HMA HEALTH

INNOVATION IN HEALTHCARE PRIVILEGED & CONFIDENTIAL

AI & Human Synergy for Superior Healthcare

asklepius.ai

Adrian Cravioto M.D. MSF. FACS. FSSO.
CEO & FOUNDER
HMA HEALTH

HMA HEALTH

Smarter Healthcare, Better Outcomes

HIGHLIGHTS

- First mover in preventive, personalized medicine based on genomics with A.I.
- We believe in the power of technology to make healthcare more efficient, accessible, and patient-centric
- Asklepius.ai as a pioneering AI-driven solution poised to transform healthcare, focusing on decreasing medical errors, early disease detection, doctor support, enhanced patient care and improve patient outcomes

THE PROBLEM

High mortality caused by cancer and chronic diseases.

High healthcare costs.

Lack of personalized medicine

No transparent costs of treatments

Doctor centric model

Limit access to preventive care

Medical Errors cause staggering damage

WHY NOW?

Advancements in technology

Patient's physical and financial health.

Early-stage disease detection

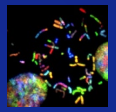
Growing demand for personalized medicine

Transparent costs and payments

Empower patients

THE SOLUTION

- **AI-Driven Synergy:** Asclepius.ai integrates seamlessly with healthcare professionals, creating a powerful synergy that maximizes both human expertise and AI capabilities.
- **Decreasing Morbidity & Mortality:** By providing predictive insights, automating routine tasks, and offering comprehensive health data analysis, Asklepius.ai aids in early disease detection and decreases medical errors, aiming to reduce morbidity and mortality rates.
- **Enhanced Patient Care:** Our AI solution empowers patients with easy access to health records, personalized health insights, and telehealth services. It offers a level of personalized care that was previously unattainable, leading to improved patient experiences and outcomes.
- **Power to the Patients:** Asklepius.ai shifts the paradigm from a doctor-centric model to a patient-centric one, giving patients more control over their healthcare journey.
- **The Future of Healthcare:** With Asclepius.ai, we're not just reacting to current healthcare issues - we're anticipating the future, setting a new standard for what healthcare can be.



- **Patient Benefits:**

  - **Early Disease Detection:** Asklepius.ai leverages complete genomic sequencing to provide a detailed understanding of a patient's genetic makeup. It utilizes advanced AI algorithms to interpret this data, thereby identifying potential health risks.
  - **Personalized Care:** Tailored to each patient's unique genetic makeup and health history.
  - **Access to Health Records:** Patients have easy access to their electronic medical records, making it easier to manage their health data.
  - **Telehealth Services:** Patients can access healthcare from the comfort of their homes, making it especially beneficial for patients living in remote areas.
  - **AI Chatbot:** A 24/7 AI chatbot provides real-time information and support to patients, answering queries and providing health recommendations.
  - **Control Over Healthcare:** Empowers patients, providing them with the tools to take control of their healthcare journey.

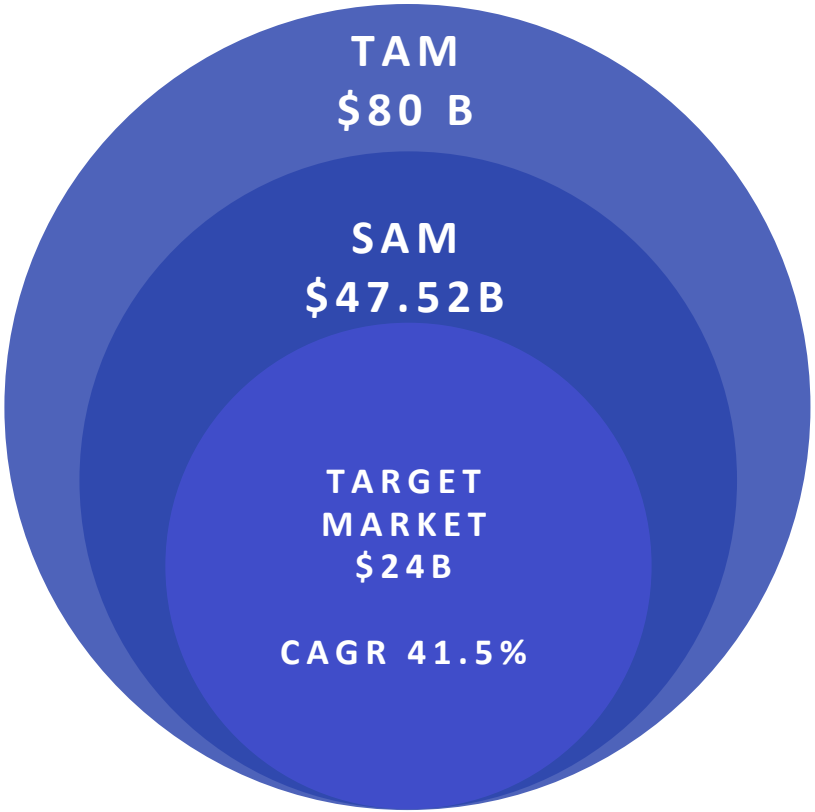
MARKET OPPORTUNITY

Total Addressable Market (TAM)
$80 Billion Personalized Medicine (USA)

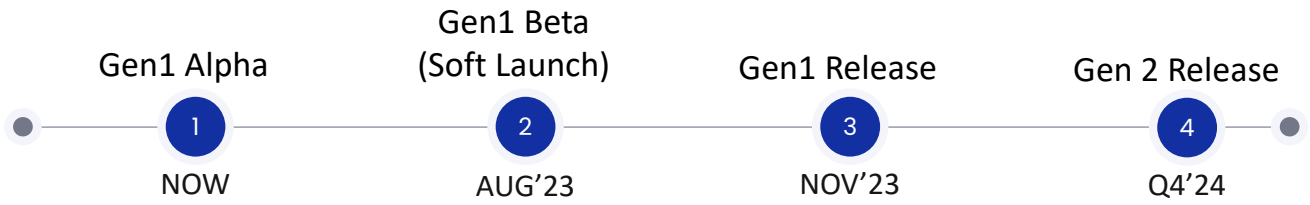
Serviceable Addressable Market (SAM)
Patients and Doctors that could benefit from using asklepius.ai $47.52 B

Target Market
AI in Healthcare Market of 24 Billion by 2025

Target Costumer
Individuals, healthcare providers, companies



Feature Rollout



Gen 1:
Clinical Assistant
Coding & Billing Assistant
Appt./Booking Scheduler
Collaboration/Coms platform

Gen 2:
Triage Assessment
Electronic Health Record Integration
Payment System (patient)
Patient portal (start)
Insurer portal (start)

The Team

Adrian Cravioto M.D.
CEO + Founder

Owen McNally
Head of AI and Statistics

Jonathan Rowley
Head of Software Development

Lisa Huron
Healthcare Business Development

Jawad Kazi
AI. Data Science

HMA HEALTH

PRIVILEGED & CONFIDENTIAL

Thank you!

CEO & FOUNDER
HMA Health

Adrian Cravioto M.D.

adrian.cravioto@hma.health
Cell Phone: +1 210 577 6228

APPENDIX

THE PROBLEM

- **High Morbidity and Mortality Rates**: Current healthcare systems struggle to decrease these rates due to inefficient processes and reactive instead of preventive care.
- **Overburdened Healthcare Professionals**: Doctors and healthcare staff face heavy workloads, resulting in less time for patient interaction and care.
- Limited Predictive Care: Despite vast amounts of health data, there is limited use of predictive data in patient care leading to missed opportunities in early intervention.
- **Doctor-Centric Model**: Traditional healthcare models put physicians in control, leaving patients feeling disengaged from their own health management.
- **Lack of Patient Empowerment**: Many patients lack the necessary tools to understand, participate in, and take control of their healthcare journey.

WHY NOW?

- **Rapid Advancements in AI**: AI technology has made incredible strides in the last few years, making the development of an AI-driven solution like Asklepius.ai possible.
- **Growing Acceptance of AI in Healthcare**: Physicians, patients, and healthcare systems are increasingly open to AI solutions in healthcare, creating a receptive market.
- **Rise of Telehealth**: Social distancing measures have accelerated the demand for telehealth services, making our solution more relevant than ever.
- **Increasing Healthcare Costs**: As healthcare costs continue to rise, the need for efficient, AI-driven solutions that can help reduce these costs is becoming more critical.

PROUDLY ARE AN AUTHORIZED RECRUITING COMPANY FOR

LETTER

doi:10.1038/nature12881

Landscape of genomic alterations in cervical carcinomas

Akinyemi I. Ojesina[1,2]*, Lee Lichtenstein[2]*, Samuel S. Freeman[2], Chandra Sekhar Pedamallu[1,2], Ivan Imaz-Rosshandler[3], Trevor J. Pugh[1,2], Andrew D. Cherniack[2], Lauren Ambrogio[2], Kristian Cibulskis[2], Bjørn Bertelsen[4], Sandra Romero-Cordoba[3], Victor Treviño[5], Karla Vazquez-Santillan[3], Alberto Salido Guadarrama[3], Alexi A. Wright[1,6], Mara W. Rosenberg[2], Fujiko Duke[1], Bethany Kaplan[1,2], Rui Wang[1,7], Elizabeth Nickerson[2], Heather M. Walline[8], Michael S. Lawrence[2], Chip Stewart[2], Scott L. Carter[2], Aaron McKenna[2], Iram P. Rodriguez-Sanchez[9], Magali Espinosa-Castilla[3], Kathrine Woie[10], Line Bjorge[10,11], Elisabeth Wik[10,11], Mari K. Halle[10,11], Erling A. Hoivik[10,11], Camilla Krakstad[10,11], Nayeli Belem Gabiño[3], Gabriela Sofia Gómez-Macías[9], Lezmes D. Valdez-Chapa[9], Maria Lourdes Garza-Rodriguez[9], German Maytorena[12], Jorge Vazquez[12], Carlos Rodea[12], Adrian Cravioto[12], Maria L. Cortes[2], Heidi Greulich[1,2,6], Christopher P. Crum[13], Donna S. Neuberg[14], Alfredo Hidalgo-Miranda[3], Claudia Rangel Escareno[3,15], Lars A. Akslen[4,16], Thomas E. Carey[17], Olav K. Vintermyr[4,16], Stacey B. Gabriel[2], Hugo A. Barrera-Saldaña[9], Jorge Melendez-Zajgla[3], Gad Getz[2,18], Helga B. Salvesen[10,11]* & Matthew Meyerson[1,2,13]

Cervical cancer is responsible for 10–15% of cancer-related deaths in women worldwide[1,2]. The aetiological role of infection with high-risk human papilloma viruses (HPVs) in cervical carcinomas is well established[3]. Previous studies have also implicated somatic mutations in *PIK3CA*, *PTEN*, *TP53*, *STK11* and *KRAS*[4–7] as well as several copy-number alterations in the pathogenesis of cervical carcinomas[8,9]. Here we report whole-exome sequencing analysis of 115 cervical carcinoma–normal paired samples, transcriptome sequencing of 79 cases and whole-genome sequencing of 14 tumour–normal pairs. Previously unknown somatic mutations in 79 primary squamous cell carcinomas include recurrent E322K substitutions in the *MAPK1* gene (8%), inactivating mutations in the *HLA-B* gene (9%), and mutations in *EP300* (16%), *FBXW7* (15%), *NFE2L2* (4%), *TP53* (5%) and *ERBB2* (6%). We also observe somatic *ELF3* (13%) and *CBFB* (8%) mutations in 24 adenocarcinomas. Squamous cell carcinomas have higher frequencies of somatic nucleotide substitutions occurring at cytosines preceded by thymines (Tp*C sites) than adenocarcinomas. Gene expression levels at HPV integration sites were statistically significantly higher in tumours with HPV integration compared with the expression of the same genes in tumours without viral integration at the same site. These data demonstrate several recurrent genomic alterations in cervical carcinomas that suggest new strategies to combat this disease.

The prevention of cervical cancer by Pap smear-based screening and treatment programs has been largely successful in resource-rich countries. However, cervical cancer is the second most common cause of cancer-related deaths in women in developing countries, in which many patients are diagnosed at advanced stages of disease with limited treatment options and poor prognosis[1]. Recent advances in targeted therapy against specific somatic alterations have transformed the management of cancers in general[10], and the discovery of new therapeutic targets in cervical cancer could improve upon current strategies to combat cervical carcinomas.

To provide comprehensive data on the landscape of genomic aberrations that contribute to cervical cancer, we investigated a cohort that included 100 patients from Norway and 15 patients from Mexico (Supplementary Notes 1–7). We performed exome sequencing of 193,094 exons, covering a median of 34.2 megabases (Mb) at a median of 89× (range: 56–122×) coverage for tumour samples and 88× (range: 69–122×) coverage for normal samples, followed by calling of somatic mutations using the MuTect algorithm[11], and identified a total of 17,795 somatic mutations across the entire data set, including 11,419 missense, 936 nonsense, 4,643 silent, 219 splice site and 29 translation start site mutations, as well as 401 deletions and 131 insertions.

The aggregate nonsilent mutation rate across the data set was 3.7 per Mb. However, squamous cell carcinomas had a higher rate of nonsilent mutations (4.2 mutations per Mb) than adenocarcinomas (1.6 mutations per Mb) (Wilcoxon $P = 0.0095$). The clinical, pathological, epidemiological and mutational characteristics of the tumours are summarized in Supplementary Figs 1–6, Supplementary Tables 1–5 and Supplementary Notes 8 and 9.

Hierarchical clustering of all 115 tumours on the basis of mutational context revealed that most tumours were characterized by previously described[12] mutational signatures: with predominantly Tp*C-to-T/G mutations and *CpG-to-T mutations (Fig. 1 and Supplementary Fig. 4). Tp*C mutations were present at a relative frequency of >0.5 in 53 (46%) tumours, and the relative frequency of Tp*C mutations was positively correlated with mutation rates, especially in squamous cell carcinomas (Fig. 1, Supplementary Note 8 and Supplementary Fig. 5). In addition, 5,648 (54%) of the 10,328 nonsilent mutations observed in squamous cell carcinomas were Tp*C-to-T/G mutations.

We performed mutation significance analyses on 79 squamous cell carcinomas and 24 adenocarcinomas. Genes were determined to be significantly mutated if recurrent mutations were found in that gene at a false discovery rate of $q < 0.1$ after correction for multiple hypothesis testing, as described previously[13] (Supplementary Note 6). Details of candidate mutation validation are presented in Supplementary Figs 6 and 7.

As expected, recurrent mutations in *PIK3CA*, *PTEN* and *STK11* were present in 14%, 6% and 4%, respectively, of 79 squamous cell carcinomas (Table 1). In addition, we found significantly recurrent mutations in *EP300* (16%), *FBXW7* (15%), *HLA-B* (9%), *MAPK1* (8%) and *NFE2L2*

[1]Department of Medical Oncology, Dana-Farber Cancer Institute, Boston, Massachusetts 02215, USA. [2]The Eli and Edythe L. Broad Institute of Massachusetts Institute of Technology and Harvard University, Cambridge, Massachusetts 02142, USA. [3]Instituto Nacional de Medicina Genomica, Mexico City 14610, Mexico. [4]Department of Pathology, Haukeland University Hospital, N5021 Bergen, Norway. [5]Tecnológico de Monterrey, Monterrey 64849, Mexico. [6]Department of Medicine, Brigham and Women's Hospital, Boston, Massachusetts 02115, USA. [7]Department of Thoracic Surgery, Fudan University Shanghai Cancer Center, Shanghai 200032, China. [8]Cancer Biology Program, Program in the Biomedical Sciences, Rackham Graduate School, University of Michigan, Ann Arbor, Michigan 48109, USA. [9]Facultad de Medicina y Hospital Universitario "Dr. José Eleuterio González" de la Universidad Autónoma de Nuevo León, Monterrey, Nuevo León 64460, México. [10]Department of Obstetrics and Gynecology, Haukeland University Hospital, N5021 Bergen, Norway. [11]Department of Clinical Science, Centre for Cancer Biomarkers, University of Bergen, N5020 Bergen, Norway. [12]Instituto Mexicano del Seguro Social, Mexico City 06720, Mexico. [13]Department of Pathology, Brigham and Women's Hospital, Boston, Massachusetts 02115, USA. [14]Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute, Boston, Massachusetts 02215, USA. [15]Claremont Graduate University, Claremont, California 91711, USA. [16]Centre for Cancer Biomarkers, Department of Clinical Medicine, University of Bergen, N5020 Bergen, Norway. [17]Head and Neck Oncology Program and Department of Otolaryngology, University of Michigan Comprehensive Cancer Center, Ann Arbor, Michigan 48109, USA. [18]Massachusetts General Hospital Cancer Center and Department of Pathology, Massachusetts General Hospital and Harvard Medical School, Boston, Massachusetts 02114, USA.
*These authors contributed equally to this work.

RESEARCH PUBLISHED IN NATURE
HTTPS://WWW.NATURE.COM/ARTICLES/NATURE12881

CEO & FOUNDER
HMA Health

Adrian Cravioto M.D.

adrian.cravioto@hma.health
Cell Phone: +1 210 577 6228

THE SOLUTION

GENOMIC TESTING AND AI

Early Detection: Identify genetic markers for diseases, allowing for early detection and prevention.

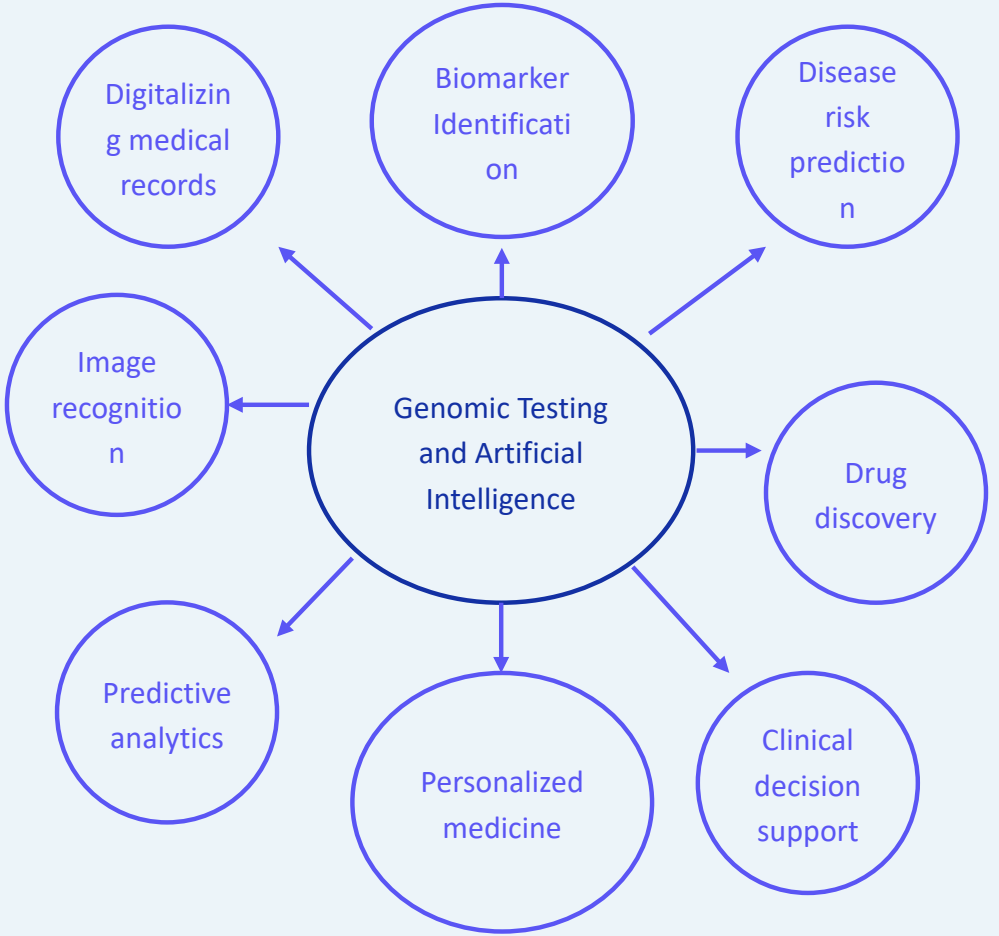
Personalized Medicine: Focusing on increasing lifespan and rejuvenation.

Improved Patient Outcomes: Leading to improved treatment plans and better patient outcomes.

Precision Medicine: Precise and targeted treatment plans that improve patient outcomes.

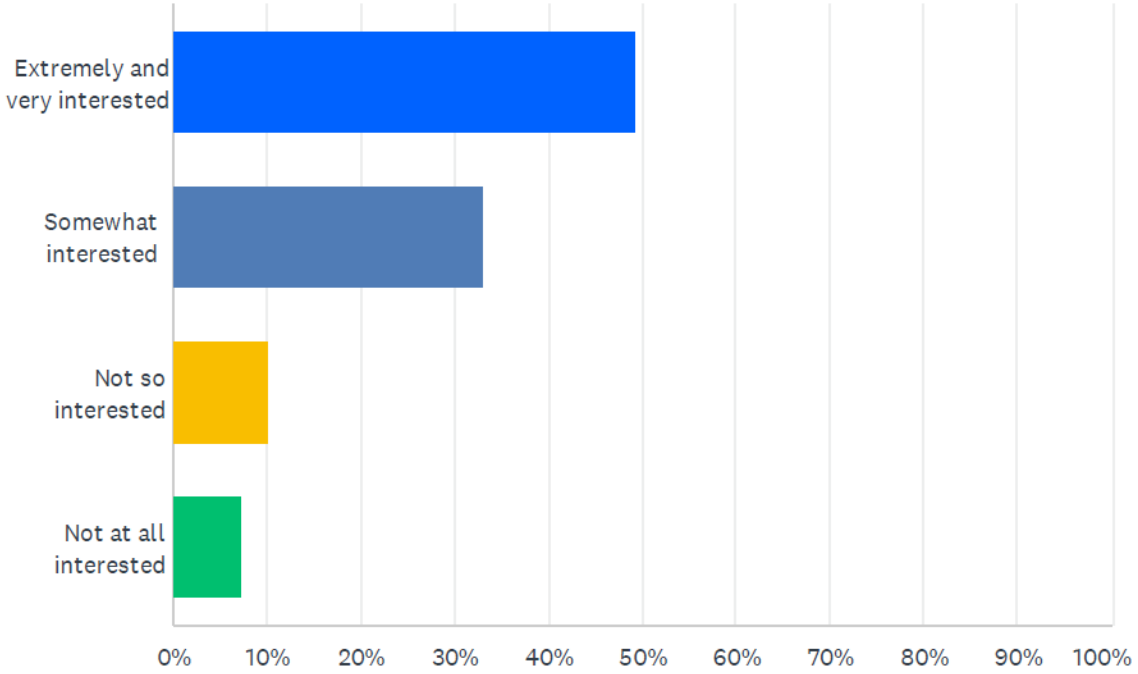
Reduced Healthcare Costs: Smart contracts can reduce costs by 65%. We can take intermediaries off.

Research. Drug discovery.



Q1 How interested would you be in a healthcare platform that uses genomic testing and artificial intelligence to detect diseases at an early stage and to provide preventive medicine?

Answered: 272 Skipped: 0



Q4 How important is personalized medicine to you when it comes to your healthcare?

Answered: 272 Skipped: 0