CureVac Conference Call, November 16, 2022

Third Quarter and First Nine Months 2022 Financial Results and Business Update

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Presenters

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Ronald Plasterk	Senior Vice President VP Science & Innovation
Pierre Kemula	Chief Financial Officer
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SARAH FAKIH

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-Werner Haas, the Chief Executive Officer of CureVac, Ulrike Gnad-Vogt, our interim Chief Development Officer, Ronald Plasterk, our Senior Vice President Science and Innovation, and Pierre Kemula, Chief Financial Officer of CureVac.

Please note that this call is a live webcast that 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, Wednesday, November 16th, 2022.

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-WERNER HAAS

Thank you, Sarah. Ladies and gentlemen, a warm welcome to this conference call from us, here at CureVac. 2022 has been a highly productive year for our company. We have significantly grown our operational bandwidth across the organization and, most importantly, our three core competencies: broad technology platform, robust product development pipeline and large GMP manufacturing capacities.

Let me give you a short overview of four key developments in these areas. First, in our prophylactic vaccine product pipeline, we continue to execute on our broad clinical development programs in COVID-19 and flu, which started earlier in 2022 in collaboration with our partner, GSK.

The ongoing four clinical trials that have successfully extended our broad technology platform into modified, as well as multivalent mRNA approaches, are on track to deliver meaningful clinical data, early next year.

Second, beyond our progress in prophylactic vaccines, the next growth driver we are moving forward with maximum speed and focus is oncology. With the acquisition of Frame Cancer Therapeutics and the partnership with myNEO, we have made an impressive start to the implementation of our expanded oncology strategy.

Today, there is an enormous gap between state-of-the-art analytical methods that provide vast amounts of data about the patient's individual cancer and current treatment options. Immuno-oncology is, particularly, suited to bridge that gap.

We intend to access and translate available data into a meaningful pipeline of new mRNA cancer vaccine candidates driven out of the

former Frame Cancer Therapeutic site in Amsterdam, which we plan to make our cancer antigen discovery hub.

Third, we progressed on the development of dedicated oncology enablers, first and foremost, the RNA printer, our automated manufacturing solution for GMP grade, mRNA vaccines and therapeutics.

In October this year, we submitted applications to the regulatory authorities for the first manufacturing licenses to support our oncology road map. Furthermore, we are advancing the development of a proprietary lipid nanoparticle, or LNP technology, that in oncology, we expect to provide additional advantages for the delivery of novel mRNA cancer vaccine candidates.

Fourth, we also presented data from the Phase I expansion study of our non-coding RNA, CV8102, at the meeting of the Society for Immunotherapy of Cancer, SITC, earlier this month.

CV8102 demonstrated a solid safety profile and preliminary efficacy in heavily pretreated patients with advanced melanoma.

In addition to those four developments, we closed the third quarter of 2022 with a solid cash position of €540.9 million, and Pierre will later talk you through the financial details.

On Slide 5, let me briefly highlight the CureVac pipeline to show you how we are leveraging our strong mRNA expertise across our three therapeutic areas of prophylactic vaccines, oncology and molecular therapy, addressing diseases with high unmet medical need.

Our most advanced area of prophylactic vaccines is driven by the technological advances of our versatile second-generation mRNA backbone. This backbone broadly spans unmodified and modified mRNA, as well as monovalent and multivalent vaccine formats to diversify and advance our product development pipeline.

All these approaches are currently being validated in four Phase I clinical trials in COVID-19 and flu that we are conducting together with GSK.

The clinical insights we expect to gain from these four studies will also accelerate the ongoing expansion of our oncology program. In this area, our strategic priority is the development of a portfolio of novel cancer vaccine candidates that can elicit strong systemic and tumor-directed immune responses, based on our second-generation backbone.

Through the implementation of synergistic technologies, we established a highly efficient antigen discovery engine. This will allow us to develop product candidates featuring differentiated new antigens, as well as tumor-associated antigens.

As already highlighted, our clinical oncology candidate, CV8102, is currently being assessed in a Phase I dose escalation trial in solid tumors and an expansion study in patients with PD-1 refractory melanoma. Ulrike will come back to the data we presented on CV8102 at the SITC.

The third therapeutic area, molecular therapy, we are developing optimized mRNA therapeutics, together with several collaboration partners that are intended to address therapeutic proteins to treat rare and metabolic diseases.

On Slide 6, let me briefly touch on a detailed overview of the four key Phase I dose escalation trials that we are currently conducting in COVID-19 and flu, together with GSK. The studies are driven by a broad technology approach to select the best performing candidates for later stage clinical development.

For COVID-19, on the left, the tested candidates include CV0501, a modified candidate encoding the Omicron variant and CV2CoV, an unmodified candidate encoding the original virus.

For flu, on the right, we are testing flu SV mRNA, a monovalent modified candidate and CVSQIV, an unmodified quadrivalent candidate. All four candidates are being tested in a one shot booster setup.

Based on our advanced second-generation backbone, they will provide an important clinical validation of our technology platform and corresponding product development.

Initial external reporting for both indications will be triggered by data that are comprehensive and meaningful enough to allow selection of the most promising candidates and determine the optimal dose for a subsequent clinical trial.

We expect to report on this data in early 2023.

Moving on from prophylactic vaccines to oncology, I will now hand over to Ulrike to walk you through our recent updates and progress in this area.

ULRIKE GNAD-VOGT

Thank you, Franz. Before we dive into the details, I would like to briefly draw your attention to our previously reported three-pillar strategy in oncology. These pillars illustrate the road map for expanding our oncology footprint, the next growth driver we are rapidly advancing beyond our progress in prophylactic vaccines.

Over the last several months, we have either started or continued to execute on each of these strategic pillars with a clear focus on the development of a differentiated cancer vaccine pipeline.

The technologies of Frame Cancer Therapeutics and MyNEO will enable us to assess novel classes of tumor antigens and identify those with the highest chance of success for potential clinical testing in alignment with the pillars in the middle and on the right.

This antigen discovery engine will be supported by the RNA printer. The automated end-to-end manufacturing solution is expected to contribute to the availability of clinical trial materials to rapidly screen new mRNA vaccine constructs in early-stage clinical studies.

As already mentioned by Franz, we are currently in regulatory review to obtain the first manufacturing licenses for the RNA printer to support the initial validation of our second-generation backbone in oncology.

This validation includes testing our second-generation backbone with different classes of tumor antigens to assess T cell-mediated immune responses as is covered by the strategic pillar on the left. I will come back to the strategic pillar later in the presentation.

First, let us take a closer look at the antigen discovery technologies we are currently establishing and how they integrate with our three core competencies in oncology.

On Slide 8, you can see an illustration of how the advanced technology and bioinformatics expertise of Frame Cancer Therapeutics and MyNEO complement our core competencies in product development and manufacturing.

The synergistic technology strongly extend our reach to the latest technologies in oncology, while being highly compatible with our own mRNA technology. They provide a powerful front end to deliver antigens that can then be developed into a deep pipeline of novel cancer vaccine candidates, along our existing expertise.

Let me now hand over the call to Ronald, the Founder of Frame Cancer Therapeutics, to walk you through the details of Frame's highly sophisticated and differentiated technology.

RONALD PLASTERK

Thank you, Ulrike. The technology, which has become part of the CureVac technology platform with the acquisition earlier this year, is dedicated to transforming the treatment of cancer by harnessing the immune system to recognize and fight tumors.

Over the next three slides, I would like to give you an overview of this technology and what sets it apart from current industry standards.

The field of immunotherapy has advanced with the progression of available technologies to extract data from patient samples, such as next-generation sequencing.

In the last 10 years, the focus was on the exome, which is all the protein coding parts of the human genome, but this represents only 1.5% of the total genetic information. Within that 1.5%, platforms have been specialized on the efficient identification of point mutations that give rise to antigens that can mostly or only be found in tumor cells and can serve, indeed, as targets for cancer vaccine candidates.

More recently, breakthrough developments in sequencing capacity have enabled the extraction of vastly larger amounts of data.

Today, we can sequence the entire genome of every patient and the tumor for about $3,000, and prices are still going down. It enables us to utilize the remaining 98.5% of genetic information, where the bulk of the antigenicity of the tumor resides.

This is where we start our neoantigen discovery engine. We perform whole-genome sequencing for every patient sample and combine it with short, as well as long-read RNA sequencing. This way, we can map the full inventory of genomic changes and know precisely what is being expressed and what is not.

Downstream of the sequencing, we generated a powerful software package to integrate all the data to retrieve the exact changes in the DNA of the tumor cells compared to healthy cells, and correlation of this data with changes in the RNA transcription of the tumor cells results in entirely new and potentially antigenic tumor antigens.

We've called these new antigens frames, which is short for neo-open reading frame proteins. We plan to apply these frames as targets for our portfolio of entirely new cancer vaccine candidates. We've

demonstrated we can go from tumor sample to vaccine design, within two weeks.

I'm now on Slide 10 to further illustrate the depth of the genetic data that our approach provides access to. Here, you can see the analysis of a real sample of a lung cancer patient from our own work.

The outer circles are both figures, number the 22 chromosomes, plus the X and Y chromosomes. The inner circles of both figures show mutations per chromosome depicted as blue dots. Each blue dot represents a potential cancer vaccine target.

The left figure illustrates the data we obtain, if we choose to do only conventional exome sequencing. The number of blue dots is restricted by sequencing only the protein coding parts of the tumor DNA. The figure in the middle illustrates the data we obtained from whole genome sequencing.

Here, of course, you get many more point mutants but, more importantly, became much more meaningful data on top of that. The case in point is the multitude of lines in the middle of the figure, which depict chromosomal rearrangements where chromosomes are tied to other chromosomes, where they should not be.

While this is a common occurrence in cancer, the number rearrangement is still staggering. Overall, there can be hundreds of such rearrangements in a common lung cancer sample. What does this difference between both data sets mean for the development of potent cancer vaccines?

Well, the main difference is that point mutations, as the name implies, represent single nucleotide changes in the encoding DNA. And consequently, the express protein only features single new amino acids.

Current personalized cancer vaccines applying this approach cover at max around 30 of such point mutation. So, about 30 changed amino acids in the vaccine. This means that vaccine is, for the most part, based on healthy or regular or wild-type genetic content.

The ability to activate the immune system based on a vaccination against the mostly wild-type derived antigen is then, of course, limited. In contrast, we are taking a very different approach.

Incorporating the totality of the genetic changes, including all the rearrangements, give rise to long stretches of genetic content that are entirely foreign to the body. This results in new antigens that are not only entirely foreign to the body but also uniquely expressed in the tumor and not in healthy tissue.

We call the entirety of these frames Framome. You can see the Framome of the lung cancer sample on the right. Every line here represents an uncoated new protein with every color in that line showing a separate amino acid.

The colors do add up to approximately here about 1,000 new amino acids in this sample, and that's a number that can easily be encoded on a small number of or even a single messenger RNA construct.

In its foreignness, this construct will look like a virus to the immune system and is expected, as also suggested by preclinical experiments, to raise a much stronger immune response.

At the end of the day, the fight between the tumor and the immune system is a numbers game, and we believe that our approach provides the best opportunity to win that game.

Having focused, so far, on the strongly extended data that we can obtain today from individual patient samples, let me now show you on Slide 11 how we can leverage our approach across different ranges with the same cancer or even across different cancer types.

What you can see here are the frames of two different lung cancer patients. We found that some of the same frames are shared between patients. In fact, shared frames, as well as shared tumor-associated antigens, occur in many different cancer types. And they offer, thus, the potential to develop cancer vaccine candidates that could be applicable to a larger group of patients.

That's why we are following two approaches for our cancer vaccine development. The first approach assesses tumor antigens shared by different cancer patients for the development of off-the-shelf cancer vaccines to benefit larger groups of patients, and the second approach is tailored to a patient's individual tumor profile.

With that, let me hand back the call to Ulrike to discuss how these approaches fit within our current oncology road map. Ulrike.

ULRIKE GNAD-VOGT

Thank you, Ronald. I am now on Slide 12 to walk you through our development plans in oncology for 2023 and beyond and how we plan to translate our mRNA technology into new cancer vaccine candidates.

You might remember that the first of our three strategic pillars highlights the validation of a second-generation mRNA backbone in oncology.

To address this pillar, we will assess how the improved performance of the second-generation backbone translates into the induction of T cells in a clinical setting. To this end, we have already started preparations to initiate two Phase I Proof of principle studies in the first and second half of '23 to assess safety and immunogenicity of the second-generation backbone, including established tumor antigens.

The first proof of principle study expected to start in the first half of '23 will assess an mRNA construct including multiple epitopes from a tumor-associated antigen in patients with surgically-resected glioblastoma multiforme.

The second proof of principle study expected to start in the second half of '23, which has an mRNA construct featuring a full-length tumor-associated antigen in patients with solid tumors with an initial focus on melanoma.

They are expected to provide a solid foundation of clinical data to accelerate the development of cancer vaccine candidates and to support subsequent regulatory review processes.

In parallel, we will be advancing the application of our antigen discovery engine to identify and validate neoantigens, as well as tumor-associated antigens for potential clinical testing. This work stream will benefit from the additional support of what we call oncology enablers.

These include primarily the RNA Printer, which will support the rapid and flexible availability of clinical trial materials. Additionally, we aim to optimize the design of cancer vaccine candidates, based on a new and proprietary LNP program for improved mRNA delivery.

Both work streams are expected to merge in 2024, based on data from the proof of principle studies and successful antigen selection in order to start cancer vaccine development programs.

Programs will encompass the two approaches Ronald has highlighted, development of off-the-shelf cancer vaccines to benefit groups of patients and cancer vaccines tailored to a patient's individual tumor profile.

Let me go more into detail about these two approaches on the next slide. Looking at the concept of shared antigens introduced earlier in this presentation, data suggests that an off-the-shelf vaccine addressing, for example, the four most frequently shared tumor-associated antigens for breast cancer can address about a quarter or even a third of all triple negative breast cancer patients.

Due to the prevalence of these shared antigens, chances are high that out of these four shared antigens, at least two will turn out to match a patient-specific tumor. With our access to tumor-associated antigens, frames and other classes of antigens from our antigen discovery engine, as well as our collaboration with MyNEO, we will evaluate possibilities to

further increase the coverage of specific patient populations with relevant off-the-shelf cancer vaccine candidate.

Our second approach is a fully personalized approach, which has the advantage of precisely tailoring a cancer vaccine to the antigens that are specific to a patient's individual tumor and are not shared with other patients. Ultimately, it will depend on the tumor and whether it can be best addressed by an off-the-shelf or personalized or combined approach.

With that, let me now shift gears and talk about the latest data update for our oncology program, CV8102.

On Slide 14, let me briefly remind you that CV8102 is a noncoding RNA optimized to activate RNA receptors that normally detect viruses, including toll-like receptor 7 and 8, as well as RIG-I.

CV8102 is injected directly into the tumor, where it mimics a viral infection that can activate the immune system to reject the tumor. CV8102 is currently being evaluated in a Phase I study consisting of two parts that assesses CV8102 as a single agent and in combination with anti-PD-1 antibodies. The dose escalation part in a range of solid tumors has already been completed.

The data on responders illustrated on the slide comes from the expansion part of the study, which assesses 40 heavily pretreated patients with PD-1 refractory melanoma at a dose of 600 micrograms. The data represents a cutoff date from August this year and show preliminary efficacy in the cohort of 30 patients treated in combination with anti-PD-1 antibodies.

Forty percent of these patients were pretreated with anti-CTLA-4 antibodies. Five of these 30 patients, or 17%, experienced a partial response, according to RECIST. The observed responses were durable for up to one year from the start of treatment.

We did not observe objective responses in the 10 patients of the single-agent cohort. In this group, 50% of patients were treated with anti-CTLA-4 antibodies.

Additional immune profiling data from the Phase I expansion study is shown on Slide 15 and is based on tumor biopsies of injected and non-injected tumors from a subset of patients, as well as blood samples from all patients.

The tumor biopsy sample shown on the left further confirms the previously reported infiltration of T cells in the tumor environment characterized by both CD4 and CD8 T cells and a corresponding decrease of the tumor cell content in one of the partial responders in the combination cohort.

On the right side of the slide, a balloon plot illustrates a gene set enrichment analysis safe on RNA sequencing from all blood samples taken before and 24 hours after the first administration of CV8102. The analysis confirms the previously reported activation of real defense pathways, led by the induction of interference.

Final data of the complete Phase I study is expected to be submitted for publication in a peer-reviewed journal in the first half of '23. Overall, the positive data of the CV8102 Phase I expansion study further demonstrates the previously reported robust safety profile and strong

ability to mobilize the immune system against injected, as well as noninjected tumors.

In the context of our strategic focus on the development of mRNA-based cancer vaccine candidates that target tumor-specific antigens, the clinically validated immunomodulatory characteristics of CV8102 represent a valuable and potentially complementary technology.

We would, therefore, only consider a potential further clinical development of CV8102, based on an integration into our cancer vaccine development, for example, as a strong immunomodulatory adjunct to a defined mRNA cancer vaccine candidate.

With this, let me hand back the call to Franz.

FRANZ-WERNER HAAS

Thank you, Ulrike. To round up the components of our oncology road map on Slide 16 and 17, let me briefly address the two oncology enablers that Ulrike already highlighted on Slide 12, the first being a new and proprietary lipid nanoparticle, or LNP program, for potential application with our cancer vaccine candidates.

The new LNP consists of an improved and PEG free lipid composition. Preclinical experiments in mice showed highly localized transcription of a rabies-based mRNA formulated with either the new non-PEG LNP or a control LNP.

Bio distribution was limited to the immune compartment and the intramuscular injection site. It showed no expression in distant organs, such as the liver, spleen and lung.

As treatment with the therapeutic cancer vaccine requires repetitive administration, maximizing expression of the encoding antigen in the immune compartment is an important goal.

We know from public studies that there seems to be a linear correlation between the amount of the activated antigen presenting cell in the immune compartment and the resulting abundance of tumor-fighting CD8 T cells. Correspondingly, the highly localized mRNA delivery was accompanied by strong cellular but also humeral immune responses.

As shown on the right side of the slide, the rabies mRNA formulated with the non-PEG LNP-generated systemic interferon alpha levels in the same range as the control LNP and was shown to raise comparable amounts of antigen-specific T cells measured via an interferon gamma ELISpot assay.

An important advantage of the new LNP program addresses the code chain logistics that still pose challenges for the distribution and long-term storage of mRNA-based vaccine.

The new LNP program was shown to enable a so-called tried presentation of a formulated mRNA, referring to the vaccine as a solid powder rather than a solution for better stability and storability.

The figures on Slide 17 show data from an ongoing stability study at 25 degrees centigrade or 77 degrees Fahrenheit, demonstrating that the mRNA is intact and securely formulated for at least 11 weeks. Overall, we are extending our technology core competencies in LNP research to add new approaches for vaccine design optimization.

Moving on to the second oncology enabler on Slide 18, I would like to look at the role the RNA Printer is envisaged to play not only in the internal expansion of our oncology pipeline, but also in the opening of new avenues for personalized mRNA-based cancer therapies.

As you know, the RNA Printer is our integrated and automated solution for the rapid manufacturing of GMP-grade mRNA vaccines and therapeutics. Designed for flexible smaller scale quantities, the RNA Printer seamlessly integrates with our antigen discovery technologies and the development of our cancer vaccine pipeline.

At the same time, the RNA Printer is expected to be uniquely suited to close the gap between the vaccine sequence and the provision of new cancer vaccines to either treat smaller group of patients or provide a fully personalized therapeutic setup.

This integration of the RNA Printer could also catalyze possible end-to-end digitization of data and data management, along the entire personalized or off-the-shelf vaccine therapy workflow.

With this, let me hand over to you, Pierre, for a review of our financial data.

PIERRE KEMULA

Thank you, Franz, and good morning and good afternoon to everyone on the call. Looking at our current cash position on Slide 19, we closed the third quarter and the first nine months of 2022 with a strong cash position of €540.9 million.

Financial statements for the first nine months of the year reflect CureVac's advanced phase of transition out of its exposure to its first-generation candidate, CVnCoV.

Cash used in operations was mainly allocated to purchases of RNA material and settling CMO contracts, as part of the wind-down activities for CVnCoV vaccine program and to capital expenditures for our new production facility.

Moving on to our profit and loss statement. Revenues decreased by €18.1 million to €11.2 million for the third quarter of 2022 and decreased by €6.1 million to €55.7 million for the first nine months of 2022, compared to the same period in 2021.

The decrease for the first nine-months period was based on a higher 2021 revenues, due to the termination of the Boehringer Ingelheim collaboration and its subsequent recognition of €10 million for the first nine months, ending September 2021.

Revenues for our two GSK collaboration increased year-on-year and amounted to a total of €52.7 million for the first nine months of 2022, compared to €49.6 million in the previous year.

Operating loss was €52.4 million for the third quarter of 2022, representing a €90.7 million decrease, compared to the third quarter of 2021.

For the first nine months ended September 30, 2022, operating loss decreased by €278.8 million to a total of €127.9 million, year-over-year. The operating result was affected by several key drivers.

Cost of sales decreased primarily due to lower expenses for CMO services. Prior year end 2021 was highly impacted by significant expenses for the setup of a European CMO network for CVnCoV.

This was partially offset in 2022 by an increase in write-off for raw materials procured to supply manufactured goods to GSK. These are now no longer expected to be used, following the transfer to GSK of reserve production capacity at the CMO.

R&D expenses decreased primarily due to significantly lower development expenses related to the completion of the large Phase IIb/III clinical trial for CVnCoV.

In line with the declining number of continuing study participants in 2022 and renegotiation of existing contracts in the first nine months of 2022, our remaining clinical trial cost estimate decreased, resulting in the reversal of €36.8 million from the provision recorded, as of December 31, 2021.

Additionally, in the first quarter of 2022, R&D cost was positively impacted by a net gain for a change in volume estimate, following the transfer to GSK of reserve production capacity at the CMO.

Other income decreased but was positively impacted by €32.5 million from GSK for reimbursement of prepayment and production activity set up at a CMO.

In 2021, other income was primarily attributable to amounts recognized from grants from the German Federal Ministry of Education and Research, or BMBF.

Financial results for the third quarter increased by €5.1 million to €4.7 million for the third quarter of 2022 and by €8.7 million to €7.5 million for the first nine months of 2022, compared to the same period in 2021.

These positive financial results were driven by foreign exchange gains and interest on cash investments. Pretax losses were €47.7 million in the third quarter and €120.4 million for the first nine months of 2022.

With this, I would like to hand back to Franz for today's key takeaways.

FRANZ-WERNER HAAS

Thank you, Pierre. And also thank you, Ulrike and Ronald. Let me quickly summarize the key takeaways from today's presentation.

Over the past several months, we continued to, strongly, increase our operational capabilities that enabled us to maximize applications for our mRNA technology across the three core competencies, including technology, product development and manufacturing.

We have expanded our clinical development pipeline by a total of four clinical trials in prophylactic vaccines this year in COVID-19 and influenza, together with GSK.

All four trials are on track and provide meaningful data with a goal to select the best performing candidates early next year and advanced preparations for potential subsequent later-stage clinical developments in 2023.

This data will also support development of our oncology program, where we have significantly expanded our technology expertise by the acquisition of Frame Cancer Therapeutics and its cutting-edge genomics and bioinformatics platform.

In 2023, we plan to start two clinical trials in oncology to integrate this highly differentiated platform with our versatile second-generation mRNA backbone to strengthen our clinical development pipeline with novel cancer vaccine candidates, supported by the RNA Printer and our new LNP technology.

Lastly, our strong cash balance in the third quarter shows the benefit from our diligent work to resolve and reallocate prior commitments from our first-generation vaccine candidate and positions us, well, to continue the execution on our priorities.

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

Sarah Fakih

With this, we would like to conclude this conference call. Thank you very much for your participation. Stay safe, and please don't hesitate to contact us, should you have any further questions. Thank you, and goodbye.