CureVac Conference Call, June 17, 2021

Results of Second Interim Analysis of CureVac's Pivotal Phase 2b/3 HERALD Study

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Presenters

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SARAH Thank you. Good morning, good afternoon and welcome to our conference call. My name is Sarah Fakih, and I am the Vice President of Corporate Communications and Investor Relations at CureVac.

Please let me introduce today's speakers.
On the call with me are Franz Haas, the Chief Executive Officer of CureVac, Ulrike Gnad-Vogt our interim Chief Development Officer and Mariola Fotin-Mleczek, CureVac's Chief Technology Officer. Pierre Kemula, Chief Financial Officer, will be available for the Q&A session after the presentation.

Please note that this call is being webcast live and will be archived on the Events and Presentations section under Investor Relations on our website.

Before we begin, a few Forward-Looking Statements: The discussion and responses to your questions on this call reflect management's view as of today, Thursday, June 17th, 2021.

We will be making statements and providing responses to your questions that state our intentions, beliefs, expectations or predictions of the future. These constitute forward-looking statements for the purpose of the Safe Harbor provisions. These statements involve risks and uncertainties that could cause actual results to differ materially from those projected.

CureVac disclaims any intention or obligation to revise any forward-looking statements. For more information, please refer to our filings with the U.S. Securities and Exchange Commission.

I will now turn the call over to Franz.

FRANZ Thank you Sarah. Ladies and gentlemen, a warm welcome to this conference call from all of us here at CureVac.

The COVID-19 environment has changed dramatically since the beginning of the pandemic and is now dominated by the evolution of the virus and the rapid spread of new and emerging virus variants.

Over the past six months, and in an increasingly challenging variant-rich environment, we have been conducting a pivotal Phase 2b/3 efficacy trial – called the HERALD study – with our first-generation COVID-19 vaccine candidate, CVnCoV.

This study is so far unmatched in geographic diversity, being conducted in 10 countries across Europe and Latin America. We believe the resulting multi-variant study presented today provide important insights into the dramatically transformed variant environment, suggesting that we were virtually fighting a different virus and a different pandemic over the last six months.

Within this environment, CVnCoV efficacy was calculated to be 47 percent on the basis of 134 adjudicated cases that met the criteria for analysis inclusion. This was calculated against any severity of disease and across all virus strains.

Efficacy data from this trial needs to be viewed against the background of comprehensive sequencing data, acquired in parallel to the accrual of COVID-19 cases within the trial.

Out of the 134 COVID-19 cases accrued and adjudicated as a basis for a first and preliminary calculation of efficacy, 124 cases were sequenced to identify the respective virus strain. The results are sobering:

From 124 sequenced, adjudicated cases, only one case can be attributed to the original virus strain the world fought all throughout 2020.

We recognize that demonstrating high efficacy in this unprecedented broad diversity of variants is challenging.

Now, let me please go into further details of the study setup before I hand it over to Ulrike for a discussion of the interim analysis.

On slide 5, you can see an overview of the general setup of the HERALD study.

Conducted in four countries in Europe and six countries in Latin America, the HERALD study represents a multi-variant study with high geographic and ethnic diversity.

Of the approximately 40,000 trial participants, about 25 percent were recruited in Europe, while about 75 percent were recruited in Latin America – a region, which in May this year was considered to be an epicenter of the COVID-19 pandemic.

Of these approximately 40,000 participants, roughly 5,000 participants, or 13 percent, were above the age of 60, while the majority of about 35,000 participants, or 87 percent, were between the age of 18 and 60. The mean age of study participants was in the range of 43 years.

Now I will hand it to Ulrike, our interim Chief Development Officer, to walk you through the case accrual process and the interim analysis outcome.

ULRIKE Thank you Franz. Please let me start by providing you with an overview of the COVID-19 case accrual process within the HERALD study, according to the study's primary endpoint. This is defined as the occurrence of first episodes of confirmed cases of COVID-19 of any severity.

Per study protocol, COVID-19 cases are eligible to be included in the vaccine efficacy calculation if they occur at least 15 days after the second vaccination – the earliest time at which the vaccine is considered to be fully protective.

COVID-19 cases occurring at least 15 days after the second vaccination undergo a stringent adjudication process, which – among other things – confirms presumed COVID-19 infections via real-time PCR and makes sure to exclude those confirmed COVID-19 participants who also test positively for a COVID-19 infection before the 15 days cutoff.
The present data analysis is based on 134 COVID-19 cases that met the stringent adjudication criteria and hence form the basis for the preliminary CVnCoV efficacy calculation.

Of these 134 COVID-19 cases, 119 cases, or approximately 90 percent, were detected in participants below the age of 60, while 15 cases, or approximately 10 percent, were detected in participants above the age of 60. This distribution corresponds well with the general age distribution within the trial.

As Franz has already highlighted, confirmed COVID-19 cases need to be seen in the context of the rapid spread of new virus variants. For some variants vaccine induced antibody neutralizing capacity can potentially be reduced.

On slide 7, let me dive deeper into the variant background, which critically determines the context and thus the interpretation of the preliminary CVnCoV efficacy.

New virus variants have been steadily spreading since the end of 2020 and have all but displaced the original virus strain.

On this slide you can see a general and non-trial related overview of the currently estimated prevalence of the four most prominent variants with a focus on the general geographies where we are conducting the HERALD study.

Presently, we are looking at four main Variants of Concern. These include:

- The Alpha strain, first detected in the UK,
- the Beta strain, first detected in South Africa,
- the Gamma strain, first detected in Brazil
- the Delta strain, first detected in India
- and the new Variant of Interest, the Lambda strain, first detected in Peru.

The ring diagrams on this slide illustrate the current estimated variant spread in South America and Europe. For your reference, the specific countries where we are conducting our Phase 2b/3 trial are marked in blue.

Because of the continuing spread of variants that has shaped this image over the last several months, we see a wide range of variants within this highly international study and have conducted comprehensive sequencing analysis to understand the dynamics of the virus in our trial.

Over the next two slides, I will go into the details of the unique variant distribution we have detected in the HERALD study.

Within the HERALD study, 124 of the adjudicated cases were sequenced, which represent approximately 93 percent of the adjudicated cases that were used for the interim efficacy analysis.

This means that the strain distribution illustrated on this slide provides important variant context around the preliminary CVnCoV efficacy of 47 percent calculated within the second interim analysis against any severity of disease, according to the primary study objective.

Of the 124 sequenced adjudicated cases, Variants of Concern, including the Alpha and the Gamma strain, represent approximately 57 percent. This is mainly supplemented by 21 percent of the Lambda or C.37 strain, originating from Peru, and 7 percent of the B.1.621 strain, originating from Colombia.

Both strains are less explored. However, C.37 was very recently added to the WHO watch-list of Variants of Interest and was assigned the name Lambda. In May, this variant was reported to be responsible for more than 80 percent of COVID-19 cases in Peru and evidence has become available for high rates of transmission in multiple countries in Latin America.

The strain is known to feature the D614G mutation, which is understood to have potentially higher transmissibility as well as two critical mutations in the receptor binding motif of the Spike protein. As the receptor binding motif is a primary target for neutralizing antibodies, this might potentially allow this variant to evade immunity.

Together with a 13 percent contribution of other strains - which further subdivide into 9 other strains with less prevalence – this adds up to a total of 13 variants, which provide direct context for the preliminary efficacy calculation.

As shown in the geographic breakdown of the total number of sequenced cases, the broad variety of variants originates primarily in Latin America, which contributed about 80 cases, or 65 percent, to the 124 sequenced cases.

In Europe, the 44 cases we observed, or 35 percent of the total, are strongly dominated by the Alpha strain in accordance with the general virus distribution there.

The variant overview provided on the next slide further extends the pool of sequenced COVID-19 cases recorded in the HERALD study to include non-adjudicated cases, providing a more detailed picture of the variant dynamics within the study.

This overview is based on a total of 474 COVID-19 cases, which were accrued and sequenced within the HERALD study irrespective of the formal COVID-19 case adjudication process, and thereby include the 124 adjudicated cases as well as 350 non-adjudicated cases.

While the majority of these cases therefore did not contribute to the efficacy calculation, they provide a more accurate and extended picture of the circulating virus variants within the study.

Overall, 29 different COVID-19 strains were identified, which cover:

- all currently designated Variants of Concern, including the Alpha, Beta, Gamma, Delta and Epsilon strain;

- Variants of Interest, including the Zeta strain as well as the newly assigned Lambda or C.37 strain first detected in Peru,

- four strains belonging to the original virus, and

- B.1.621 and B.1.1.519 with high prevalence in Colombia and Mexico, respectively.

In accordance with the variant mix in the group of adjudicated cases, diversity was again more pronounced in Latin America compared to Europe, where the Alpha strain dominates.

I am now on slide 10 to briefly touch on the preliminary vaccine efficacy data from the second interim analysis.

First, let me remind you again that preliminary vaccine efficacy of 47 percent was calculated for the prevention of COVID-19 cases of any severity and across all strains.
Although the study was not statistically powered to provide separate sub-population efficacies, the preliminary data show trends for age and strain related efficacy.

For age related trends, the interim results suggest efficacy in younger participants but did not allow to conclude on efficacy in the age group above 60.

For strain related trends, interim data suggests an efficacy range within the most prevalent strains of the 13 different COVID-19 variants identified within the adjudicated cases applied for efficacy calculation.

We will now continue to final analysis on the basis of approximately 80 more cases compared to the second interim analysis, which we expect in approximately two to three weeks. Based on the addition of new cases the efficacy readout is expected to change.

I am now on slide 11 to briefly update you on the safety and reactogenicity profile of CVnCoV on the basis of the first 2,000 participants recruited within the HERALD study.

The two 12 microgram vaccinations of CVnCoV are shown to be well tolerated. As previously reported for CVnCoV, and in line with other mRNA-based COVID-19 vaccines, the majority of events were mild to moderate and accumulated around fatigue, headache, muscle pain or myalgia, and chills, and only few fever events were recorded.

We were particularly pleased to see that there was no increase in the severity of side effects after the second vaccination compared to the first vaccination – both reactogenicity profiles are comparable.

The data is further stratified according to trial participants between the age of 18 to 60 and participants above the age of 60. As expected, side-effects are generally more pronounced but still in a well-tolerated range within the group of 18- to 60-year-old study participants compared to study participants above the age of 60.

Overall, this safety profile is fully in accordance with the safety profile reported for other mRNA-based vaccines and further confirms the safe applicability of CVnCoV.

Let me now hand back the call to Franz for a short summary of key messages and next steps.

FRANZ Thank you Ulrike.
Let me quickly summarize key messages from the present interim analysis and outline the next steps.

Our technology had to prevail in one of the most challenging COVID-19 environments.

While we were hoping for a stronger outcome of this second interim analysis, we see trends that indicate efficacy in younger age groups, below the age of 60, as well as potentially differentiated efficacy per strain – as far as the conclusions from this interim data readout with limited statistical power allow.

We will now move to the final analysis, which we expect within the next two to three weeks and which will be carried out on the basis of more than 200 cases to confirm age and strain related trends and also look at disease severity. These cases will also be characterized by accompanying sequencing data.

Data from the final analysis will allow us to look further into the efficacy we see in participants below the age of 60 – and please note again, this takes into account efficacy against any severity of disease within a challenging variant environment.

Final analysis will also allow us to better understand the unprecedented broad diversity and dynamics of variants in all trial countries, which had an impact on vaccine efficacy.

We remain fully committed to supporting ending the pandemic. Following the final analysis, we will carefully assess the most appropriate regulatory pathway.

Lastly, we have a strong second-generation candidate lined up in our COVID-19 pipeline, which we are co-developing in partnership with GSK and which we intend to bring into the clinic within the next four months based on promising preclinical data.

For the last part of the presentation, let me now hand over to Mariola for a quick look at new preclinical data of our second-generation COVID-19 vaccine candidate, which targets faster improved immune responses at even lower doses to primarily meet the challenge of emerging new variants via multivalent vaccines as well as combination vaccines for potential protection against multiple infectious diseases in a single vaccine.

MARIOLA Thank you Franz.

To further counter the ongoing spread of new virus variants, on slide 13 I would like to introduce you to second-generation COVID-19 vaccines, which we are co-developing together with our partner GSK on the basis

of a new mRNA backbone. This new mRNA backbone differs from the setup of our first-generation vaccine candidate, CVnCoV, and was generated on the basis of our learnings over the past year.

Based on non-chemically modified mRNA, the second-generation mRNA backbone features targeted optimizations, focusing on improved mRNA translation for increased and extended protein expression as well as improved immunogenicity.

It thereby targets the ability to rapidly induce improved immune responses compared to CVnCoV. These characteristics will be key for the development of multivalent vaccines as well as combination vaccines.

The second-generation data illustrated on slide 14 are central proof of concept data, applying to the second-generation COVID-19 vaccine candidate, CV2CoV. The data form part of a larger preclinical dataset in non-human primates, which is currently being generated in collaboration with the Harvard Medical School.

The so far unpublished data is based on animals immunized with CV2CoV or CVnCoV, according to the vaccination schedule applied in humans, which includes two vaccinations with a 12 microgram dose on day 0 and day 28.

The neutralizing antibody titers shown here strongly confirm the functionality of the advanced second-generation approach for rapid and strong immune response.

The onset of neutralizing antibodies occurs faster for CV2CoV than for CVnCoV. Already 2 weeks after first vaccination, CV2CoV antibodies show good antibody titers and while the second vaccination on day 28 efficiently boosts antibody titers for both candidates, it leads to a more pronounced booster effect of CV2CoV.

The full data publication will be made available through a scientific manuscript over the next weeks.

With this, we conclude our presentation and would now like to open the webcast to your questions.

SARAH With this we would like to conclude this conference call. Thank you very much for your participation, stay safe and please do not hesitate to contact us should you have any further questions.

Thank you and goodbye.