Coconut synthesis report on gaps for priority collecting and conservation LOA 2014/44

Technical report

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Abstract

Based on the information available from COGENT, important gaps persist in the affiliated germplasm collections, e.g. for large parts of Polynesia, Melanesia, Micronesia, Australia, Indonesia, Malaysia, India, Myanmar, Madagascar, Kenya and Somalia, among regions where coconut is likely to be native. SSR marker data for 86 coconut populations were analyzed to study the distribution of genetic diversity, using Jost's J_1 index. The Indo-Pacific region presents the highest diversity, with hotspots in Vanuatu, Papua New Guinea, South East Asia, and East Africa. Atlantic shores, where the coconut was introduced in historical times, appear less diverse. However, this picture is incomplete, as many neighboring areas correspond to gaps in collections and genetic studies.

The potential impact of climate change on coconut distribution was anticipated for the year 2050, using three climate models (BCC-CSM1-1, CCSM4, and HadGEM2-ES) and three gas emission/radiative forcing scenarios (rcp4.5, rcp6.0, and rcp8.5). All results converge in predicting a very strong increase of areas climatically suitable for the coconut, thus discarding a global negative impact of climate change per se. This seems reassuring in terms of genetic erosion risk, as well as production. However, a few regions, including southeastern India and Bangladesh, would be negatively affected. Due the eastward shift of favorable areas around the Bay of Bengal, Bangladesh could lose about half of his coconut production areas.

The 0.2-0.4m sea-level rise expectation for 2000-2050 might be doubled in case the West Antarctic Ice Sheet has already been set into motion. Even so, its impact on coastal coconut populations should be negligible for continents and large islands, where shoreline retreat should be modest, compared to the extension of climatically suitable areas. The situation would be different for distant, small and low-lying islands, as well as delta areas, particularly in the Indo-Pacific region, where rising rates are up to thrice the global rate. Thus, there are severe threats on the Maldives, Laccadive, and Mascarene archipelagos, and on the myriad of far Polynesian, Micronesian, and Melanesian islands, all regions hosting an important diversity of coconut germplasm, not well studied so far. Flooding threats will increase on the shores of eastern India and the Bay of Bengal, increasing the pressure on coconut and people.

1. General development of the research

The 4000 USD research budget was mostly used to fund a 4-month internship. Five candidates were shortlisted for an interview, among a total of 33 from 11 countries, before Valentin Wolf, an MSc student from the University of Göttingen, was finally selected. As Valentin could start working at CIRAD from the 20th of April, his internship was extended up to the 20th of August. After training on the structure of our coconut data (distribution and genetic diversity) and on Ecological Niche Modeling, he initiated a bibliographical research on global warming effects and future climate models, as well as models for the prediction of coastline evolution. However, the latter aspect was not much developed because available data do not allow reliable predictions.

As a complement to earlier research on coconut distribution, the distribution of coconut genetic diversity was mapped.

To anticipate the response of coconut distribution to global warming for the year 2050, three Earth System Models (ESMs) and three Representative Concentration Pathways (RCP) scenarios were selected. Globally, the predictions showed no major negative effects on current coconut producing areas located on large land masses, except for the Indian subcontinent. Thus climate evolution only appears to be a significant threat in this region, whereas sea-level rise must be considered a significant threat on distant low-lying islands and deltas of the Indo-Pacific basin.

2. Results from previous research

2.1. Coconut distribution model

In 2013-14, Prune Komba Mayossa and Geo Coppens d'Eeckenbrugge used Maxent to infer global coconut potential distribution from 1875 coconut palm observation sites for current climatic conditions, as described by 19 bioclimatic variables consisting of average temperature, total precipitation, their extreme monthly and trimestral values and seasonality indices, with a resolution of 2.5 minutes (Worldclim database; Hijmans et al., 2005). The resulting distribution map (Figure 1) was validated in several countries (Colombia, India, Sri Lanka, Vietnam, Philippines, and Australia). As expected, it shows the prevalence of tropical coastal areas, and more particularly small islands, in terms of climate suitability. Suitable climates are also found far inland, in humid equatorial regions, where the plant is practically absent (e.g. Congo basin) or very recently introduced (e.g. Amazon).

2.2. <u>Collecting gaps for coconut germplasm referenced in the Coconut Genetic Resources</u> <u>Database</u>

From this work, Geo Coppens d'Eeckenbrugge and Alvaro Ullivari derived a map showing collecting gaps at global scale (Figure 2), to be included in a section of COGENT's Strategic Plan. Some suitable regions are not or very poorly represented in the COGENT-affiliated germplasm collections: the northern fringe of Australia, much of Indonesia and Malaysia, parts of India, Myanmar, the eastern coast of Madagascar, Kenya and Somalia in eastern Africa, which are all regions where coconut is likely to be a very ancient introduction and/or a component of the native vegetation. The many distant tropical islands (Mascarene islands, Maldives, Laccadive in the Indian Ocean, Polynesia, Melanesia, and Micronesia, in the Pacific ocean), whose situation and climates are highly favorable for the development of well differentiated coconut populations, have not been systematically explored. Several archipelagos are not represented in the COGENT collections. Coconut germplasm from the far Pacific has also been introduced on the Pacific shores of America, however they are poorly represented, with only an old accession from Sullana, northern Peru, and none from Colombia and Ecuador. Among regions of historical introduction, i.e. along the Atlantic tropical shores, the Gulf of Guinea appears to be poorly collected, and tropical America is only represented by accessions from Mexico and Panama. The case of the Amazonian and Congo basins is less important. Although they present favorable environments for the coconut, these populations are of very recent introduction and, presumably, their diversity is low. Appendix A reminds the conclusions of the analysis of Bourdeix et al. (2005), which are still valid.

2.3. Prioritization from genetic analyses

In the same period, Luc Baudouin reviewed a number of regions that would need further characterization (and possibly conservation) in the coconut cultivation area¹. Six understudied regions of potential scientific interest were more particularly identified: 1) The Eastern Indian Ocean, between Thailand and Bangladesh and the Maldives. 2) The Polynesian outliers including Palau, the Marianas and the Marshall Islands. 3) French Polynesia, Hawai'i and the Midway Islands. 4) Tanzania, 5) Colombia, Ecuador and Isla de Coco, 6) isolated islands where coconut grows spontaneously e.g. in Eastern Samar (Philippines) and in Cocos (Keeling) Islands.

¹Use of molecular markers to contribute to the identification of priority coconut accessions in the framework of the Global Strategy for Conservation and Use of Coconut Genetic Resources. (LOA 2013/25)





Figure 1. Coconut potential distribution (without irrigation). Dark green areas correspond to marginal climatic conditions; light green to orange areas correspond to increasingly favorable climates. Based on data assembled by Komba Mayossa and Coppens d'Eeckenbrugge in 2013.





Figure 2. Origins of accessions inventoried in the COGENT CGRD database (blue dots). Coconut suitable areas (see Fig. 1) are represented with a green-to-red color gradient according to their distance from the closest collecting site: yellow between 220 and 320 km, red to deep red beyond 420 km. Dark grey areas correspond to marginal climates for coconut growth and development.

3. Distribution of genetic diversity

We computed molecular allele richness indices based on the genotyping data of 778 coconut palms from 86 Tall populations (genebank accessions or populations sampled *in situ*). The data were obtained through the Generation Challenge program "Molecular characterization of tier 2 (orphan) crops" for coconut (see details in Appendix B). The simplest allele richness index is the observed allele number. However, it is strongly influenced by the number of observations (for a given population, it is roughly proportional to the logarithm of the number of observations, due to the presence of rare alleles). To minimize this effect, we used the diversity index J_1 proposed by (Jost, 2008). It is an "effective" allele number (i.e. if all allele have the same frequency, the value of the index is the number of alleles), however, the contribution of the rare alleles is minimized, thus making the value less dependent on the number of observation. It is equal to the exponential of the Shannon index.

The Shannon index values were computed for each locus with the point-to-grid richness analysis tool in DIVA-GIS, with a $0.5\times0.5^{\circ}$ grid and a circular neighborhood of 4° . They were converted into the J_1 index of Jost, and then averaged. The result is presented at Figure 3, which shows the effective allele number (J_1). Plotting allele number and J_1 as a function of the logarithm of sample size shows that the latter index is effective in reducing the effect of sample size, except perhaps in the North of Vanuatu where 103 palms were sampled. In any case, this region is known to be especially diverse, both phenotypically and genetically.

As expected, the highest diversity is found in the Indo-Pacific region where the crop originated, with hotspots in the western Pacific Ocean, particularly in Vanuatu, but also in Papua New Guinea, South East Asia, and East Africa. Slightly less diversity has been found in southern India/Sri Lanka. This picture is however far from complete, as some of these areas appear to be densely collected (e.g. Papua New Guinea and Vanuatu, Philippines, Sri Lanka), whereas neighboring areas (e.g. Solomon Islands, Indonesian Papua, Malaysian Borneo, southern Sulawesi) have not or very little been collected/studied. Other potential hotspots in Somalia and Madagascar have also been neglected. Most materials collected in India are not listed in the COGENT database, hampering the analysis of their relative contribution to germplasm diversity.

Areas where the coconut was introduced in historical times (tropical Atlantic shores) appear logically less diverse; however the distribution of their diversity cannot really be deduced from Figure 3, because of the many under-represented red areas of Figure 2.





Figure 3. Distribution of coconut genetic diversity (Jost's J_1 index), according to currently available data (30 SSR loci, 778 individuals from 86 populations).

Color code for effective number of alleles:



4. Global change potential impact on coconut genetic resources

4.1.Climate change direct effect on coconut geographic distribution

The response of coconut distribution to global warming was anticipated for the year 2050 following three Earth System Models (ESMs): BCC-CSM1-1 (Beijing Climate Center Climate System Model), CCSM4 (Community Climate System Model), and HadGEM2-ES (Hadley Global Environment Model 2 - Earth System). The corresponding bioclimatic data were obtained from the 2.5 minutes spatial resolution global climate models, downloaded from the Worldclim website (worldclim.org). These three future climate models were selected according to their components and resolution (IPCC, 2013a). The respective foci of the models were an additional selection factor. In particular, we thrived for a representation of the tropical areas of the world including a realistic modeling of the monsoon.



percentiles (light/dark grey) of the literature.

Four new Representative Concentration Pathways (RCP) scenarios were introduced in the fifth assessment report of the Intergovernmental Panel on Climate Change (IPCC); (i) rcp8.5 (radiative forcing reaches more than 8.5 W/m² by 2100 and proceeds to rise afterwards); (ii) rcp6.0 (radiative forcing reaches around 6.0 W/m² by 2100 and proceeds to rise afterwards); (iii) rcp4.5 (radiative forcing is stabilized around 4.5 W/m² by 2100); (iv) rcp2.6. (radiative forcing peaks around 3 W/m² and starts to decline before 2100).

The RCP scenarios include spatially resolved data sets of the change in land use and the gaseous emissions for each sector. Annual greenhouse gas concentrations and the anthropogenic emissions are provided until 2100. Integrated assessment models, simple climate models, atmospheric chemistry and global carbon cycle models provide the basis for the RCPs scenarios (IPCC, 2013b). We did not extrapolate the model for the RCP2.6 scenario. Indeed, since global policies have unfortunately not been able to reduce greenhouse gas emissions, this scenario is not realistic anymore. As shown by van Vuuren (2011) the RCP2.6 scenario indicates a peak of CH4 emission around 2010 and a peak of CO2 emission around 2020. Although RCPs do not represent socioeconomic scenarios, RCP 4.5

can be viewed as a moderate mitigation policy scenario, while RCP 8.5 can be viewed as corresponding to high-end business-as-usual emissions (Kopp et al., 2014).

The convergence between models of potential coconut distribution for future conditions was strikingly good across climatic models, and even across RCP scenarios. This allowed us a quite synthetic presentation of our results for medium and large land masses (Figure 5).



Figure 5A. Potential coconut distribution for modern climate (based on current presence data assembled in 2014), and potential coconut distribution predicted for 2050 under the RCP 4.5 scenario, for three climate models (BCC-CSM1-1, CCSM4, and HadGEM2-ES).



Figure 5B. Potential coconut distribution predicted for 2050 under the RCP 6.0 and RCP 8.5 scenarios, for three climate models (BCC-CSM1-1, CCSM4, and HadGEM2-ES).



Figure 6. Predicted evolution of climatically suitable areas (km²) for rainfed coconut by 2050, under three RCP scenarios and three climate models (only HadGEM2-ES model for the bar charts). 'Average suitability' corresponds to a 10% training omission threshold in the Maxent model (separating marginal conditions, dark green on first map, from suitable conditions, light green), 'high suitability' (>33% training omission, yellow areas), and 'very high suitability' (>67% training omission, orange areas). See also Appendix C.

Global warming does not appear to threaten present areas of coconut cultivation. Instead, all models predict a very strong increase of climatically suitable areas, with no significant evolution within currently favorable areas. However, there are some exceptions to this trend, particularly in India, Bangladesh and Myanmar. Figure 6 presents the particular case of these three countries, and the evolution of climatically suitable areas based on the HadGEM2-ES model.

According to the predictions presented in Figure 6, the western and southwestern coastal favorable areas of India would be positively affected by global warming, as well as in the states northeast of Bangladesh. Fortunately, these correspond to the major production areas of the country. The situation would be quite different in the South and along the northeastern shores of the country, where suitable areas would suffer a significant reduction under all three warming scenarios. Around the Bay of Bengal, coconut favorable areas would shift to the East. As this move would not be compensated for Bangladesh, this country could lose about half of his coconut favorable areas. On the contrary, climatic conditions would improve very significantly along the shores of Myanmar, where future coconut suitable areas would be more than twice as large, as compared to present.

The global extension of coconut favorable climatic areas predicted by all climatic scenarios and models is very reassuring in terms of genetic erosion risk assessment. In terms of production, the picture is less clear, because the choice of a crop plant depends not only on the environment, but also on historical and cultural factors, as well as on pest and disease evolution (Chakraborty et al., 2000) and "economic competition" from other tropical plants that could be also favored by warming conditions. In the case of India and Bangladesh, where coconut is a particularly important crop plant, both production and genetic resources may be affected by future shifts in cultivation areas. For the Bay of Bengal, we must keep in mind that this region is irrigated by a dense river network, opening possibilities for irrigation, a factor not taken into account by our models. In India, this factor may also be important, as coconut irrigation has allowed the northward expansion of coconut cultivation into many climatically marginal areas. Again, the future situation will depend much on the pressure on water and, concerning agricultural water, on competition among crops.

Naresh Kumar and Aggarwal (2013) have used two climatic scenarios and a simulation model (InfoCrop-COCONUT) to assess the impact of climate change on coconut in India, for 2030 and 2080. According to their study, climate change is projected to increase coconut productivity in the western ans southern coastal states, as well is in the states northeast of Bangladesh, while negative impacts are projected for the eastern coastal states. Although they were developed with very different data and methods, these predictions are globally consistent with ours.

4.2. Threats related to sea level rise

So far, most sea-level rise has been related directly to ocean thermal expansion and ice sheet loss; the contribution of global deglaciation will get more and more important in the near future (Parris et al., 2012; Rignot et al., 2014). While climate change models converge relatively well, giving consistency to predictions of future coconut suitable areas, there is no general model to predict regional variations in sea-level rise, and even less consequent shoreline modifications.

A first difficulty for a global scale study like ours comes from the fact that sea-level rise is not uniform. Rates of sea level rise over broad regions can be several times larger or smaller than the global mean sea level rise for periods of several decades, due to (1) fluctuations in ocean dynamics, heat content, and salinity, (2) perturbations in the Earth's gravitational field and crustal height, (3) glacial isostatic adjustment, and (4) vertical land motion (Parris et al., 2012; Kopp et al., 2014). Thus, static-equilibrium effects lead to a strong tendency for greater-thanglobal sea-level rise in the central and western Pacific Ocean (Kopp et al., 2014). Indeed, since 1993, the regional rates for most of the Indian Ocean and the Western Pacific are up to three times larger (currently up to 10mm/yr) than the global mean, while those for the Eastern Pacific are near zero or negative (IPCC, 2014; Parris et al., 2012). Furthermore, high tides and wave height must also be taken into account to anticipate coastal flooding risks. Finally, shoreline modifications also depend on highly dynamic processes, combining erosion processes and the possible accumulation of materials brought from the sea. So far, such processes have only been modelled at local scales (e.g. Le Cozannet et al., 2013). In the case of small tropical islands, the vitality of protective coral reefs may constitute a positive factor, whereas high human population densities often hamper processes of "natural" adaptation, favoring instead the building of inefficient defenses. We got in touch with Patrick Barnard, a geologist who is working for the U.S. Geological Survey. He is in the process of assimilating and producing the water level data that are needed for modeling water levels, including for coconut favorable areas. He wrote us in July 2015 that his target is about a year out.

According to Kopp et al. (2014), global sea-level rise is nearly indistinguishable between RCP 2.6 to RCP 8.5, up to the middle of the current century, remaining around 0.2-0.4m between 2000 and 2050. By 2050, deglaciation in the Antarctic alone accounts for half the variance among projections for RCP 8.5. Kopp et al. (2014) project a very likely mean sea-level rise of 0.5-1.2 m by 2100, under the RCP 8.5 scenario. In addition to this "baseline" case, Strauss et al. (2015) envisage a second "triggered" case, making a major adjustment assuming that an inevitable collapse of the West Antarctic Ice Sheet has already been set into motion. This sector is of global significance since it contains enough ice to raise global sea level by 1.2 m (Rignot et al., 2014).

For the prediction of changes in the distribution of the coconut, the exercise of modeling shoreline is not only impractical, but also superfluous for continent and large islands. In fact, even a pessimistic prediction of a 2m-rise over the century (ca.0.5-0.6m from now to 2050, according to Parris et al., 2012) would be negligible in relative terms, as compared to the direct effects of climate change predicted by climate and distribution modeling. Thus, sea level rise mostly threats coconut germplasm (and human population) survival in distant, small and low-lying islands, as well as delta areas, which are constituted of great extensions of low alluvial lands.

Concerning distant islands, there are severe threats on the Maldives and Laccadive archipelagos, as well as smaller archipelagos around the Mascarene islands, in the Indian Ocean, and on the myriad of far Polynesian, Micronesian, and Melanesian islands, particularly if we consider that sea-level rise rate in the Indo-Pacific is thrice the global rate. These regions in the eastern Indian Ocean and western Pacific Ocean are likely to host an important diversity of coconut germplasm, which has not been well studied so far.

Delta and other extensive low littoral regions in southern and southeastern Asia are also particularly threatened (Figure 7). Thus flooding threats will increase even more on the shores of eastern India and the Bay of Bengal, as well as those of Myanmar, particularly in the South. Such areas are also found in the South of Thailand and Vietnam, where coconut genetic diversity is relatively important.



Figure 7. Areas below 5 m above sea level –masl- (red) and between 5 and 10 masl (yellow) in southern and southeastern Asia, according to NASA's SRTM elevation model (Shuttle Radar Topography Mission; http://topex.ucsd.edu/WWW_html/srtm30_plus.html).

5. Conclusions

In complement to the phylogeographical approach of Gunn et al. (2011), we have mapped the distribution of coconut genetic diversity as approached from currently available data. As expected, diversity appears to be higher in the presumed area of origin and domestication of the coconut, i.e. in the Indo-Pacific region, and more particularly in the western Pacific and between Southeast Asia and northern Australia. The emerging picture is a significant improvement over the last similar exercice (Bourdeix et al., 2005), however it is still incomplete, as many potentially important areas have been undercollected or their genetic resources understudied. Furthermore, comparable genetic diversity data are mostly lacking for the distant low islands of the Indian Ocean (Laccadives, Maldives) and of Polynesia and Micronesia in the Pacific Ocean, whose climates are particularly favorable for the plant.

We have assessed the potential impact of climate change on the distribution of coconut, extrapolating our ENM-derived coconut distribution model to future climates, using a combination of three climate models and three RCP scenarios. The results are remarkably convergent. They consistently indicate that, quite generally, future climates will not threat directly current coconut populations/cultivation. Instead, they predict a strong extension of climatically favorable areas in the future. However, climate change may affect coconut germplasm and production indirectly, through its effect on other organisms (parasites, competing crops), including human societies (e.g. population displacement in coastal habitats). In a few cases, climate change should affect important production zones, shifting climatically favorable areas along the coasts of India or even reducing them, as in Bangladesh. The latter is thus doubly threatened by climate change, directly and, indirectly, by sea-level rise and consequent flood risk.

The negative impact of sea-level rise on coastal coconut populations should be negligible on continents and large islands, as shoreline retreat should be modest, compared to the extension of climatically suitable areas. The situation is different on small and low-lying islands. In terms of genetic erosion, coconut genetic resources are particularly threatened in distant low islands of the Indian Ocean (Islands of the Maldives and Laccadives) and the Pacific Ocean (Polynesia, Micronesia, East Melanesia). Furthermore, both native and cultivated coconut germplasm from these islands, which is likely to contribute significantly to the important diversity of the Indo-Pacific basin, has been poorly explored and studied.

Publication of the present research

The internship of Valentin Wolf ended on August 20. Although some additional work, including the present report, was carried out after this date, the preparation of an article for an international audience would not have been possible within the remaining two months. This publication work will have to be planned, and coordinated along our other activities on coconut, which we shall remind here.

The present research has been based on our first GIS-based approach of coconut distribution, developed during the internship of Prune Komba Mayossa, whose results have been partly used in COGENT's Strategic Plan (e.g. presenting coconut distribution and crossing it with germplasm collections to identify collecting gaps; see 2.1. and 2.2.). This document has not been published so far. A paper where coconut morphological and genetic diversity is related to current and past coconut distribution models is being prepared. Logically, the present research should be published after this first work and the Strategic Plan. Another potentially

important point to discuss before defining a consistent publication strategy is that the components of the present research have also been considered in the Darwin initiative preliminary proposal that was recently approved.

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Appendix A. Prioritization of collecting gaps according to Bourdeix et al. (2005; section "Mapping coconut genetic diversity")

Some areas remain clearly under-represented in national and international genebanks, which are listed below, in a subjective ranking of priority:

1. The west coast of South and Central America (except Mexico and Panama, which have already been surveyed). Germplasm collecting is presently being conducted in Guatemala. These studies are essential, considering the problem of the Lethal Yellowing Disease and the history of coconut in this region;

2. A large part of Micronesia, including the Caroline and Mariannas Islands;

3. The eastern part of Polynesia, including the Tuamotu and the Marquesas Islands and Hawaii;

4. Irian Jaya and the Moluccas archipelago;

5. The tropical coasts of Australia and the Cocos/Keelings Islands, where putative wild coconut occurs (Williams 1990; Leach et al. 2003);

6. Madagascar. Seafarers from Southeast Asia reached this island probably around the sixth century AD and settled there. Molecular biology studies show that they probably introduced coconut seednuts with them, and new diversity developed thereafter; and 7. Other more localized areas like Somalia, Myanmar, Laos and Sarawak in Malaysia.

Some of the areas that are suggested here (such as Micronesia, eastern Polynesia, and the Cocos/Keelings Islands) represent only a very small part of the coconut world, in terms of cultivated area and economic value. However, these areas could prove to be extremely important for coconut diversity.

Appendix B: Analysis of coconut genetic diversity distribution: source of data, list of microsatellite markers, and of populations.

Data base:

(http://tropgenedb.cirad.fr/tropgene/JSP/interface.jsp?module=COCONUT)

Markers:

CnCir 126, CnCir 2, CnCir 206, CnCirA3, CnCirA9, CnCirB12, CnCirB6, CnCirC12, CnCir C5, CnCirC7, CnCirE10, CnCirE12, CnCirE2, CnCirF2, CnCirG11, CnCirH4', CnCirH7, CNZ03, CNZ42, mEgCIR2739, mEgCIR3400, mEgCIR3750, CNZ40, CnCir F3', CnCir 119, Cncir H11, CnCir I4, CnCir E1, CnCir 215, CnCir 147

<u>List of accessions and effective sample sizes</u> (this is the number of data points divided by 30. Due to missing data, the sample size is not an integer):

Andaman Ordinary Tall (11), Baibara Tall (5), Ballesteros Tall Tarraq (7), Baybay Tall (8), Brazilian Tall (53), Brazilian Tall Praia Do forte (4), Brazilian Talll (11), Calangute Tall (3), Cambodia Tall Koh Rong (5), Cambodia Tall Ream (5), Cameroon Kribi Tall (5), Comoro Moheli Tall (7), Cook Islands Tall (5), Dau Tall (6), East African Tall (4), East African Tall Kenya (4), East African Tall Kimanga (5), East African Tall LBS (5), East Sepik Tall Vokio (5), East Sepik Tall Yangoru (3), Gazelle Peninsula Tall (10), Gazelle Peninsula Tall Natava \many fruited\ (4), Gazelle Peninsula Tall New Massawa (5), Gazelle Peninsula Tall Pellavarua (5), Hainan Tall (7), Indian East Coast Tall (7), Indian West Coast Tall (6), Jamaica Tall (4), Kappadam Tall (1), Kar Kar Tall (5), Karkar Tall Guanaga (5), Karkar Tall Kinim (8), Karkar Tall Ulatava (4), Kiwai Tall Boze (4), Laccadive Micro Tall (5), Laccadives Ordinary Tall (3), Lubuk Pakam Tall (5), Madang Yellow tall (4), Malayan Tall (10), Manus Tall (5), Markham Valley Tall (6), Markham Valley Tall Liara Village (5), Markham Valley Tall Markham Farm (10), Marshall Island Tall (5), Mexican Atlantic Tall (9), Mexican Pacific Tall Colima (14), Mexican Pacific Tall Guerrero (11), Mexican Pacific Tall Michoacan (14), Mexican Pacific Tall Nuxco (4), Milne Bay Tall Siagara (3), Mozambique Tall (12), Namatanai Tall Etalat (5), Namatanai Tall Karu Village (5), New Caledonia Tall (7), Niu Leka Dwarf (7), Palu Tall (5), Panama Tall (10), Panama Tall Aguadulce (13), Panama Tall Cr (19), Panama Tall Monagre (19), Pandan Tall (6), Poligolo Tall (3), Rennell Island Tall (12), Rotuman Tall (5), Sakhi Ghopal Tall (5), San Ramon Tall (11), Sarawak Tall (3), Sawarna Tall (5), Solomon Island Tall (6), Sri Lanka Tall (19), Ta Tall (7), Tagnanan Tall (14), Tahiti Tall (4), Takome Tall (5), Tenga Tall (5), Thailand Tall (18), Tonga Tall (5), Tuvalu Tall (17), Vailala Tall (5), Vailala Tall Keakea (5), Vanuatu Tall (134), West African Tall (4), West African Tall Benin (10), West African Tall Côte d'Ivoire (10), West New Britain Tall Gaungo (5), West New Britain Tall Naviro (4).

Appendix C: Data for Figure 5: predictions for evolution of climatically suitable areas (km²) for coconut production (without irrigation) from present to 2050, under three RCP scenarios, according to the HAD climate model. 'Average suitability' corresponds to a threshold of 10% training omission in the Maxent distribution model (separating marginal conditions, dark green on the maps, from suitable conditions, light green on the color maps), 'high suitability' (33% training omission threshold, yellow areas), and 'very high suitability' (67% training omission threshold, orange areas).

	World	India	Bangladesh	Myanmar
Good conditions				
Current climate	7,623,870	235,541	115,776	58,693
RCP 4.5	12,312,907	257,752	77,237	118,213
RCP 6.0	12,163,443	259,467	103,939	133,178
RCP 8.5	10,589,132	237,418	53,781	116,185
Very good conditions				
Current climate	2,384,847	72,209	64,606	13,377
RCP 4.5	5,241,154	77,933	20,268	47,860
RCP 6.0	4,941,794	94,231	31,446	48,377
RCP 8.5	4,492,489	64,291	16,633	58,376
Excellent condition	S			
Current climate	496,350	18,350	6,051	1,268
RCP 4.5	1,871,307	25,926	6,228	8,986
RCP 6.0	1,769,688	28,598	13,218	12,335
RCP 8.5	1,859,922	22,095	3,109	11,045