

Repare Therapeutics

Insight that enriches. Precision that empowers.

CORPORATE PRESENTATION

Q1 2023

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RP-6306, a first-in-class, oral PKMYT1 inhibitor, drives genomic instability in CCNE1amplified tumors with Ph 1 monotherapy and multiple combination trials ongoing



Robust pipeline of SL-based therapeutic opportunities, including Polθ and a pipeline of advanced preclinical opportunities



Balance Sheet of \$344M funds Repare through multiple value-creating milestones into 2026



Camonsertib (RP-3500 / RG6526), a potential best-in-class ATR inhibitor with durable responses and clinical benefit in Ph 1/2 and strategic validation through Roche partnership





Proprietary genome-wide CRISPR-enabled SNIPRx platform, focused on genomic instability and DNA damage repair, enabling novel target identification and differentiated patient selection insights

HERAPEUTICS

Proven experience in drug discovery and development



Leadership Team





Daniel Durocher, PhD

- Developed CRISPR SL platform
- Deep DNA repair knowledge
- Lunenfeld-Tanenbaum Research Institute (LTRI) & professor at University of Toronto



Agnel Sfeir, PhD

- DDR and cancer pathway investigator
- Pioneer in Polθ, genome instability
- Professor, MSKCC



Frank Sicheri, PhD

- Globally recognized structural biologist, expert in eukaryotic cell signaling, drug mechanism of action
- LTRI & professor at University of Toronto



Focused on precision oncology for untapped cancer lesions



Repare has identified several novel and proprietary targets to date



Robust pipeline of SL-based precision oncology therapeutics

		SL	Pair	ן					
		Lesion Network	Drug Target	Discovery	IND-Enabling	Phase 1/2	Pivotal	Anticipated Milestones	Rights
Clinical	Camonsertib (RP-3500 / RG6526)	ATM + 16 STEP ² lesions	ATR	Ph1/2 TRESR: Monotherapy Ph1/2 TRESR: PARP (talazoparib) Combo Ph1/2 ATTACC: PARP (olaparib/niraparib) Combo Ph1/2 TRESR: Gemcitabine Combo Ph2 CCTG BASKET IST Ph1 MYTHIC: Mono + Camonsertib Combo Ph1 MAGNETIC: Gemcitabine Combo Ph1 MINOTAUR: FOLFIRI Combo			 H1'23 initial PARP combination data Summer/Fall '23 initial gemcitabine combination data 	Reche REPARE THERAPEUTICS	
	PKMYT1 inhibitor RP-6306	CCNE1, FBXW7, PPP2R1A	PKMYT1				 2023 Ph2 Basket IST start H1'23 Ph1 carboplatin combination study start H1'23 initial Ph1 monotx data Q4'23 initial Ph1 combination data 	REPARE THERAPEUTICS	
Preclinical	Undisclosed	Undisclosed	Undisclosed				 H1'23 IND-enabling studies Late '23/Early '24 Clinic 	REPARE THERAPEUTICS	
	Polθ inhibitor	BRCA1/2 + others	ΡοΙθ	-				 2024 Clinical entry 	
Discovery	SNIPRx [®] platform	Additional SL targets in advanced stages of development						REPARE THERAPEUTICS	
		Discovery and validation of new SL precision oncology targets							Bristol Myers Squibb
									DEDADE

THERAPEUTICS



SNIPRx[®] platform



SNIPRx® platform for synthetic lethal ("SL") drug discovery







SNIPRx® campaigns mine targeted genomic instability lesions



We have mined an initial 16 largely mutually exclusive tumor lesions representing ~30% of all tumors



STEP² screens expand patient population tailored to each program



STEP² screens: SNIPRx Targeted Expansion of Patient Populations

- Expands patient populations beyond those identified by original SL pair
- STEP² insights enable precision medicine-driven clinical trials





REPARE THERAPEUTICS

Ull Bristol Myers Squibb™

Multi-target discovery collaboration with Bristol Myers Squibb to leverage Repare's proprietary SNIPRx[®] synthetic lethal discovery platform to identify multiple oncology drug candidates

~\$65M upfront

Including \$50M non-dilutive cash and \$15M equity investment

~\$3 billion

Potential total milestone payments in addition to royalties (~\$300M/program)

Target focused

Includes both small molecule SL targets and "undruggable" targets outside our focus

Discovery only

Repare retains all rights to its remaining pipeline





PKMYT1 inhibitor RP-6306





RP-6306 exploits vulnerabilities caused by increases in CCNE-1, not previously considered a druggable target



Preclinical data differentiates as potent and highly selective, with anti-tumor activity especially in combination



Many affected tumor types, including gynecological and gastrointestinal malignancies



Synthetic lethal combinations with CCNE1 amplified, FBXW7 loss, PPP2R1A, and other STEP² genes aid in patient selection



CCNE1 amplification drives genome instability



CCNE1-overexpression drives premature entry into S-phase and overloads the DNA replication machinery, resulting in genome instability



PKMYT1: strong hit in a CCNE1-overexpression ("O/E") SL screen

PKMYT1 (also known as Myt1):

- Membrane-associated serine/threonine protein kinase
- Member of WEE1 protein kinase family
- Negatively regulates the G2/M transition of the cell cycle by inactivating CDK1
- Not previously linked to CCNE1 amplification

 CCACKET amplification is synthesic lethal with both the synthesic lethal with the synthesic lethal

> werexpression disrupts CDK1 homeostasis at least in part through an early activ of the MMB–FOXM1 mitotic transcriptional program. We conclude that PKMYT.



- Genome-wide CRISPR screen
- PKMYT1 was the highest scoring druggable hit
- PKMYT1 was also a high scoring hit in the DepMap



PKMYT1 selectively regulates cyclin B-CDK1 complexes





	Parameter	RP-6306
Potency	Enzyme potency (IC ₅₀ , nM)	3
	HCC1569 CDK1 T14 phosphorylation (IC ₅₀ , nM)	20
	HCC1569 cell viability (EC ₅₀ , nM)	19
	PKMYT1 selectivity over WEE1 (cell-based)	>100-fold
	CYP inh (3A4, 2D6, 2C9, 1A2, 2C19)	all >30 µM
erties	Hepatocytes: rat, dog, human Cl _{int} (µL/min/10 ⁶ cells)	28, <6, <6
E Prop	Human plasma protein binding	79%
ADME	Rat PK (%F, t _{1/2})	44%, 2.6h
	Dog PK (%F, t _{1/2})	74%, 5.5h



Tumor cell lines with CCNE1-Amp are **hypersensitive** to PKMYT1 inhibition compared to cells with normal CCNE1 levels

RP-6306 profile:

- Highly potent and selective inhibitor
- PanLabs Lead Profiling screen on 68 assays showed no significant activity at 10 µM
- No activity (>100 µM) in patch clamp assays for hERG, hNaV1.5, and hCaV1.2 ion channels
- Favorable pre-clinical PK profile
- Low potential for clinical drug-drug interactions



RP-6306 selectivity on CCNE1-O/E cells vs. WEE1 inhibition



- PKMYT1 inhibition results in a 39-fold increase in sensitivity in CCNE1-O/E FT282 cells vs. wild type
 - WEE1 inhibits both wild type and CCNE1-O/E cells



RP-6306 inhibits growth of multiple CCNE1-amplified xenograft tumors



RP-6306 anti-tumor activity seen or demonstrated at doses well below MTD



RP-6306 + gemcitabine synergize to drive regression with tolerability



- Xenograft tumors continue to regress after dosing cessation with several mice having no measurable tumor detected
 - Measured three times a week, mice at each dose level experienced <7% (monotherapy) and maximum of 10% (gemcitabine combo) body weight loss

Gemcitabine dosed once a week and RP-6306 dosed twice daily; CCNE1 CN = 14



STEP² screen identified FBXW7 as sensitive to PKMYT1 inhibition

- E3 ubiquitin ligase that targets proteins, such as CCNE, for proteasomal degradation
- **FBXW7** Frequently mutated in tumors
 - Inactivating mutations can increase CCNE levels





RP-6306 inhibits growth of FBXW7 mutant PDX models



- RP-6306 is active across tumor models with clinically relevant hotspot mutations
 - Pre-clinical data supports expanding patient populations for RP-6306



Top 10 tumor types with highest prevalence of CCNE1 amplification and FBXW7 mutations deficiency



CCNE1 amplification or FBXW7 loss occurs in multiple cancers with significant unmet medical need

These lesions are largely mutually exclusive and represent distinct patient populations



Source: TCGA

RP-6306 clinical program profile and objectives



Targeting tumors with STEP² genomic alterations, including CCNE1 amplification, FBXW7 loss, PPP2R1A

Trial summary & development objectives:

Eligibility:

Any solid tumor with STEP² gene alterations per local NGS or FISH with subsequent retrospective central confirmation

Early Program Objectives:

- 1. Safety, tolerability, dose and schedule Phase 1
- 2. Efficacy in tumors with STEP2 gene alterations: several Proof of Concept (POC) studies
- 3. Multiple RP-6306 based combination POC trials

RP-6306 profile/plan

- Orally available ATPcompetitive inhibitor
- Maximized potency and specificity
- Genomically defined, tumor-specific and tumor agnostic indications
- Early combination testing





RP-6306 initial global clinical trial program





Note: Phase 2 study is an investigator-sponsored basket trial planned with the Canadian Cancer Trials Group (ClinicalTrials.gov Identifier: NCT05605509).



Camonsertib (RP-3500 / RG6526) ATR inhibitor



Overview of camonsertib: a potential best-in-class ATR inhibitor





Oral ATR inhibitor and Repare's first clinical therapeutic candidate (now partnered with Roche) ATR is a critical DNA Damage Response ("DDR") protein with a central role in



Began monotherapy trial in July 2020; progressed three combination trials with compelling rationale American Association for Cancer Research[®]

Clinical validation of ATR/ATM SL relationship disclosed by Repare at AACR-NCI-EORTC (Oct 2021) and AACR (Apr 2022)

Differentiation driven by:

Potential best-in-class profile (safety and efficacy)

replication stress

regulation of

- Enhanced chemical properties (potency and selectivity)
- Proprietary patient selection insights to expand addressable patient populations



Overview of camonsertib clinical trial program

Trial results to date support expanded clinical development now partnered with Roche







Ph1/2 monotherapy trial demonstrated proof of concept in ovarian cancer





Safety Potency



Selectivity

Compelling rationale for ATRi combination therapy with PARPi, radiotherapy and PD-1/L1

Potential for best-in-class safety, potency and selectivity

Proprietary patient selection insights to expand addressable patient populations



Clinically relevant benefit in advanced ovarian cancer

Ovarian cancer patients were heavily pretreated with platinum and PARPi therapies



*2 additional pts are included in the swim plot that started Tx on PARPi combination for ≤3w and switched to monoTx; duration of Tx calculated from start of monoTx. **Platinum refractory/resistant: progression on platinum or a platinum-free interval of <6 mo. CBR: OR or ≥16w on therapy without progression



Clinically relevant benefit in patients with *BRCA1/2* mutated tumors





CBR (OR or ≥16w on therapy without progression) was 48% for BRCA1 population, and 36% for BRCA2

Durable clinical benefit in patients with ATM LOF tumors



CBR (OR or ≥16w on therapy without progression)



Anti-tumor activity is largest in tumors with biallelic loss of function

Biallelic gene loss of function (LOF) is an emerging biomarker for synthetic lethal therapies

(Not reported by routine clinical NGS assays)

47% vs. 15%

CBR significantly higher in biallelic tumors (p=0.02)

Longer PFS for biallelic (17 weeks) vs non-biallelic (11 weeks) for all subjects (not shown)

Central NGS assay, SNiPDx, (AACR 2022 poster #2801) determines biallelic LOF, germline status and CHIP alterations in TRESR

Further analysis in additional patients ongoing; Confirmation in prospective studies required

Nature. 604 (7907), pp. 749-756 (Apr 2022). https://doi.org/10.1038/s41586-022-04638-9

Clinical benefit rate (%) in biallelic vs. nonbiallelic tumors





Expected, manageable anemia; potentially best in class safety profile at well studied doses

	5d on/2d off (N=25)			3 d on/4 d off (N=95)		
Preferred Term	Grade 3 N (%)	Grade 4 N (%)	All Grade N (%)	Grade 3 N (%)	Grade 4 N (%)	All Grade N (%)
Any TRAE	14 (56.0)	1 (4.0)	22 (88.0)	28 (29.5)	4 (4.2)	81 (85.3)
Anemia	13 (52.0)	0	20 (80.0)	23 (24.2)	0	58 (61.1)
Fatigue	1 (4.0)	0	7 (28.0)	2 (2.1)	0	26 (27.4)
Neutrophil count decreased	3 (12.0)	0	6 (24.0)	10 (10.5)	3 (3.2)*	25 (26.3)
Nausea	0	0	3 (12.0)	0	0	22 (23.2)
Platelet count decreased	2 (8.0)	1 (4.0)	7 (28.0)	5 (5.3)	1 (1.1)**	17 (17.9)
Decreased appetite	0	0	4 (16.0)	0	0	14 (14.7)
Diarrhea	0	0	0	0	0	13 (13.7)
Vomiting	0	0	3 (12.0)	0	0	9 (9.5)
White blood cell count decreased	0	0	1 (4.0)	4 (4.2)	0	11 (11.6)
Dyspnea	0	0	5 (20.0)	0	0	6 (6.3)

Detailed safety analysis at 3/4 schedule at various dose levels reported at AACR-NCI-EORTC, December 2021 (Yap et al., oral presentation, #4950) and ESMO-TAT, March 2022 (Fontana et al, oral presentation #202). No incidences of Gr4 anemia reported. * 2/3 with documented "outlier" high exposure. ** at 200mg non-tolerated dose level. No Grade 5 TRAE reported.



- Induces cell death in ATM-deficient cancer cells
- Compromises the stabilization of DNA replication forks
 - Is associated with increases in DNA double-strand breaks





Inhibition

of ATR

Repare discovered a network of alterations that are SL pairs with ATRi





Camonsertib patient opportunity with STEP² selection tools



Represents expanded, clinically relevant populations with unmet medical needs Average prevalence of ~2% (ATM) to ~10% (STEP² genes) across multiple tumors



Source: *TCGA; Not weighted for tumor prevalence

STEP² approach identifies genes to predict combination response



Significant synergy demonstrated by combination of camonsertib and PARP inhibitors



- Identified tumors with STEP² genes sensitive to the combination of camonsertib and PARP inhibitors
- The activity observed at low doses of camonsertib and PARPi could lead to efficient anti-tumor activity and potentially address know PARPi toxicities
- Significant new approach to select patients for response to combinations



-/-: Genomically Altered

Camonsertib monotherapy data suggests potentially best-in-class ATRi

Potentially best-in-class safety profile confirmed with larger cohort and longer observation time

- Long-term tolerability further show; anemia non-cumulative, no new adverse safety findings
- Potency/selectivity/PK differentiation increasingly clear



Large trial size (N=120) allowed for comprehensive assessment of dose and schedule

 Multiple dose/schedules rigorously tested to maximize patient benefit and evaluate tumors/molecular alterations to convincingly see a path to further development (AACR 2022)



POC in ovarian cancer clearly demonstrated – engagement with regulator(s) in near-term

- 25% OR, 75% CBR and PFS 8+mo in PARPi and platinum pretreated patients with ovarian cancer
- Several long/deep ovarian cancer tumor responses (BRCA1, SETD2, RAD51c)



Early data supports further exploration of POC for ATM and STEP² alterations

- Current data suggests need for further efficacy exploration meaningful CBR noted in early data
- Tools identified to potentially better select ATM LOF and improve clinical outcomes
- Additional validation of STEP² platform opportunities beyond ATM and BRCA1 LOF



Camonsertib collaboration with Roche announced June 2022

Long-term, global camonsertib collaboration with U.S. co-development, profit/cost share and co-promotion option







Key terms of the collaboration with Roche





Collaboration adds resources and extends funding into 2026 assuming robust development plans

Repare to complete ongoing TRESR and ATTACC clinical studies



Leading precision oncology company focused on synthetic lethality



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