing regimens, the new dual therapy could be a very viable option. Nevertheless, the single-arm design of this study is a limitation, and further studies, like phase III trials, are needed to confirm the use of this new combination in later lines of therapy^{112,117}. In parallel, better predictive biomarkers should also be investigated, in order to ensure a significant clinical response among the subgroups.

Other Studies

An example is a study involving 30 patients with resectable clinical stage III or oligometastatic stage IV melanoma without prior ICI therapy, that evaluated the safety and efficacy of relatlimab and nivolumab as neoadjuvant and adjuvant therapy¹¹⁸. This study followed an earlier trial comparing nivolumab and ipilimumab with nivolumab alone, also in the neoadjuvant and adjuvant settings¹¹⁹.

Remarkably, the neoadjuvant combination of nivolumab and relatlimab demonstrated positive results. A complete pathological response (pCR) was observed in more than half of the patients (57%), with 70% of patients experiencing some clinical response¹¹⁸. In contrast, pCR rates were significantly

lower with nivolumab plus ipilimumab and nivolumab monotherapy (45% and 25%, respectively)¹¹⁹. Moreover, recurrence-free survival (RFS) rates were 97% and 82% in the first and second year, respectively, after treatment with the novel dual therapy¹¹⁸.

Regarding safety, no grade 3-4 irAEs were reported in the neoadjuvant setting. Contrarily, 26% of patients experienced irAES in the adjuvant setting, which raises the question of whether adjuvant therapy is necessary following an effective neoadjuvant regimen¹¹⁸. When comparing these results with both arms of the previous trial, the difference in safety is striking. Indeed, 27% of combination patients had their surgery postponed due to immunotherapy toxicity and 73% reported grade 3 TRAEs¹¹⁹.

Despite the small sample size and the need for further studies, these data are very encouraging, as neoadjuvant

therapy with LAG-3 and PD-1 blockade shows lower toxicity and a higher efficacy and tolerability than previous regimens.

Beyond relatlimab, other anti-LAG-3 therapies are currently under investigation, including fianlimab, an anti-LAG-3 human monoclonal antibody. Interestingly, fianlimab in combination with cemiplimab, an anti-PD-1 monoclonal antibody, has shown promising results in preclinical studies. This new dual immunotherapy is undergoing several phase III clinical trials¹¹².

Eftilagimod alfa (IMP321), bi-specific antibodies targeting LAG-3 and CTLA-4 (XmAb22841) or PD-1 and LAG-3 (RO7247669 and INCA32459), and other innovative anti-LAG-3 molecules, such as INCAGN02385, are also being evaluated^{102,112}. Table 3, lists the ongoing clinical trials targeting anti-LAG-3 molecules.

Table 3. Ongoing clinical trials investigating relatlimab and other anti-LAG-3 molecules in melanoma¹²⁰⁻¹³⁶

Agent	NCT Number	Condition	Focus	Phase	Status
Relatlimab	NCT05704647	Active melanoma brain metastases	Evaluate the efficacy and safety of nivolumab and relatlimab combination	II	Recruiting
	NCT03743766	Unresectable or metastatic melanoma without prior treatment	Evaluate the antitumor activity of relatlimab and nivolumab	II	Active, not recruiting
	NCT05625399	Untreated metastatic or unresectable melanoma	Compare nivolumab and relatlimab subcutaneous fixed-dose combinations with intravenous administration	III	Recruiting
	NCT04552223	Metastatic uveal melanoma without prior treatment	Evaluate the efficacy (ORR) of nivolumab and relatlimab combination	II	Active, not recruiting
	NCT06295159	Locoregionally advanced melanoma	Compare nivolumab plus relatlimab, nivolumab and ipilimumab in neoadjuvant therapy	I	Recruiting

Table 3. Ongoing clinical trials investigating relatlimab and other anti-LAG-3 molecules in melanoma¹²⁰⁻¹³⁶ (cont)

Agent	NCT Number	Condition	Focus	Phase	Status
Relatlimab	NCT05002569	Completely resected stage III-IV melanoma	Compare adjuvant therapy of nivolumab plus relatlimab with nivolumab monotherapy	III	Active, not recruiting
	NCT05418972	High risk, clinical stage II cutaneous melanoma	Evaluate the efficacy of nivolumab and relatlimab in the neoadjuvant setting	II	Recruiting
	NCT05704933	Surgically resectable melanoma brain metastases	Evaluate the safety and feasibility of nivolumab with ipilimumab or relatlimab	I	Active, not recruiting
	NCT05077280	Metastatic uveal melanoma	Evaluate the safety and tolerability of nivolumab and relatlimab with radiotherapy	II	Recruiting
Fianlimab	NCT05352672	Untreated unresectable locally advanced melanoma or metastatic melanoma	Compare the efficacy of fianlimab and cemiplimab combination against pembrolizumab	III	Recruiting
	NCT06246916	Unresectable or metastatic melanoma	Compare the efficacy and safety of fianlimab and cemiplimab with nivolumab and relatlimab combination	III	Recruiting
	NCT05608291	Completely resected high-risk melanoma	Compare the efficacy and safety of fianlimab combined with cemiplimab against pembrolizumab	III	Recruiting
	NCT06190951	Resectable stage III and IV melanoma	Compare the efficacy of fianlimab and cemiplimab combination against pembrolizumab	II/III	Not yet recruiting
XmAb22841	NCT05695898	Metastatic melanoma refractory to prior ICI immunotherapy with and without central nervous system disease	Evaluate the safety and tolerability of XmAb22841 (CTLA-4 X LAG-3) in combination with XmAb23104 (PD-1 X ICOS)	Ib/II	Active, not recruiting

Table 3. Ongoing clinical trials investigating relatlimab and other anti-LAG-3 molecules in melanoma¹²⁰⁻¹³⁶ (cont)

Agent	NCT Number	Condition	Focus	Phase	Status
INCAGN02385	NCT04370704	Advanced melanoma	Evaluate the safety and tolerability of INCAGN02385 (Anti-LAG-3) + INCAGN02390 (Anti-TIM-3) and INCAGN02385 + INCAGN02390 + INCMGA00012 (Anti-PD-1) combinations	I/II	Active, not recruiting
RO7247669	NCT04140500	Metastatic melanoma	Evaluate the safety and tolerability of RO7247669 (Anti PD-1 and LAG-3)	I/II	Recruiting
INCA32459	NCT05577182	Unresectable or metastatic melanoma	Evaluate the safety and tolerability of INCA32459 (Anti PD-1 and LAG-3)	I	Recruiting

Abbreviations: CTLA-4 - Cytotoxic T-Lymphocyte-Associated Protein 4; ICOS - Inducible T Cell Costimulatory; LAG-3 - Lymphocyte-Activation Gene 3; ORR - Objective Response Rate; PD-1 - Programmed Cell Death Protein 1 Receptor; TIM-3 - Mucin Domain-Containing Protein 3.

Conclusion and Future Perspectives

Melanoma is a complex and deadly skin cancer, characterized by several pathways of development and a high mutational load. In its most advanced stages, melanoma has a severe prognosis. Progress in immunotherapy, particularly ICIs, have therefore become extremely important, making this therapy the cornerstone of the treatment of advanced melanoma.

Relatlimab, the first approved anti-LAG-3 antibody, in combination with nivolumab, has shown promising clinical results in the treatment of untreated and refractory advanced melanoma, as well as in the adjuvant and neoadju-

vant settings. However, multiple critical questions remain unanswered.

As discussed in this review, the precise mechanism of action of LAG-3 is still unclear. Since LAG-3 plays an important role in the immunoregulation of melanoma and other human cancers, further work is needed to elucidate its mechanism of action, as this knowledge is undoubtedly essential for the optimal use of any anti-LAG-3 immunotherapy and for future research into new molecules targeting this IC.

Regarding the combination therapy of relatlimab and nivolumab, this review has highlighted its clinical results, with safety results standing out compared to

other first-line therapies. In fact, this was a key factor in its approval, as ICI immunotherapy is associated with many adverse events, many of which are serious and lead to treatment discontinuation. Nevertheless, additional studies are required to evaluate the efficacy and safety of this combination in patient subgroups beyond those included in the aforementioned clinical trials, such as brain metastases or rare melanoma subtypes.

Additionally, given the recent approval of this novel dual therapy, long-term data on PFS and OS are still needed, along with the identification of predictive biomarkers. Immunotherapy is an expensive treatment and is associated with resistance and tolerability, so the existence of accurate biomarkers would ensure a rigorous selection of patients who would actually benefit clinically from this therapy, sparing them from unwanted side effects and treatment failure.

Apart from LAG-3, other ICIs, such as T cell immunoglobulin and mucin domain-containing protein 3 (TIM-3) and T cell immunoglobulin and ITIM domain (TIGIT) also hold the potential to revolutionize melanoma treatment. The emergence of these and other novel molecules, alongside the several anti-LAG-3 agents currently undergoing clinical trials, points to a promising future for therapeutic strategies in advanced melanoma.

Through sustained innovation and rigorous pursuit of unanswered questions, immunotherapy with anti-LAG-3 is expected to maintain its position at the forefront of advanced melanoma treatment. Continued progress in this field could therefore, unquestionably, lead

to further improvements in the efficacy and safety of ICIs therapies, ultimately enhancing both survival outcomes and quality of life for patients.

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